The 3rd International Congress of

Laboratory Diagnosis

February 15-18, 2024

North Khorasan University of Medical Sciences | Ardebil University of Medical Sciences | Ghazvin University of Medical Sciences | Bam University of Medical Sciences | Arak University of Medical Sciences | Urmia University of Medical Sciences | Jahrom University of Medical Sciences | Isfahan University of Medical Sciences | Tabriz University of Medical Sciences | IAU | Tehran University of Medical Sciences | Nasim Institute | Shahid Beheshti University of Medical Sciences and Health Services

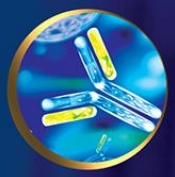
LD CONGRESS

3RD INTERNATIONAL CONGRESS OF LABORATORY DIA

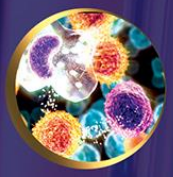
FEB 15-18, 2024 - VIRTUAL CONGRESS

Biochemistry

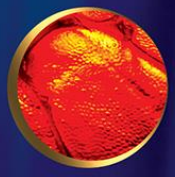
Pathology



Immunology

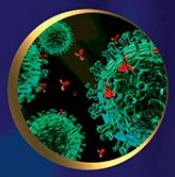


Microbiology



Hormonology

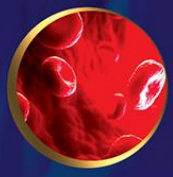
Mycology



Virology

Parasitology

Medical Genetics



Hematology

Scientific Sponsor

BioTechnology Publications

Financial Sponsor

NASIM Tashkhis Azma DIAGNOSTICS

Submission deadline
December 23, 2023
Top poster evaluation criteria
ldcongress.com/award-poster
Top oral evaluation criteria
ldcongress.com/award-oral

Registration and Submission
www.ldcongress.com
Online Workshops
ldcongress.com/online-workshop
Contact
info@ldcongress.com

WWW.LDCONGRESS.COM

Financial Sponsor

IDEAL DIAGNOSTICS NETWORK

Financial Sponsor

PISHTAZTEB DIAGNOSTICS

1. **A brief overview of effective and interfering factors in the healing process of surgical wounds and chronic wounds (Review)**

Shabnam Akbari,[1,*]

1.

Introduction: Background and purpose: Today, reducing pain and rapid healing of surgical wounds (acute) and chronic wounds are discussed by researchers. Wound healing is the process of structural and functional reconstruction of injured tissues. Damage to the skin can lead to contamination and disruption of the body's homeostasis. When an acute injury occurs, extensive cell migration, proliferation, and differentiation, synthesis of extracellular matrix components, scar formation, and restoration of blood flow and oxygen supply to the tissue are part of They are a complex adjustment of improvement and restoration. Wound healing, a natural biological process in the human body, is achieved through four precise and highly programmed stages: homeostasis, inflammation, proliferation, and regeneration. For a wound to heal successfully, all four steps must occur in the proper order and time frame. However, chronic wounds do not follow this sequence of events and can challenge the most experienced physician if underlying factors interfere with wound healing are not identified. The purpose of this article is to provide recent information on factors that interfere with the response to tissue injury, impair wound healing, and factors that accelerate healing.

Methods: The article is a review and does not have materials and methods

Results: Recent findings: Carbohydrates, along with fats, are the main source of energy in the wound healing process for surgical patients or sick patients. Protein is one of the most important nutritional factors affecting wound healing. Protein deficiency can impair capillary formation, fibroblast proliferation, proteoglycan synthesis, collagen synthesis, and wound regeneration. Vitamins C (L-ascorbic acid), A (retinol), and E (tocopherol) have strong antioxidant and anti-inflammatory effects. Vitamin C deficiency leads to impaired healing and is associated with reduced collagen synthesis and fibroblast proliferation, reduced angiogenesis, and increased capillary fragility. Wound oxygenation status is a key factor in wound healing outcomes. Oxygen is intricately involved in numerous biological processes, including cell proliferation, angiogenesis, and protein synthesis, which are required to restore function and tissue integrity. Wound tissue hypoxia is usually greater in the center of the wound. Hypoxemia, caused by vascular dysfunction, is a key factor limiting wound healing. Correction of hypoxemia through the administration of supplemental oxygen (O2) can have a significant beneficial effect on wound healing. Many drugs, such as those that interfere with clot formation or platelet function, or inflammatory responses and cell proliferation, can affect wound healing. These agents include common

medications (glucocorticoid steroids, non-steroidal anti-inflammatory drugs, or NSAIDs) that have a significant effect on wound healing. Systemic glucocorticoids (GC), often used as anti-inflammatory agents, are well known to inhibit wound healing through anti-inflammatory effects and suppression of wound cellular responses, including fibroblast proliferation and collagen synthesis. Most chemotherapy drugs are designed to induce rapid cell division and angiogenesis and therefore inhibit many pathways that are relevant to wound healing. These drugs inhibit the synthesis of DNA, RNA, or protein and thus reduce fibroplasia and neovascularization of wounds.

Conclusion: Conclusion: Nutritional needs of wounds are complex and complex nutritional support is useful for healing acute and chronic wounds. Proteins, carbohydrates, arginine, glutamine, polyunsaturated fatty acids, vitamin A, vitamin C, vitamin E, magnesium, copper, zinc, and iron play a significant role in wound healing, and their deficiency affects wound healing. Both the absence and presence of oxygen affect wound healing. New therapeutic approaches that take advantage of cellular hypoxia sensing and response mechanisms and recreate the precise application of oxygen therapy in hypoxic tissue areas, as well as therapeutic approaches targeting oxygen and redox sensing signaling pathways, are very promising. Consequently, the successful treatment of any acute or chronic wound depends on the identification and management of factors for each individual.

