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POSTERS

Amrina Rasyada et al., J Bacteriol Infec Dis 2019, Volume 3

A CASE REPORT: ACUTE PANCREATITIS AS A RARE COMPLICATION OF WEIL'S DISEASE IN INDONESIA

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Background: Weil's disease is a severe form of leptospirosis and caused by a pathogenic strain of *Leptospira*, one of rare clinical manifestation is acute pancreatitis. Diagnosis of acute pancreatitis based on clinical manifestation and laboratory finding. In this study, author reports that Weil's disease with acute pancreatitis as the main complication during the rainy season in Jakarta, Indonesia.

Case Presentation: They reported a case of 43 years old man suffering Weil's disease with acute pancreatitis. The patient complained with right upper abdominal pain (VAS 7-8), gastrocnemius pain, fever, vomitus, jaundice, discoloration of stool, brown urination and history of digging the grave one week before admission. Physical examination found hypotension, ictero hemorrhagic of sclera and epigastric pain. In laboratory finding thrombocytopenia, increasing of bilirubin, ureum, creatinine, amylase and lipase, hypoalbuminemia and negative hepatitis viral serologic; Abdominal ultrasonography found nephrolithiasis bilateral and full of sludge in bile duct mimicking to cholelithiasis. 48 hours later, this patient had clinical regression and procalcitonin was 10, then admitted to the intensive care unit. They gave rehydration, inotropic, carbapenem class antibiotic and supportive therapy. Two days later, IgM *leptospira* (+), decreasing of PCT, amylase and lipase, the clinical signs improved. Then the patient recovered without sequelae after 11 days of admission.

Conclusion: This rare case defined that acute pancreatitis should be identified early to reduce morbidity and mortality rate in Weil's disease.

BIOGRAPHY

Amrina Rasyada has been graduated from Faculty of Medicine of Andalas University as Medical Doctor. She works as a full timer General Practitioner in Hermina Jatinegara Hospital in emergency department.

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Ummi Shahieda Lazaroo et al., J Bacteriol Infec Dis 2019, Volume 3

STRUCTURAL AND FUNCTIONAL PREDICTION OF THE HYPOTHETICAL PROTEINS FROM *PSEUDOMONAS AERUGINOSA* PA7

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Pseudomonas aeruginosa is the most frequently isolated bacterium among those gram-negative rods that are obligated aerobes. It is one of the important opportunistic human pathogens, causing severe chronic respiratory infection in a patient with underlying conditions such as cystic fibrosis (CF) or bronchiectasis. The emergence of multi-drug resistance *Pseudomonas aeruginosa* strain in clinically isolated demands the development of better or new drugs against this pathogen. The objective of this study is to assign a precise function to hypothetical protein (HPs), whose functions are unknown. With the help of various bioinformatics tools, the extensive functional analysis of these hypothetical proteins was performed. This study combines a number of bioinformatics tools including Blastp, Pfam, interproscan, SMART, PSLpred, CELLO, signal peptide, expasy's protParam tool, virulenPred, vicmPred to gain information about the conserved regions, families, pathways, interactions, localizations and virulence related to a particular protein. The hypothetical proteins present in *Pseudomonas Aeruginosa* PA7 genome was extensively analyzed and annotated, out of 1350 hypothetical proteins, 25 proteins are catalytic domains, 31 proteins are enzymes, 46 proteins are integral membrane proteins, 72 proteins are transporters, 104 proteins are binding proteins, 404 proteins sequences contain a domain of unknown function (DUF) and 540 proteins cannot be functionally determined by any of the tools. The outcomes of this study may be helpful for a better understanding of the mechanism of pathogenesis and in finding novel therapeutic targets for *Pseudomonas aeruginosa*.

BIOGRAPHY

Ummi Shahieda Lazaroo is an undergraduate student from Management and Science University, Malaysia currently she is doing her final year Bachelor in Bioinformatics (Hons). Currently her research focusing on finding novel drug target for antimicrobial resistant bacterial pathogens using computational aided drug design. Her research interests are in computational biology and bioinformatics.

