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REVIEW ARTICLE

RESEARCH ARTICLES

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Molecular and Cellular Biomedical Sciences

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Sandra F, Esposti MD, Ndebele K, Gona P, Knight D, Rosenquist M, et al. Tumor Necrosis Factor-Related Apoptosis-Inducing Ligand Alters Mitochondrial Membrane Lipids. Cancer Res. 2005; 65(18): 8286-97.

Book
Murray PR, Rosenthal KS, Kobayashi GS, Pfaller MA. Medical microbiology. 4th ed. St. Louis: Mosby; 2002.

Chapter in a book:
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.

Dissertation/Thesis/Essay:
Arlauckas SP. Near infrared fluorescent choline kinase alpha inhibitors for cancer imaging and therapy [Dissertation]. Philadelphia: University of Pennsylvania; 2015.

Part of Website/Monograph:
Medline Plus [Internet]. Bethesda: US National Library of Medicine; ©2009. Diabetic Kidney Problems [update 2015 Nov 2; cited 2015 Nov 16]. Available from: https://www.nlm.nih.gov/medlineplus/diabetickidneyproblems.html/.

Conference Paper:
Fledelius HS. Myopia and significant visual impairment: global aspects. In: Lin LLK, Shin YF, Hung PT, editors. Myopia Updates II: Proceedings of the 7th International Conference on Myopia 1998 Nov 17-20, Taipei. Tokyo: Springer; 2000. p.3-17.

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CONTENT

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RESEARCH ARTICLES

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Abstract

DDC 616.042
Meiliana A, Dewi NM, Wijaya A (Prodia Clinical Laboratory, Bandung, Indonesia)
Cancer Genetics and Epigenetics in Cancer Risk Assesment
Mol Cell Biomed Sci. 2021; 5(2): 41-61
Abstract (English)
Compared to the normal tissues, cancer cells tend to have higher proliferation rate and often lost their ability to undergo apoptosis. In addition, cancer cells can separate themselves from their original tissue thus causing metastasis in other part of body. While undergoing program cell death, disordered cellular programming can happen. The main causes of this cellular programming anomaly are epigenetic and genetic alterations, which have been known as two separate mechanisms in carcinogenetic. A recent outcome of whole exome sequencing of thousands of human cancers has been the unexpected discovery of many inactivating mutations in genes that control the epigenome. These mutations have the potential to disturb the DNA methylation patterns, histone modifications, and nucleosome positioning, hence, the causing gene expression alternation. Genetic alteration of the epigenome therefore contributes to cancer just as epigenetic process can cause point mutations and disable DNA repair functions. Epigenetic mechanisms changes could cause genetic mutations, and genetic mutations in epigenetic regulators could cause epigenome changes. Knowing that epigenome play a major role in the hierarchy of gene control mechanisms suggests that mutations might have impact on multiple pathways related to cancer phenotype. This pinpoint the fact that recently, the way the genes are organized and controlled are suggested to be a relevant factor for human carcinogenesis.
Keywords: cancer genetic, cancer epigenetic, oncogens, tumor suppressor genes, driver mutation, passenger mutation

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DDC 611.018166
Sari BA, Zahra AT, Tasti GP, Maritska Z (Master of Biomedical Science, Faculty of Medicine, Sriwijaya University, Palembang, Indonesia)
Healing the Fundamental Unit of Heredity (Gene Therapy): Current Perspective and What the Future Holds
Mol Cell Biomed Sci. 2021; 5(2): 61-7
Abstract (English)
The ability to make precise adjustments to the human genome has been a goal of healing in which gene also introduces as the fundamental unit of heredity, in biomolecular technology in genetic diseases have opened new knowledge such as gene therapy. Gene therapy is a technique to repair DNA where its usage is to treat the malignancy and inherited genetic diseases. Gene therapy is a choice to the genetic cloth that goals to remedy a sickness this is hard to deal with or perhaps has no treatment. Currently, gene remedy is done in approaches to patients, specifically embryonic cells and somatic cells, every *in vivo* and *ex vivo*. Moral considerations with modification of the difficulty's cells and oversight of regulation and reagents want to be taken into consideration within the gene therapy project. Applications for using gene remedies have begun to be widely used, which include in case of maximum cancers, coronary heart disorder, infectious sicknesses, and others. Gene therapy has spread to a wide range of applications then go beyond the modification of genetic disorders. Advances in genetic modification of cancer cells and immunity and the use of viruses and bacteria to control cancer cells have resulted in many clinical trials and product developments for cancer treatment. The miracles and blessings of gene therapy are might believe, but even though they are being studied and developed now and, in the future, so that the desire for gene therapy may be even better future.
Keywords: gene therapy, genetic recombination, gene therapy application