Keywords: Wound healing, biological biomolecules, oxygen, drugs, chemotherapy

A comprehensive review of the clinical biomarkers in gastric cancer (Review)

Fatemeh jeldani,[1,*]

1. Department of Microbiology, Faculty of Basic Siences, Lahijan Branch Islamic Azad University, Lahijan, Guilan, Iran.

Introduction: Abnormal growth in the cells of any part of the stomach causes gastric cancer (GC). According to the database of research, GC is presently the 5th most common cancer diagnosis worldwide. This cancer caused 9.6 million deaths worldwide. Infection with microorganisms such as Helicobacter pylori, eating habits, obesity, tobacco, alcohol consumption, and the use of NSAIDs are risk factors for stomach cancer. A biomarker is a characteristic element which objectively measured and evaluated as an indicator of normal biological processes, pathogenic processes, or pharmacologic responses to a therapeutic intervention. Therefore diagnostic techniques related to cancer biomarkers in addition to helping early diagnosis of cancer, in the fields of investigating cancer progression, response to cancer treatment, and recurrence of cancer are beneficial. This study aims to review existing knowledge on the clinical, and biomolecular biomarkers in gastric cancer.

Methods: A comprehensive search was conducted in MEDLINE, EMBASE, Scopus, and other databases to discover published articles related to clinical biomarkers in gastric cancer with search terms included, clinical biomarkers, gastric cancer, miRNA, diagnosis, prognosis, and related keywords. Several articles were found in the surveyed databases. Only the most relevant ones were published in high-impact factor journals were selected.

Results: based on our results, disturbances in gene expression, DNA methylation, and non-coding regulatory RNAs can contribute to the initiation and development of gastric cancer. Currently, the most widely used markers for stomach cancer diagnosis in clinical practice are CEA, CA19-9, and CA72-4. Some genes such as FCER1G, MRPL14, SOSTDC1, TYROBP, and C3 are expressed at a high level and associated with the occurrence of GC in H. pylori infection. Another important parameter in the development of various cancers is DNA methylation changes. Defective DNA methylation in CDH1, CHFR, DAPK, GSTP1, p15, p16, RARÎ², RASSF1A, RUNX3, and TFPI2 has been considered as a serum biomarker for the diagnosis of GC. Up-regulation of 14 miRNAs particularly miR-21, miR-30b, and miR-26b are associated with gastric cancer.

Conclusion: Many biological molecules such as genes, proteins, and miRNA can be applied as potential biomarkers for early diagnosis, prognosis, and novel molecular therapies in gastric cancer. Overall, this review highlights the significant clinical biomarkers in gastric cancer.

Keywords: clinical biomarkers, gastric cancer, miRNA, diagnosis, prognosis

A novel method for evaluating the biological activity of recombinant human interleukin-1 receptor antagonist (rhIL-1RA) produced in E. coli (Research Paper)

Kianoush Dormiani,[1,*] pendar shojaei,[2] sanaz sedghi esfahani,[3]

1. 1. Department of Animal Biotechnology, Cell Science Research Center, Royan Institute for Biotechnology, ACECR, Isfahan, Iran
2. Department of Animal Biotechnology, Cell Science Research Center, Royan Institute for Biotechnology, ACECR, Isfahan, Ira
3. Department of Animal Biotechnology, Cell Science Research Center, Royan Institute for Biotechnology, ACECR, Isfahan, Ira

Introduction: Human interleukin-1 (hIL-1) is a pro-inflammatory cytokine that plays a critical role in controlling inflammatory responses. In the case of a continuous response, this process causes serious tissue damage and auto-inflammatory diseases such as rheumatoid arthritis. Human interleukin-1 receptor antagonist (hIL-1RA) is an antagonist of hIL-1 receptor that inhibits the signaling pathway of hIL-1 and subsequently reduces the severity of autoimmune disease. In this study, recombinant hIL-1RA protein was expressed into soluble form in E. coli. Accordingly, the present study was designed to set up a simple and accurate method to evaluate the biological activity of the recombinant hIL-1RA protein. For this purpose, NIH3T3 fibroblast cells were treated with hIL-1RA protein and after that, the process of inflammation was induced through treatment with Lipopolysaccharide (LPS). consequently, higher expression of hIL-1Î² reduced the cell viability of NIH3T3 cells. Then, the bioactivity of pre-treated recombinant hIL-1RA protein by antagonizing the IL-1 receptor was evaluated using MTS assay. Based on our findings, 1000 ng/ml of the recombinant hIL-1RA protein was successfully able to rescue the survival of the LPS-treated NIH3T3 cells by 82 %.

Methods: For the MTS assay test, NIH3T3 cells were counted and 1 Ã— 102 cells/ml were seeded in 96-well plates. After 24 h and following cell adhesion, recombinant hIL-1RA and commercial hIL-1RA (Peprotech) were added separately at final concentrations of 10, 100, 500, and 1000 ng/ml. Two hours later, 100 Âµg/ml LPS was added to each well. After 24 h of LPS treatment, the cells were subjected to the MTS assay to determine the viability of NIH3T3 cells. 20 Î¼l of the MTS/PMS reagent was added to each well and incubated at 37 Â°C for 3 h. At the end of incubation, absorbance was measured at 490 nm, and after normalization, the viability of NIH3T3 cells was calculated

Results: The results showed that there was no significant difference between the recombinant hIL-1RA activity and the commercial protein (Peprotech) as the positive control. Both of these proteins similarly neutralized the cytotoxic effect of hIL-1Î² and improved NIH3T3 cell viability from 82% (after treatment

with LPS) to 96% (after adding hIL-1RA proteins). It is noteworthy that the rescue of cell viability by hIL-1RA proteins was dose-dependent.

Conclusion: Using this simple and reliable approach, the biological activity of recombinant hIL-1RA was estimated in comparison to a standard protein. This study indicated that however, treatment of NIH3T3 cells with LPS decreased the cell viability, the recombinant hIL-1RA protein was able to rescue, the cell survival, and thus the functionality of recombinant IL-1RA protein was confirmed by antagonizing IL-1 receptor and reduction of inhibitory effect of LPS on the viability of NIH3T3 cells.

