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Rosenberg GA. Matrix metalloproteinase and proteolytic opening of the blood-brain-barrier in neuroinflammation. In: deVries E, Prat A, editors. The Blood-brain Barrier and Its Microenvironment Basic Physiology To Neurological Disease. New York: Taylor and Francis Group; 2005. p.335-58.

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Tubagus Djumhana Atmakusuma, Andhika Rachman, Ni Ken Ritchie p.145-52

Abstract

DDC 599.935

Jusni LFJ, Patricia, Rosadi BL (Faculty of Medicine and Health Science, Atma Jaya Catholic University of Indonesia, Jakarta, Indonesia) Alteration in 11 Beta-Hydroxysteroid Dehydrogenase Type-2 (*HSD11B2*) Gene as A Potential Candidate Parameter for Early Detection of Intrauterine Growth Restriction (IUGR) Events

Mol Cell Biomed Sci. 2021; 5(3): 98-103

Abstract (English)

Intrauterine Growth Restriction (IUGR) incidence in Indonesia ranks in the top 10 of the highest in Asia. It is the main perinatal death cause. IUGR also impairs fetal neurodevelopment, which can affect the development of children until later ages. Lack of 11β-hydroxysteroid dehydrogenase type-2 (11β-HSD2) enzyme is influenced by changes in the coding gene, *HSD11B2*, one of IUGR's causes. The main diagnostic method of IUGR at this time is by using Doppler ultrasound. However, Doppler ultrasound has several limitations as many cases are not detected. Its clinical predictive value in various women is poor, as Doppler ultrasound is not recommended for use in the first trimester, detection of abnormalities in the second trimester seems to be too late for helpful interventions. The study aim is to present an overview concerning *HSD11B2* gene alteration in an non-invasive prenatal testing (NIPT) as a possible diagnostic parameter for early detection in IUGR infants. This literature review is based on selected articles and studies taken from the Pubmed, Proquest, and EBSCO databases. A total of 4 studies reported the tendency for DNA methylation and decreased expression of the *HSD11B2* gene in IUGR cases. Changes in the *HSD11B2* gene have the potential to become a diagnostic parameter in the early detection of infants with IUGR. Further study and investigation of this possibility are needed.

Keywords: intrauterine growth restriction, HSD11B2, early detection, diagnostic, non-invasive prenatal testing

DDC 614.433

Soleha W, Iswanti FC (Master's Programme in Biomedical Sciences, Faculty of Medicine, Universitas Indonesia, Jakarta, Indonesia) Innate Immune Response to House Dust Mite Allergens in Allergic Asthma

Mol Cell Biomed Sci. 2021; 5(3): 104-14

Abstract (English)

Asthma is a major health problem and one of the leading causes of death in the world. The prevalence of asthma in Indonesia is high, with a recurrence >50%. Allergic sensitization in asthma is mainly caused by house dust mite (HDM) allergens, both from the mite's body and its contaminants (e.g., lipopolysaccharides). HDM allergens stimulate several pathways in the innate immune response based on the HDM allergen groups that sensitize them. The innate immune response to HDM allergen exposure occurs when pattern recognition receptors (PRRs) recognizes the allergen, thereby stimulating respiratory epithelial cells to release cytokines, namely, thymic stromal lymphopoietin (TSLP), interleukin-25 (IL -25), and IL-33. The release of IL-25 and IL-33 activates group 2 innate lymphoid cells (ILC2) to release Th2-type cytokines (i.e., IL-5 and IL-13), resulting in allergic airway inflammation via IgE secretion by B cells, recruitment of eosinophils, and respiratory tract remodeling. Dendritic cells induce an adaptive immune response through Th2 activation in the sensitization and effector phases. Other mediators that contributed to the innate immune response include C-C motif chemokine ligand 20 (CCL-20) and granulocyte-macrophage colony-stimulating factor (GM-CSF). A deeper understanding of the components and mechanisms involved in innate immunity against HDM allergens creates the potential to develop alternative therapeutic targets for allergic asthma treatment. **Keywords:** house dust mite allergens, innate immunity, allergic asthma, respiratory epithelium, inflammatory cytokines

DDC 615.321

Tjajaindra A, Sari AK, Simamora A, Timotius KH (Faculty of Medicine and Health Sciences, Krida Wacana Christian University, Jakarta, Indonesia)

The Stem Infusate and Ethanol Extract of *Physalis angulata* Inhibitory Activities against α-Glucosidase and Xanthine Oxidase *Mol Cell Biomed Sci.* 2021; 5(3): 115-20

Abstract (English)

Background: Infusate of the whole plant of *Physalis angulata* is used traditionally for the remedy of various diseases including diabetes and gout. This study focused on the stem of *P. angulata*. The objectives of this study were to investigate the potential of the stem infusate (INPA) and ethanol extract (EEPA) of *P. angulata* as inhibitors of α-glucosidase and xanthine oxidase.