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DDC 616.39
Ekaputri DS, Sidiartha IGL, Pratiwi IGAE (Department of Child Health, Faculty of Medicine, Universitas Udayana/Sanglah General Hospital, Denpasar, Indonesia)
Low Total Lymphocyte Count as the Risk of Hospital Acquired Malnutrition in Children
Mol Cell Biomed Sci. 2021; 5(2): 68-72
Abstract (English)
Background: Hospital Acquired Malnutrition (HAM) is characterized by inadequate nutritional therapy and the risk of developing malnutrition during the hospital stay. In clinical practice, there are many measurements to determine nutritional status. Total lymphocyte count (TLC) is associated with impaired function of immune system in malnutrition. The purpose of this study was to evaluate the prognostic value of TLC to the occurrence of HAM in pediatric patients.
Materials and method: This an observational study with a prospective cohort design. Subjects were assessed for weight at the first day of hospitalization, then the subjects were followed until they were discharged. Body weight was re-measured on discharge to determine the presence or absence of HAM. This research was conducted at Sanglah Hospital from May-December 2019. Subjects who met the inclusion and exclusion criteria were enrolled in the study.

Results: Among 120 subjects, 55 subjects or 45.8% were malnourished on admission. Subjects with a low TLC compared to a normal TLC had a 3.9-fold risk of experiencing hospital acquired malnutrition (95% Confidence Interval: 1.59 to 7.19, *p*=0.001). Subjects who had a low TLC had HAM of 61.8%, while subjects who had a normal TLC had HAM of 32.3%. In multivariate analysis, low TLC was the only risk factor for HAM in this research.

Conclusion: This study proved that low TLC is the risk of HAM. Total lymphocyte count could be used as predictor of the risk of HAM in hospitalization children.

Keywords: hospital malnutrition, total lymphocyte, children

DDC 616.3623

Nababan SHH, Khairunissa ST, Erfan E, Nafrialdi, Krisnuhoni E, Hasan I, Gani RA (Internal Medicine Department, Faculty of Medicine, Universitas Indonesia, Cipto Mangunkusumo General Hospital, Jakarta, Indonesia)

Choline-deficient High-fat Diet-induced Steatohepatitis in BALB/c Mice

Mol Cell Biomed Sci. 2021; 5(2): 74-81

Abstract (English)

Background: Non-alcoholic steatohepatitis (NASH) is an expanding cause of chronic liver disease worldwide, including Indonesia, with higher risk progression to cirrhosis and hepatocellular carcinoma. Preclinical experiments using several mice models have been conducted to clarify its complex pathogenesis. This study was designed to investigate whether BALB/c mice on a choline-deficient high-fat diet can be used as a model for NASH.

Materials and Methods: BALB/c male mice were fed choline-deficient L-amino acid-defined high-fat diet (CDAHFD) or a standard diet for six weeks. The body and liver weights, liver histology, and plasma biochemistry were analyzed. The relative expression levels of tumor necrosis factor (TNF)α, transforming growth factor (TGF)β1, collagen-1α1 (COL1α1), glutathione peroxidase 1 (GPx1), and uncoupling protein 2 (UCP2) genes in the livers were analyzed using a two-step real time-polymerase chain reaction. Liver fatty acids composition was analyzed using gas chromatography with flame ionization detector (GC-FID).

Results: CDAHFD induced steatohepatitis in BALB/c mice with increased plasma levels of alanine aminotransferase. The liver of CDAHFD-fed BALB/c mice showed upregulated relative expression levels of TNFα, TGFβ1, COL1α1, GPx1, and UCP2 genes. The liver fatty acid analysis showed a significant accumulation of saturated fatty acids (SFAs) and an increased ratio of n-6/n-3 polyunsaturated fatty acids (PUFAs) in the livers of CDAHFD-fed BALB/c mice.

Conclusion: This study suggests that CDAHFD can induce steatohepatitis in BALB/c mice and therefore may be used as NASH mice model.

Keywords: steatohepatitis, fatty liver, choline-deficient high fat diet, BALB/c

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DDC 617.522

Wihastyoko HYL, Sidarta EP (Department of Plastic and Reconstructive Surgery, Faculty of Medicine, Universitas of Brawijaya/Dr. Saiful Anwar General Hospital, Malang, Indonesia)

The Expression of TGF-β1, p38 MAPK, and ERK-1 Protein in Cleft Affected Tissue of the Lip: An Observational Study

Mol Cell Biomed Sci. 2021; 5(1): 82-7

Abstract (English)

Background: Cleft lip is a congenital birth defect caused by many proteins. Transforming growth factor (TGF)-β1, p38 mitogen-activated protein kinase (MAPK) and extracellular signal-regulated protein kinase (ERK)-1 are proteins which regulate proliferation and apoptosis role during intrauterine period. This study aimed to observe the expression of these proteins in cleft affected tissue of the lip.