Keywords: hIL-1, hIL-1RA, Lipopolysaccharide, NIH3T3 fibroblast cell, MTS assay

A review of aptamer-based biosensors for Staphylococcus aureus detection (Review)

Zahra Ghorbani,[1,*] Sana Yahyazadeh Jasour,[2]

1. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Department of Microbiology, School of Biology, College of Science, University of Tehran, Tehran, Iran

Introduction: Staphylococcus aureus is a gram-positive and spherical bacterium known as one of the most important bacterial pathogens. This bacterium can cause food poisoning and various infectious diseases by producing enterotoxin. This opportunistic and common pathogen in humans can cause a wide range of skin infections to pneumonia and sepsis. Staphylococcus aureus infections are easily transmitted and usually exist in air, water, soil, human skin, etc. Therefore, its rapid identification is critical to treat and prevent the spread of infection.

Methods: Many detection methods have been introduced, including bacterial culture with genotype and phenotype detection tests, polymerase chain reaction methods, ligase chain reactions, and enzyme-linked immunosorbent assay. These techniques, despite their high sensitivity, are time-consuming methods and require a lot of facilities and costs. Also, the existence of expert staff and advanced laboratories is essential.

Results: Recently, the attention of researchers has been drawn to providing methods with high sensitivity but simple and cheap. Therefore, by using aptamers, new biosensors have been designed that successfully detect Staphylococcus aureus in various samples.

Conclusion: In this article, recent studies related to aptamer-based biosensors for the rapid detection of Staphylococcus aureus and the replacement of aptamers with antibodies have been discussed.

Keywords: Aptamer, Staphylococcus aureus, biosensor, SELEX

A review: mesenchymal stem cell-based therapies for Autoimmune Diseases (Review)

Helia Keshavarzi,[1,*]

1. bagerolulum research center

Introduction: Autoimmune disease [AID also called autoimmune disorder] is a result of immunological imbalance and intolerance. In such a condition, an immune response is produced against the healthy tissues or substances in our body. About 80 different types of autoimmune disorders are found to affect various systems and organs in the body. Current treatments for these diseases, such as immune suppressive agents, have long-term side effects and require lifelong treatment. As a result, researchers are exploring alternative and more efficient therapy options. Mesenchymal stem cells (MSCs) have recently been identified as a potential novel therapeutic option for autoimmune disorders. They have been found to have a significant immune-regulatory effect against autoimmune disorders, inhibiting NK proliferation and activity, as well as suppressing T/B cell proliferation and dendritic cell maturation. As a result, MSCs have gained increased interest in treating autoimmune disorders.

Methods: The papers included in this article were obtained from PubMed and MEDLINE databases. The following medical subject headings were used: â€œstem cell therapyâ€□, â€œautoimmune diseaseâ€□, â€œregenerative medicineâ€□, â€œmesenchymal stem cellsâ€□, and â€œAutoinflammatory diseaseâ€• .

Results: MSCs possess the ability to differentiate both in-vivo and in-vitro into different lineages, which include adipose, bone, cartilage, muscle, and myelosupportive stroma. Isolation of MSCs can be done from bone marrow, skeletal muscle, adipose tissue synovial membranes, connective tissues in adults, cord blood, and products of placenta. Allogeneic MSCs can be transplanted into a patient without preconditioning and still have positive clinical effects on the subject without acute toxicity. MSCs possess the following abilities that make them a clinical success. 1. Homes to inflammation site when delivered intravenously following tissue injury. 2. Differentiates into a variety of cells. 3. Secretes multiple bioactive molecules that facilitate recovery of injured cells and inhibition of inflammation in return. 4. Lacks immunogenicity and possesses immunomodulatory functions. MSCs can also migrate and engraft at the inflammation site when administered locally or systemically, and downregulate pathogenic immune response triggered in Graft versus Host Disease (GVHD) and AID such as multiple sclerosis, autoimmune diabetes, and rheumatoid arthritis. Particularly for diabetes, studies demonstrated that systemic administration of MSCs could prevent or reduce the development of type 1 diabetes in a NOD mouse model. The

MSCs were found to decrease the incidence of diabetes, reduce T cell and CXCL9-positive macrophage accumulation in the islets, and increase islet beta cell area and insulin content. This suggests that MSCs have potential as a therapeutic option for preventing or treating autoimmune side effects, such as type 1 diabetes, associated with immune checkpoint inhibitors. Additionally, many scientists believe that the beneficial effects of MSCs are owing to the paracrine activity of MSCs not to their cell replacement properties or differentiation properties. The paracrine activity of MSCs could be considered a novel therapeutic perspective in order to develop a safe and potentially more advantageous alternative to MSC-based therapy i.e. cell-free strategies. Notably, MSC-derived extracellular vesicles are an example of the paracrine activity of MSCs. MSC therapy is widely used and can be delivered through intravenous or intra-arterial injection. The route of administration is chosen based on the application, and MSC therapy can be either autologous or allogeneic. Both types of therapy are used to treat inflammatory diseases such as systemic lupus erythematosus, Crohn's disease, multiple system atrophy, multiple sclerosis, amyotrophic lateral sclerosis, and stroke.

Conclusion: Clinical studies have shown promising results for the potential use of MSCs in treatment, but it has not yet become a standard therapy. Concerns about the tumorigenic potential of MSCs have led to the exploration of MSC-derived EVs as a cell-free alternative. While preclinical and clinical studies have shown positive results for using MSC-derived EVs to treat autoimmune disorders, this approach is still in the early stages of development and research. Overall, MSCs may be a new and emerging treatment modality for autoimmune diseases, but further comprehensive investigations are needed before they can be widely used in clinical applications.