Materials and method: INPA and EEPA were determined for their α -glucosidase and xanthine oxidase inhibition activities *in vitro*, whereas antioxidant activity was determined by 2,2-diphenyl-1-picryl-hydrazyl-hydrate (DPPH) assay. Reference inhibitors were used for comparison. The total phenolic compounds were also estimated.

Results: EEPA had more concentrated phenolic than INPA which were 7.96 and 0.08 mgGAE/g dried biomass, respectively. INPA and EEPA inhibited α -glucosidase considerably, with IC50 of 149.11 and 409.86 μ g/mL, respectively (acarbose was 130.66 μ g/mL). However, they inhibited xanthine oxidase weakly, with IC50 of 0.546 and 2.643 mg/mL, respectively, compared with allopurinol 0.005 mg/mL. EEPA scavenged DPPH radicals very weakly (16.04 mg/mL) compared to BHT (0.021 mg/mL), whereas no activity was observed for INPA.

Conclusion: The stem infusate and ethanol extract of P. angulata are able to inhibit the activity of α -glucosidase, thus can be further explored for sources of bioactive compounds with α -glucosidase inhibition activity.

Keywords: α-glucosidase, infusate, ethanol extract, *Physalis angulata*, stem, xanthine oxidase

DDC 616.92

Puspitasari D, Rusli EA, Husada D, Kartina L (Department of Pediatric, Dr Soetomo General Hospital/Faculty of Medicine, Universitas Airlangga, Surabaya, Indonesia)

Escherichia coli and Klebsiella pneumonia as the Most Common Bacteria Causing Catheter Associated Urinary Tract Infection Mol Cell Biomed Sci. 2021; 5(3): 121-6

Abstract (English)

Background: Healthcare-Associated Infections (HAIs) are the result of a reaction between taint agents that infected the patient when the patient is hospitalized. A Study from The Center for Disease Control and Prevention shows that most HAIs in hospital are urinary tract infection, most of the infection incident in patient are caused by catheter. Catheter indwelling is notable in medical sphere. This study aimed to inquire case number of Catheter-Associated Urinary Tract Infection (CAUTI) in Dr. Soetomo General Hospital, the feature of CAUTI patients, the type of bacteria that cause CAUTI, and what is the relation among sex and bacteria colony.

Materials and Methods: An analytic observational study with the population of pediatric hospitalized patients of Dr. Soetomo General Hospital was conducted in January-December 2017. Samples collected were positive urine culture from pediatric hospitalized patients. Information regarding the bacteria that cause CAUTI, gender, and length of catheter usage were collected.

Results: There were total 140 samples of positive urine culture in pediatric patient, and 38.5% was diagnosed as CAUTI. Overall CAUTI was often found in male subjects (51.9 %), and similar with ≤1-year old patients which also often found in male subjects (60.8%). The highest length of catheter usage was 3-5 days (42.5%). All subjects had fever as a clinical sign and 83.3% had suprapubic pain. *Escherichia coli* and *Klebsiella pneumoniae* infections were highly discovered. There was an association between gender and urine culture colony count (*p*=0.02).

Conclusion: CAUTI is commonnly found in Dr. Soetomo General Hospital, and two bacteria that cause the most infection were *E. coli* and *K. pneumoniae*.

Keywords: catheter, urinary tract infection, healthcare associated infection

DDC 543.65

Arlinda D, Oktoberia IS, Karyana M (National Institute of Health Research and Development, Ministry of Health of Indonesia, Jakarta, Indonesia)

Validation of a Liquid Chromatography/Tandem Mass Spectrometry Assay for the Quantification of Plasma Dihydroartemisinin Mol Cell Biomed Sci. 2021; 5(3): 127-36

Abstract (English)

Background: Insufficient plasma level of dihydroartemisinin (DHA) can select resistance and will further hinder malaria elimination program. We investigated clinical applicability of a validated liquid chromatography/tandem mass spectrometry (LC-MS/MS) assay to quantify plasma concentration of DHA in healthy subjects from a single oral administration of fixed dose combination of Dihydroartemisinin-Piperaquine.

Materials and Methods: Micro-elution solid-phase extraction in a 96-well plate format was used to prepare the samples. DHA separation happened in Acquity UPLCTM BEH C18 column (50 × 2.1 mm, 1.7 μm). Mobile phase was a mixture of acetonitrile-ammonium acetate 10 mM pH 3.5 (50:50, v/v) at 0.3 mL/minute flow rate. Waters Acquity UPLCTM H-Class system coupled with triple quadruple mass spectrometry in positive electrospray ionization mode was used for detection. The internal standard was a stable isotope labelled DHA.