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ACCEPTED ABSTRACTS

J Bacteriol Infec Dis 2019, Volume 3

GENOME CHARACTERISTICS OF A *CAMPYLOBACTER JEJUNI* 63A ISOLATED FROM CALIFORNIA GULL EXCRETA

Jingrang Lu[1], Scott P Keely[1], Sharon Yelton[2] and **Nicholas Ashbolt[1]**
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Campylobacter jejuni is not only a major cause of human gastroenteritis in western countries due to food and water contamination, but it is also associated some outbreaks of Guillain-Barre´syndrome (GBS). *C. jejuni* 63A was isolated from California gull excreta, which was in the meanwhile found to be a major strain of *Campylobacter* species in Sandhill crane (a migratory bird) excreta as well. The novel isolate is 99% identical to *C. jejuni* strain ICDCCJ07001, which was isolated from a GBS patient according to several gene sequences of mapA, aspA, atpA, glnA, glyA and tkt. The genome of 63A was sequenced with an Illumina HiSeq sequencing platform, assembled and compared with the strain ICDCCJ07001. It revealed that the 63A genome consisted of 1,697,260 base pairs (bp) with the GC content 30.47%. The virulence loci and virulence-associated genes evaluated were found to be 98-99% identical to the equivalent genes in ICDCCJ07001. Some sequence differences were found in 63A compared to ICDCCJ07001. For example, eight differences were observed in Invasion Antigen B, 22 were observed in cadF, and 12 were observed in surface-exposed lipoprotein (jlp A). Strain-specific assays of the 63A based on prophage similar sequences were designed, which could be used for some water fowl *C. jejuni* source tracking and further pathogenic animal model experiment.

J Bacteriol Infec Dis 2019, Volume 3

MECHANISMS AND MANAGEMENT OF INFLUENZA AND ITS RELATED PNEUMOCOCCAL PNEUMONIA IN JAPAN

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Influenza-related pneumonia is an important complication of influenza and it has been suggested that excessive inflammatory reactions, including "cytokine storm", may contribute to the mechanisms underlying severe pneumonia. Human data and mouse model which co-infected with influenza virus and *Streptococcus pneumoniae* show increased severity of illness caused by the elevation of cytokines/chemokines and mice with genetic knock-out of immune molecules such as Toll-like receptor-related IRAK-M also show hyper-immune responses and reduced survival following influenza virus infection. Such findings suggest that innate immune responses and excessive neutrophil activation might be related to severe inflammatory changes in the lungs, and immune-modulatory therapy, including macrolides may thus be effective against severe influenza-related pneumonia. In Japan, author had five anti-influenza agents and could choose each agent dependent on influenza and pneumonia severity. Among them, peramivir can be administered by drip infusion and used not only for the most severe patients but also for the ambulatory outpatients who have some medical issues. In addition, new anti-influenza agent: 'Baloxavir marboxil' which is 'Cap-dependent endonuclease inhibitor' has been started to use. The insurance system supports early administration of them with antibiotics and as a result, they might be able to have very low influenza-related mortality. Today, their management style for influenza, including vaccination and infection control team activity will be introduced.

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IMMUNOPROFILING OF NON-TUBERCULOUS MYCOBACTERIAL INFECTION PATIENTS REVEAL GLOBAL T CELL DYSFUNCTION AND INDIVIDUALS AT RISK

John J Miles[1, 2, 3, 5], Viviana P Lutzky[1], Champa N Ratnatunga[1, 2, 3], Daniel J Smith[1, 4], Andreas Kupz[2], Denise L Doolan[1, 2], David W Reid[1, 4], Rachel M Thomson[3, 4] and **Scott C Bell[1, 3, 4]**

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The increasing global incidence of non-tuberculous mycobacterial (NTM) infection is of growing concern. New evidence of person-to-person transmission of multidrug-resistant NTM adds to the global alarm. The reasons why certain individuals are at risk of these infections is unknown. Using high definition flow cytometry author studied the immune profiles of two groups of at risk NTM patients and matched controls. The first group was cystic fibrosis (CF) patients and the second group was elderly individuals. CF patients with active NTM infection or a history of NTM infection exhibited a unique surface T cell phenotype with a marked global deficiency in TNFα production. Immune-based biomarkers were determined that could identify CF individuals at risk of NTM infection with a regression model of AUC=1. In contrast, elderly individuals with NTM infection exhibited a separate T cell phenotype underlined by the high prevalence of exhaustion markers and dysregulation in type I cytokine release. Collectively, these data will be of significant diagnostic and prognostic value for NTM patient management and could be used to identify new therapeutic pathways and new targets to correct T cell dysfunction.

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EFFECTIVE STRATEGIES IN ADDRESSING VACCINE HESITANCY

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Vaccines play a vital role in ensuring every individual, regardless of where they live can have a healthy start to life. Health system in each country is an important element of public health programs that aim to deliver life-saving vaccines, thus, understanding the threat to trust is essential in explaining vaccine acceptance. Overcoming hesitancy requires detection, diagnosis and tailored intervention as there is no simple strategy that can address all of the barriers to vaccine acceptance. In this presentation, author will discuss evidence-based literature reviews and meta-analysis that have examined the effectiveness of different interventions to reduce vaccine hesitancy and enhance vaccine acceptance.