Keywords: Autoimmune disease, Stem cell therapy, Regenerative medicine, Mesenchymal stem cells

A Systematic Review of MicroRNA Expression in Rheumatoid Arthritis and Related Autoimmune Diseases (Review)

Shadi Nazari Fard,[1] Hadis Rahimi,[2] Fatemeh Ahmadpour,[3,*]

1. Department of Biochemistry and Genetics, School of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Department of Biochemistry and Genetics, School of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Department of Biochemistry and Genetics, School of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran

Introduction: Rheumatoid arthritis (RA), a complex autoimmune disease, involves dysregulation of the immune system. MicroRNAs (miRNAs) have emerged as crucial regulators of gene expression and potential biomarkers for autoimmune diseases. This systematic review aims to provide a comprehensive overview of miRNA expression profiles in various autoimmune diseases, with a focus on RA. The review analyzes studies investigating miRNA expression in different immune cell types, emphasizing CD4+ T cells, CD8+ T cells, and B cells, in patients with RA. Autoimmune diseases, including RA, involve dysregulation of the immune system. MiRNAs, small non-coding RNA molecules, play a pivotal role in post-transcriptional gene regulation and have been implicated in the pathogenesis of autoimmune disorders. This section introduces the significance of understanding miRNA expression patterns in autoimmune diseases

Methods: A systematic search of major databases (PubMed, Scopus, etc.) was conducted to identify studies investigating miRNA expression in RA and related autoimmune diseases. Inclusion and exclusion criteria were applied to select relevant studies. Data extraction focused on the types of immune cells analyzed, patient populations, and key findings.

Results: MicroRNA Expression in CD4+ T Cells: This section reviews studies that have explored miRNA expression profiles in CD4+ T cells from RA patients, including miR-146a, miR-363, and miR-498. It summarizes consistent findings, discrepancies between studies, and potential implications for RA pathogenesis. MicroRNA Expression in CD8+ T Cells: A detailed analysis of miRNA expression in CD8+ T cells in the context of RA and autoimmune diseases, incorporating miR-155 and its functionally linked gene, suppressor gene of cytokine signaling 1 (SOCS1). This section discusses the functional relevance of identified miRNAs and their association with disease severity. MicroRNA Expression in B Cells: Focusing on the role of miRNAs in B cells, this section reviews studies investigating miRNA expression in CD19+ B cells from RA patients, including miR-21-5p, miR-223-3p, miR-486-3p, and miR-23a-3p. It discusses how dysregulated miRNAs may contribute to aberrant B cell function and autoantibody production. cross-Cutting Themes

and Future Directions: A synthesis of common miRNA signatures across different immune cell types, highlighting potential therapeutic targets and biomarkers, including STAT3, PRDM1, and PTEN. This section also discusses gaps in current research and proposes avenues for future investigations.

Conclusion: Summarizes key findings from the systematic review, emphasizing the importance of understanding miRNA dysregulation in RA and related autoimmune diseases. Concludes with implications for future research and the potential clinical utility of miRNAs as diagnostic or therapeutic targets.

Keywords: Rheumatoid arthritis, MicroRNAs, Autoimmune Diseases.

A systematic review on laboratory criteria for diagnosis of SLE (Review)

Sayyid Ali Hosseini,[1,*]

1.

Introduction: Systemic lupus erythematosus (SLE) is an autoimmune disease that causes inflammation and damage in various parts of the body, including the skin, joints, kidneys, brain, and heart. The exact prevalence of classic systemic lupus (SLE) in Iran is not known, but some studies have shown that its prevalence is almost similar to the global average in Iran. That is, about 50 to 70 per 100,000 people per year, including young and vulnerable women. SLE can lead to serious complications such as kidney injury, brain damage, heart failure, and so on, so the importance of early diagnosis and appropriate therapeutic intervention in this disease is very high. Given the importance of this topic, in this study, were examined the latest diagnostic methods and tests for SLE.

Methods: In this systematic review, it was conducted based on the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta Analyzes) protocol. To search for articles, PubMed and Scopus databases were used until Setember2023. Articles that included detailed information about clinical and laboratory criteria for clinical diagnosis of SLE also met the inclusion criteria.

Results: The diagnosis of SLE is made through a combination of clinical signs, blood tests, and diagnostic tests. In general, the usual tests to diagnose SLE (systemic lupus erythematosus) include: ANA (Antinuclear Antibodies) test: This test checks if there are antibodies against the nuclear structures of cells in your body. ANA is usually positive in more than 90% of people with SLE, but positive results of this test can also be seen in other diseases. Immunofluorescence Assays: These tests check if antibodies are attached to specific structures in cells. These tests can be useful in the diagnosis and investigation of SLE. Anti dsDNA test: This test checks if there are antibodies against dsDNA in your body. This test is usually positive in active cases of SLE. Acceleration rate test (ESR): This test is a measure to determine the acceleration rate of red blood cells in the test tube. An increase in ESR is usually seen in patients with SLE and indicates the presence of inflammation in the body. Complement Test: This test examines whether the level of complement (a series of proteins important to the immune system) is a reaction to normal inflammation and immunity. Decreased complement levels are commonly seen in patients with SLE. In addition, newer tests such as immune system efficiency tests, genetic tests, and molecular tests such as Polymerase Chain Reaction (PCR) are also being developed and used to diagnose SLE.

Conclusion: The anti-nuclear antibody (ANA) test has a high sensitivity for diagnosing SLE, meaning that in most cases, if a person has SLE, this test will be positive. However, it should be noted that this test may also be positive in healthy individuals. This means that it has a high false positive rate, so that when the test is positive, the person being tested may not have any signs of SLE. Therefore, anti-nuclear antibodies (ANA) alone cannot help diagnose SLE and require other tests and clinical evaluation by a doctor. For example, information that needs to be obtained includes clinical signs and symptoms, medical history, blood tests such as inflammation and anti-double stranded DNA (anti-dsDNA) tests, histology, and other tests. Of course, with the passage of time and the progress of science, we hope that more suitable and better ways and methods will be found to diagnose and treat SLE.