Results: Calibration curve was linear with a correlation coefficient >0.995 over a concentration range of 1–1,000 ng/mL. Bias and variation for accuracy and precision were in the range of 15% (20% at the lower limit of quantification). Using 5 μL sample, lower limit of quantification was 1 ng. Matrix effect was less than 15%. The method was successfully applied to investigate the pharmacokinetics of DHA from five healthy subjects, although carry over and the role of anticoagulants were not tested.

Conclusion: The LC-MS/MS assay for the quantification of plasma DHA was validated for selectivity, linearity, lower limit of quantitation, accuracy, precision, matrix effect and stability. Although clinical applicability was demonstrated, this method was to be improved to address the not-tested validation parameters.

Keywords: dihydroartemisinin, liquid chromatography/tandem mass spectrometry assay (LC-MS/MS), malaria, Indonesia

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DDC 616.614

Ramadhanti R, Helda (Public Health Study Program, Faculty of Public Health, Universitas Indonesia, Depok, Indonesia)

Association of Hypertension and Chronic Kidney Disease in Population Aged ≥18 Years Old

Mol Cell Biomed Sci. 2021; 5(3): 137-44

Abstract (English)

Background: Chronic kidney disease (CKD) is a global public health problem, due to the increasing prevalence and incidence of kidney failure, poor prognosis, and required high costs for its treatment. Hypertension as the dominant risk factor for CKD also has a high prevalence which keep increasing in DKI Jakarta. This study aimed to determine the association between hypertension and the incidence of CKD in people aged ≥18 years old in DKI Jakarta Province.

Materials and Methods: This was a quantitative research with an analytic cross-sectional study design. The data source used was secondary data obtained from Basic Health Research (Riset Kesehatan Dasar/Riskesdas) 2018. There were 7,141 samples that matched the inclusion and exclusion criteria.

Results: The proportion of CKD and hypertension in people aged ≥18 years old in DKI Jakarta Province were 0.5% and 16.6%, respectively. There was a significant association between hypertension and CKD with a prevalence odds ratio (POR) of 3.140 (95% CI: 1.527-6.453) after being adjusted by the age variable. Several other characteristics such as age (POR = 3.912; 95% CI: 1.932-7.918), diabetes mellitus (POR = 3.412; 95% CI: 1.405-8.285), heart disease (POR = 7.323; 95% CI: 3.158- 16.982), and physical activity (POR = 2.324; 95% CI: 1.148-4.703) were also significantly associated with the incidence of CKD.

Conclusion: Someone who has hypertension has 3.14 times (95% CI: 1.527-6.453; p-value = 0.002) chance of suffering from CKD compared to someone who does not have hypertension after being controlled by the confounding variable, age.

Keywords: chronic kidney disease, hypertension, DKI Jakarta, Basic Health Research 2018

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Donor HLA Genotyping using Polymerase Chain Reaction-Sequence Specific Primers (PCR-SSP) as Method for Acquiring **Donor Panel in Platelet Refractoriness**

Mol Cell Biomed Sci. 2021; 5(3): 145-52

Abstract (English)

Background: Evaluation and identification of HLA antibodies in the recipient's serum is of utmost importance prior to transplantation and transfusion. HLA typing is a steppingstone in proposing a donor panel. In order to obtain the HLA typing, Polymerase Chain Reaction-Sequence Specific Primers (PCR-SSP) can be performed.

Materials and method: This is a preliminary study to determine HLA polymorphism by HLA genotyping in 43 blood donors. DNA from the samples was isolated using commercial kits according to the standard protocol. The DNA then was amplified using PCR-SSP methods and analyzed using the provided set in the kit.

Results: This study found that the most frequent HLA-A alleles was HLA-A*24 (41.9%). For HLA-B alleles, the most common was HLA-B*15 (28%). Most frequent HLA-A-B haplotypes was HLA-A*24-B*15 (11.3%). The results from this study concurs with that of previous study. However, some alleles might vary due to difference in study population. Determining HLA-typing is of paramount importance in an ethnically diverse country such as Indonesia. In contrast to homogenous caucassian country, difference in ethnicity might cause platelet refractoriness due to incompatibility. HLA-typing would also guide the diagnostic workup and required treatment strategy for platelet

Conclusion: From the HLA typing using PCR-SSP in blood donors in Jakarta, we found that the most frequent alleles were HLA-A*24 and HLA-B*15; and the most frequent haplotypes were HLA-A*24-B*15. This study should be upscaled to include larger population and ethnic groups to obtain complete profile of Indonesian population.

Keywords: platelet refractoriness, HLA, donor, PCR-SSP, transfusion medicine

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