Materials and Methods: A descriptive study by examining the TGF-β1, p38 MAPK, and ERK-1 immunohistochemical expression of cleft affected tissue of the lip was conducted. Subjects were patients that were participating for the social event held by Plastic Surgery Department, Faculty of Medicine, Univesitas Brawijaya, on December 3-12, 2012 in Nusa Tenggara Timur. Excess lip mucosa (waste tissue) during the operation were stored in 10% formalin then stained by immunohistochemistry for TGF-β1, p38 MAPK, and ERK-1. We counted the average protein expression under the light microscope with 1000x magnification for 20 different fields of view, randomly.

Results: Paraffin blocks from 30 subjects were selected. The mean p38 MAPK expression was found to be highest, with the average of 8 per field of view; followed by the mean TGF-β1 expression, with the average of 5 per field of view; and the mean ERK-1 expression was found to be the lowest, with the average of 2 per field of view.

Conclusion: Expression of p38 MAPK and TGF-β1 are higher than ERK-1, suggesting that p38 MAPK is in the same signalling pathway as TGF-β1, while ERK-1 is lower, as its role as anti-apoptotic. This is consistent with several previous studies showing that all proteins took part in the development of cleft lip or craniofacial development. Further study needs to be conducted to determine which protein plays the bigger role.

Keywords: cleft lip, TGF-β1, p38 MAPK, ERK-1

DDC 617.735

Edwar L, Ariyanto IA, Tanudjaja SA, Sitompul R, Lee S, Price P (Department of Ophthalmology, Faculty of Medicine, Universitas Indonesia, Jakarta, Indonesia)

Interleukin-1A May Illuminate Differential Effects of the Retinal Artery Caliber in HIV Patients

Mol Cell Biomed Sci. 2021; 5(2): 88-92

Abstract (English)

Background: Retinal artery caliber (RAC) is narrower in human immunodeficiency virus (HIV)-infected patients beginning antiretroviral therapy (ART). We aimed to assess associations between variations in genes encoding inflammatory mediators and natural killer receptors and retinal artery caliber (RAC) in HIV patients beginning ART.

Materials and Methods: Seventy-nine HIV positive patients beginning ART with less than 200 cluster of differentiation (CD) 4 T-cells/µL were recruited. Examinations were performed before ART (V0) and at months 3, 6 and 12 (V3, V6, V12). The study was approved by ethics committees and informed consent was obtained from each subject.

Results: Right and left RAC of the HIV patients were narrower than healthy controls (p=0.016 for right RAC) and narrowed further on ART, but demographic associations with the right and left RAC were not identical. Here we show that polymorphisms in genes encoding NK receptors or TNF activity had no significant impact, but right RAC was associated with carriage of allele 2 at IL1A+4845 (p=0.037 after 12 months on ART).

Conclusion: Overall the paradoxical reduction in the RAC in HIV patients responding to ART was not modified by genotypes known to affect NK cell function or TNF responses, but IL1A genotype may modify the decline in the right RAC.

Keywords: anti-retroviral therapy, CMV, HIV, IL1A, retinal artery caliber

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DDC 362.1981

Anwar AA, Abdullah N, Padjalangi AN, Hamid F, Mappeware NA, Lukas E (Obstetrics and Gynecology Department, Faculty of Medicine, Universitas Hasanuddin, Makassar, Indonesia)

Serum Leptin Concentration is Correlated to Insulin Resistance in Polycystic Ovary Syndrome (PCOS) Patients

Mol Cell Biomed Sci. 2021; 5(2): 93-7

Abstract (English)

Background: Leptin resistance which leads to excessive circulating leptin levels is thought to affect ovarian function. This study aimed to study the correlation between serum leptin levels with insulin resistance in patients with polycystic ovary syndrome.

Materials and method: This cross-sectional study was undertaken in several teaching hospitals in Makassar, Indonesia. We included patients diagnosed with polycystic ovary syndrome (PCOS) aged 18-40 years old. Serum leptin levels were examined in all eligible subjects using the enzyme-linked immunosorbent assay (ELISA) method. The results obtained were further analyzed statistically.

Results: Approximately 53 PCOS subjects were included in this study, 25 subjects with insulin resistance and 28 subjects without insulin resistance. After examining serum leptin levels, we found that leptin is directly proportional to insulin resistance (p<0.001). We even found a strong positive correlation between serum leptin levels with homeostatic model assessment for insulin resistance (HOMA-IR) levels (r=0.659; p<0.001). Leptin was found to be independent of HOMA-IR, not influenced by confounding factors such as body mass index (BMI) (p=0.090).

Conclusion: There was a significant correlation between serum leptin levels and HOMA-IR values in PCOS patients. This correlation was found to be significant regardless of patient's BMI, therefore is considered to have a direct effect on insulin resistance in PCOS.

Keywords: polycystic ovary syndrome, leptin, insulin resistance, HOMA-IR

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