Keywords: SLE, ANA, Anti dsDNA, ESR

Acute myeloid leukemia encourages bone marrow mesenchymal stromal cells to express PI3K/AKT pathway genes through exosome secretion (Research Paper)

Maryam Nabigol,[1] Mehdi Allahbakhshian Farsani,[2,*]

1. Department of Hematology and blood bank, School of Allied Medical Sciences, Shahid Beheshti University of Medical Sciences, Tehran, Iran
2. Department of Hematology and blood bank, School of Allied Medical Sciences, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Introduction: Introduction: Acute Myeloid Leukemia (AML) is a heterogeneous clonal disorder characterized by the uncontrolled expansion and differentiation arrest of myeloid cells. While a wide range of therapeutic approaches have been developed for this neoplasm, therapy resistance and relapse are still the main obstacles. Currently, it is well known that the components of the bone marrow microenvironment, including mesenchymal stromal cells (MSCs), play a crucial role in leukemia growth and inducing anti-apoptotic signals, resulting in treatment failures of AML. PI3K/AKT signaling is one of the pathways involved in leukemic cell growth, whose hyperactivation in MSCs is associated with leukemogenesis. It is important to note that the interaction between MSCs and AML cells occurs either through direct cell-to-cell contact or indirectly through soluble mediators, including cytokines or extracellular vesicles (EVs). Exosomes are membrane-bound EVs that transfer various cargoes of chemicals and have an important role in pathophysiological conditions. In AML, leukemia-derived exosomes transform MSCs to create a microenvironment that promotes chemoresistance and leukemia survival. In this study, we examined the influence of AML-derived exosomes on the alteration in the expression of genes (PI3K, AKT, and mTOR) involved in PI3K/AKT signaling as a favoring leukemia pathway.

Methods: Methods: Exosomes were isolated from the HL-60 cell line. The morphology, size, and CD markers of isolated particles were assessed using TEM (Transmission Electron Microscopy), DLS (Dynamic Light Scattering) technique, and flow cytometry, respectively. Exosomal protein content was assessed using a BCA protein assay in order to determine the concentration of exosomes. MSCs were co-cultured with 20, 50, and 80 Î¼g/mL concentrations of AML-exosomes. The effect of AML-exosomes on the MSCs' metabolic activity was evaluated by an MTT assay. Gene expression analysis was performed by qRT-PCR.

Results: Results: Isolated exosomes were mostly positive for exosomal CD markers, including CD9, CD63, and CD81. According to the DLS results, the isolated particles' size range was between 70-110 nm. Our results demonstrated that treatment with 50 Î¼g/mL of AML-exosomes increased MSCs' metabolic activity, while exposure to 80 Î¼g/mL of exosomes

decreased the metabolic activity of these cells (P<0.05). Additionally, qRT-PCR results showed that PI3K, AKT, and mTOR were significantly upregulated in response to the treatment with exosomes in MSCs.

Conclusion: Conclusion: Since PI3K/AKT signaling is involved in leukemogenesis, our findings suggest that AML-exosomes induce MSCs to express PI3K/AKT genes and activate this pathway, which may contribute to the initiation and development of AML in the bone marrow microenvironment.

Keywords: Keywords: Acute myeloid leukemia, Exosome, Mesenchymal stromal cell, PI3K/AKT signaling pathway

Acute promyelocytic leukemia (APL) Detection (Review)

Shahla Rahmani,[1,*] Mahsa Loran Esfahani,[2] Sahar Ghiasi,[3]

1. MSc of Hematology and Blood banking Department of Medical Laboratory Sciences, School of Allied Medicine, Kermanshah University of Medical Sciences, Kermanshah, Iran
2. MSc of Hematology and Blood banking Department of Medical Laboratory Sciences, School of Allied Medicine, Kermanshah University of Medical Sciences, Kermanshah, Iran
3. MSc of Hematology and Blood banking Department of Medical Laboratory Sciences, School of Allied Medicine, Kermanshah University of Medical Sciences, Kermanshah, Iran

Introduction: Adult acute myeloid leukemia (AML) is a type of cancer in which the bone marrow makes a large number of abnormal blood cells. Leukemia may affect red blood cells, white blood cells, and platelets. There are different subtypes of AML. Acute promyelocytic leukemia (APL) is a subtype of AML. This leukemia occurs when genes on chromosome 15 switch places with some genes on chromosome 17, and an abnormal gene called PML::RARA is made. The PML::RARA gene sends a message that stops promyelocytes (a type of white blood cell) from maturing. APL usually occurs in middle-aged adults.

Methods: APL tests for diagnosis: Full blood count (FBC) measures the number of each type of cell in blood, Bone marrow biopsy Itâ€™s not normally possible to diagnose APL with just a blood test. There may be leukaemia cells in bone marrow that arenâ€™t in blood yet. Cytogenetics Specialist doctors will look at chromosomes 15 and 17 in the abnormal cells. If these chromosomes are mixed up, this confirms a diagnosis of APL. Polymerase chain reaction (PCR) test will check cells from bone marrow sample for the PML/RARA gene, because only people with APL have this gene. Immunophenotyping (flow cytometry), looks at the pattern of proteins on the surface of leukaemia cells. Together with the other tests, it helps doctors to confirm whether patient have APL or another type of leukaemia.

Results: Problems with severe bleeding and blood clots may occur. This is a serious health problem that needs treatment as soon as possible. Bleeding can become life-threatening if itâ€™s not treated straight away, So patient may need regular blood and platelet transfusions to lower risk of bleeding. Treatment of newly diagnosed APL includes: All-trans retinoic acid (ATRA) plus arsenic trioxide (ATO) for low-risk to intermediate-risk disease. ATRA plus combination chemotherapy followed by ATO for high-risk disease.

Conclusion: There are also some other tests you will need once youâ€™re diagnosed: Blood clotting system tests APL can affect the blood clotting

system in body, and increase the risk of bleeding and blood clots. General health tests: Patient will have a general health check to assess how patient is likely to cope with the side effects of treatment. This will involve a range of tests to check patient's heart, liver and kidney function, and may include screening for HIV and hepatitis.

Keywords: Acute promyelocytic leukemia, APL, PML::RARA, Diagnosis, AML

An overview of the GRAIL test as a novel laboratory approach for detecting circulating tumor DNA (Review)

Alireza Khanahmad,[1,*]

1. Department of Hematology and Medical Laboratory Sciences, Faculty of Allied Medicine, Kerman University of Medical Sciences, Kerman, Iran

Introduction: Cancer treatment is a major challenge for medical systems worldwide. It is proven that the decrease in mortality of malignancies is associated with early diagnosis. Limitations of the currently available laboratory tests such as the possibility of false results, invasive sampling, and high costs have made clinical and laboratory scientists design new panels for cancer diagnosis. Imaging, application of the biosensors, evaluation of the biomarkers, and investigation of the circulating tumor DNA (CT-DNA) have been introduced as cancer screening strategies in recent years. Small DNA fragments with a short half-life shed by tumor cells into the blood circulation are called CT-DNA. Apoptosis, necrosis, or active secretion are the possible mechanisms of releasing CT-DNA. In addition, Tumor origin, tumor stage, gender, and age are mentioned as variable factors that affect CT-DNA levels. Although detecting CT-DNA in the bloodstream is a hard procedure due to the simultaneous presence of circulating normal DNA, several laboratory tests are designed to evaluate the level of CT-DNA including GRAIL, IvyGene, CancerSEEk, ELSA-seq, PanSeer, and TEC-Seq. This study overviews the GRAIL (Gallery) test as a new strategy of CT-DNA evaluation for cancer screening.

Methods: A comprehensive search of the related keywords was done in the PubMed database. The most recent English articles were included.

Results: Machine learning and artificial intelligence (AI) are the basis for detecting and differentiating DNA methylation patterns of normal and tumor-circulating DNA in the GRAIL test. The test can screen and diagnose more than 50 types of malignancies by evaluating a panel with more than 100000 methylation sites in the whole genome of CT-DNAs. Several multi-centered and multi-patient clinical trials have investigated the efficacy of the GRAIL test. Studies showed that the GRAIL test can hold promise in the early-stage diagnoses of cancers. Thus, utilizing this test can result in a subsequent 39% reduction in 5-year mortality of cancers and a 26% reduction in overall cancer-related mortalities. However, the development of survival in cancer patients is highly dependent on cancer type. For example, an altered stage of diagnosis improves the survival rate for patients with prostatic cancer but does not affect the survival rate for patients with ovarian cancer.

Conclusion: Designing new strategies for early-detecting neoplasms is undeniably crucial. Among recently designed strategies, the GRAIL test is the

most widely investigated multiple cancer early detection (MCED) test. However, its pros and cons are not fully identified.

Keywords: GRAIL test, gallery test, circulating tumor DNA, neoplasm, screening

Anticancer effects of Epigallocatechin gallate based on Molecular Interactions (Research Paper)

Ghazal Rezazadeh Anbarani,[1,*] Bita Behboodian,[2]

1. Department of Biology, Faculty of Basic Sciences, Mashhad Branch, Islamic Azad University, Mashhad, Iran
2. Department of Animal Science, Kashmar Branch, Islamic Azad University, Kashmar, Iran

Introduction: Cancer is a major public health problem that is caused by abnormal growth of cells. There is no one single cause for cancer. Scientists believe that many factors produce cancer diseases. Ultraviolet, ionizing radiation, chemical carcinogens, components of tobacco smoke, alcohol, and biological carcinogens, such as viruses, and bacteria are reported factors. Most of these factors cause changes in genetics and affect the way cells work, and how they grow and divide. Removal of damaged and abnormal cells is possible through programmed cell death which is called apoptosis. Most anticancer drugs in clinical oncology are related to apoptotic signaling pathways to trigger cancer cell death. BCL-2 is a member of the BCL-2 family that inhibits apoptosis. Bcl-2 is widely believed to be an apoptosis suppressor gene. Overexpression of this protein in cancer cells may block or delay the onset of apoptosis. Therefore, inhibitors of the BCL-2 protein may have anticancer properties. In this Computational study, we investigate Molecular Interactions and anticancer effects of Epigallocatechin gallate by inhibiting BCL-2.

Methods: The investigation focused on the anticancer effect of Epigallocatechin gallate. Firstly, Hyperchem software was used to draw the Epigallocatechin gallate. The structure of the ligand was searched and drawn based on carbon atoms in this software. Subsequently, desired atoms were substituted for carbon atoms and energy optimization was carried out. Next, the BCL-2 protein (known for its role in inhibiting apoptosis) with a code of 4-MAN was extracted from https://www.rcsb.org/ and reviewed using Discovery software. The primary form of the protein in this software revealed its presence along with water molecules and co-crystal parts. In order to prepare the protein for analysis, unnecessary components such as water molecules and co-crystal parts were eliminated using specialized software. Autodock Vina was used for the docking of the studied ligand into the protein. Finally, all pharmacokinetic properties of Epigallocatechin gallate were thoroughly examined by utilizing the http://swissadme.ch/index.php website.

Results: After docking, Epigallocatechin gallate has formed two hydrogen bonds with amino acid ARG143 and one hydrogen bond with amino acid ALA146. This ligand possesses one Pi-cation connection. The binding energy level between the ligand and the protein is -7.842 kcal/mol. Investigations into

pharmacokinetic features were also studied. The molecular weight of this ligand, which has the formula C22H38O11, is 478.53. There are eleven receiver hydrogen atoms and nine donor hydrogen atoms. This compound is soluble with a low rate of GI absorption, TPSA: 53.200 Ã…Â², and lipophilicity: -2.97.

Conclusion: Considering the good energy level and interactions that were seen in the active site of the enzyme, it can be concluded that this ligand has inhibitory potential. However, the data is theoretical and in silico, and must be examined in clinical situations.

Keywords: Epigallocatechin gallate, BCL-2, Anticancer, Apoptosis, Inhibitor.

ANTIMICROBIAL PEPTIDES IN BIOMEDICAL APPLICATIONS (Review)

Dr. Issa Layali,[1] Zahra Toolabie,[2] Negin Mansouri,[3] Melika Chalook,[4,*]

1. Department of Biochemistry andÂ Â Â Â Â Â Â Â Â Â Biophysics, faculty of Advanced Sciences and Technology, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, IranÂ Â Â Â Â Â Â Â Â Â Â Â Â Â Â Â
2. Bachelorâ€™s student, Microbiology Group, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran
3. Tehran. Shariati street. Khaghani street , DaneshÂ dead end, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran
4. Bachelorâ€™s student, Microbiology Group, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran

Introduction: According to a 2014 report by WHO, antimicrobial resistance is a growing challenge that must be addressed. This resistance poses a significant problem for the treatment of diseases and infections and is typically caused by mutation, gene transfer, long-term or improper use of antimicrobials, survival of microbes after antimicrobial consumption, and the presence of antimicrobials in agricultural feeds, as well as hospital and medical device-induced biofilm infections. These issues affect millions of lives and require urgent innovative preventive approaches. One potential solution to these problems is antimicrobial peptides (AMPs), which are widely present in the environment. The biomedical field has a high demand for AMPs, which is an emerging topic involving both natural and synthetic pathways and some of which are currently undergoing clinical testing for approval. AMPs were discovered in 1939 by Rene Dubos isolated an antimicrobial agent named gramicidin from a soil Bacillus strain which protected mice from pneumococcal infection. Peptides can be categorized in multiple ways based on activity, mechanism of action, or structure and sequence. AMPs interact with bacterial cell membranes, impacting construction of the membrane, leading to cell death. AMPs can recruit and activate immune cells, controlling inflammation and increasing cell killing. AMPs also produce a variety of immune responses like activation, attraction, and differentiation of white blood cells. Immune cells also produce AMPs and can be the first line of defense against invading microbes. AMPs are mostly amphipathic, cationic peptides that display antimicrobial activity against bacteria, fungi and viruses, for example in bacteria they interact with specific constituents of the bacterial cell envelope resulting in depolarization, destabilization or disruption of the bacterial plasma membrane leading to bacterial cell death. Naturally occurring AMPs have been used as design templates for synthetic AMPs, some of which have reached the stage of clinical trials like the he synthetic peptide IDR-1018 prevented biofilm formation by S.aureus and other species by blocking ppGpp which is a signal molecule in biofilm formation.

Methods: Currently the most commonly used method of obtaining AMPs is chemical synthesis. In clinical trials and commercial markets, large quantities of AMPs are needed to fulfil basic scientific study requirements. Isolation from natural sources and chemical synthesis are not costeffective, For cost-effective production of large peptides biological systems such as bacteria and yeast are required, Escherichia coli and yeast are two major systems used to produce recombinant antimicrobial peptides. Summarising over many years scientists have developed methods of obtaining AMPs not only through their direct isolation from organisms but also chemical methods for the synthesis of these peptides and finally more efficient methods of obtaining recombinant AMPs by genetic engineering.

Results: AMPs isolated from vertebrates are studied due to their potency against a wide range of microorganism. The most commonly found and highly investigated antimicrobial peptides are Defensins and Cathelicidins. Defensin is positively charged antimicrobial peptide composed of 29â€“34 amino acids in a sheet structure and Cathelicidin is a multifunctional peptide that has conserved pro-peptide sequences and is identified as an N terminal signal peptide. Crohnâ€™s disease can be eliminated by inducing Defensins. In patients suffering from periodontitis, Defensins play a critical role in bone repairmen and also they have the capability to suppress inflammatory cytokines and is also used in therapy for the herpes simplex virus. The potency of Cathelicidins LL-37 was examined on human MDMs and THP-1 cells, which were infected with Mycobacterium tuberculosis these cells were infected with the M.tuberculosis for four hours, followed by treatment with 1 g/m of LL 37 for 24 h, it was concluded that LL-37 mediates the activation of autophagy via the P2RX7 receptor and inhibits the growth of Mycobacterium tuberculosis. In another study the Cathelicidins peptides have shown antifungal activity against Fusarium, Aspergillus, Cryptococcus, and Candida.

Conclusion: AMPs can be used as new therapeutics, enhancing antimicrobial treatment and reducing resistance. Despite challenges associated with the of AMPs including stability and half-life issues, the market is expected to benefit from growing interest in innovative therapeutics containing antimicrobial peptides for rare diseases.

Keywords: amps, antimicrobial, peptides

Apoptosis in Lung Cancer: A Dualistic Role and Therapeutic Implications (Review)

Asal Teimoori,[1] Maryam Seyedolmohadesin,[2,*]

1. Bachelor's student. Department of Microbiology, Faculty of Advanced Science and Technologies, Tehran Medical Science, Islamic Azad University, Tehran, Iran.
2. Department of Genetics, Faculty of Advanced Science and Technologies, Tehran Medical Science, Islamic Azad University, Tehran, Iran.

Introduction: Apoptosis, a tightly controlled process of programmed cell death, plays a pivotal role in regulating tissue of growth and development, immune responses to infections and injuries, and various physiological processes. Inthe context of lung cancer, apoptosis assumes multifaceted role, exhibiting both beneficial and a detrimental aspects. When cancer cells succumb to apoptosis, it contributes to curbing tumor growth and to dissemination. However, resistance to apoptosis by cancer cells fosters their proliferation and metastasis,exacerbating the malignancy.

Methods: To comprehensively investigate the role of apoptosis in in Lung cancer, an extensive literature search was conducted across PubMed, Google Scholar, and NCBI databases. This search yielded 22 relevant articles that were meticulously reviewed and analyzed to gain a deeper understanding of this topic.

Results: Several mechanisms orchestrate the regulation of apoptosis in lung cancer. Epigenetic alterations, such as DNA methylation, can modulate gene expression, impacting apoptosis susceptibility. Notably,DNA methylation of the p76INK4a gene, which encodes a protein inhibiting cyclin-dependent kinases (CDKs),a is frequently observed in lung cancer This dysregulation of CDKs derails cell cycle regulation, potentially leading to apoptosis resistance. Mutations genes that regulate apoptosis alsos significantly influence acel'ss susceptibility to this1 process.The p53 gene stands as a crucial regulator of apoptosis. In lung cancer, mutations in p53 are commonly encountered. This gene normally functions as a tumor suppressor, preventing cells with damaged DNA from replicating However, mutated / P53 loses its regulatory capacity, allowing damagedc cells to proliferate despite their increased likelihood of malignancy. This genetic aberration fosters the development of apoptosis-resistant tumors. Furthermore, tumors can produce antiapoptotic proteins that inhibit the execution of apoptosis. One notable example is survivin, an antiapoptotic protein that blocks the activation of caspases, enzymes essential for apoptosis initiation. Excessive survivin production can prevent cancer cells from undergoing programmed cell death.

Conclusion: The intricate interplay of these regulatory mechanisms dictates the susceptibility of of lung cancer cells to apoptosis. Understanding these molecular pathways holds immense promise for the development of targeted and effective therapies that selectively eliminate cancer cells while preserving normal tissue functionality. By targeting these regulatory elements, we c can harness the therapeutic potential of apoptosis to combat lung cancer more effectively.

Keywords: Apoptosis, Lung Cancer, Epigenetics, Tumorigenesis

Apoptosis induction by Ganoderic Acid-A via increase Autophagy-Related Genes in Nalm-6 cells (Review)

Hanie Shafiee,[1,*] Gholamhossein Tamaddon,[2] Reza Fotouhi,[3]

1. Department of Hematology and Blood bank, Department of Medical Laboratory Sciences, School of Paramedical Sciences, Shiraz university of medical Sciences, Shiraz,Iran
2. Department of Hematology and Blood bank, Department of Medical Laboratory Sciences, School of Paramedical Sciences, Shiraz university of medical Sciences, Shiraz,Iran
3. Department of Biotechnology, School of Medicin, Qom University of Medical Sciences, Qom, Iran.

Introduction: Acute lymphoblastic leukemia (ALL) is the most common leukemia in children, which is associated with a high relapse rate despite prevalent therapies. Ganoderic acid A (GAA) is one of the bioactive compounds of Ganoderma lucidum, which possesses potential antileukemic properties. This study aimed to investigate the effect of the GAA extract on the expression of autophagic genes and the autophagy induction in the ALL cell line.

Methods: NALM-6 cells were cultured in vitro, and the optimal treatment concentration of GAA was determined by an MTT assay. Flow cytometry was used to determine the death of NALM-6 cells caused by GAA treatment by utilizing FITC-conjugated propidium iodide (PI) and annexin V staining. The expression levels of autophagic genes LC3, BECLIN, ATG5, ATG10, FIB200, and AMBRA before and after treatment with GAA were monitored using real-time polymerase chain reaction.

Results: The results of the MTT test indicated that the half maximum inhibitory concentration (IC50) of leukemic cells after 48 hours of treatment with G. lucidum is 140 Î¼g/mL. In addition, the flow cytometry results showed an increase of 40.5% in apoptosis and death of cells at a 140-Î¼g/mL concentration of GAA after 48 hours. Besides, GAA treatment up regulated expression levels of LC3 (P = 0.024), BECLIN (P = 0.035), ATG5 (P = 0.024), ATG10 (P = 0.024), FIB200 (P = 0.024), AMBRA (P = 0.024) in NALM-6 compared to the control groups.

Conclusion: GAA can induce apoptosis in NALM-6. It also increases the expression of autophagy genes.

Keywords: Acute Lymphoblastic Leukemia, Ganoderic Acid A, Autophagy

Assessing the Efficacy of the MacMaster Fecal Technique in Identifying Oxfendazole efficacy in Parascaris equorum (Research Paper)

Negar Najafifard,[1] Fatemeh Jalousian,[2,*] Negar Hemmati,[3]

1. DVM student, faculty of veterinary medicine, Tehran university
2. Department of parasitology, faculty of veterinary medicine, Tehran university
3. DVM student, faculty of veterinary medicine, Tehran university

Introduction: The McMaster method is widely used in veterinary parasitology to accurately measure the quantity of eggs in stool samples. The technique employs a McMaster slide, which includes a chamber where a specific volume of stool suspension is added. Researchers examine the checkered pattern on the slide to count the number of eggs present in each square. This method is particularly valuable for monitoring resistance to anti-parasitic drugs. To assess resistance, the number of parasite eggs in fecal samples is counted both before and after treatment, and the results are subsequently compared. The MacMaster method is highly regarded as an effective, cost-efficient, and time-saving approach for evaluating resistance to anti-parasitic treatments. The main objective of this study was to evaluate the effectiveness of Oxfendazole as a treatment for Parascaris equorum infections in stable horses located in Tehran province.

Methods: In this study, we collected a total of 38 samples of horse fecal samples directly by performing rectal touch. These samples were then transferred to the parasitology laboratory at the Faculty of Veterinary Medicine, University of Tehran. To detect the presence of Parascaris equorum eggs, we employed a flotation technique with saturated sodium chloride solution (1.202g/m density at 25Â°C). The eggs of P. equorum are easily distinguishable from those of other parasites and measure approximately 90-100 Âµm in diameter. Subsequently, we counted the number of eggs in each sample using the McMaster method. For horses diagnosed with Parascaris equorum infection, we administered treatment with oxfendazole. After the completion of treatment, we conducted a follow-up sampling on the fourteenth day, and the stool samples collected after this period were further examined using the McMaster method.

Results: The results of the stool test showed that 4 horses, which were 10.5% of the tested population and aged 36 months or older, were infected with Parascaris equorum. The average egg count per gram of feces in these infected horses was determined to be 625Â±132.28. After treating these 4 infected cases with oxfendazole, a subsequent test was conducted on the 14th day to evaluate the effectiveness of the drug. The results displayed acceptable efficiency of the treatment, as the average number of eggs

observed in the feces on the 14th day after treatment was 28.29Â± 25.5. Furthermore, the drug exhibited an efficiency rate exceeding 65%.

Conclusion: The present study discovered the presence of Parascaris equorum infection in horses kept in stable conditions. The significant daily excretion of Parascaris equorum eggs makes a stool test a suitable method for detecting the presence of Ascarid eggs. To date, there have been no reported incidents of Parascaris equorum developing resistance towards fenbendazoles on a global scale. However, the emergence of resistance to this specific anthelmintic among cyathostomins presents a significant challenge. The study's findings exhibited a marked reduction in Fecal Egg Count (FECRT>95%) and a Low Confidence (LCL>90%) when employing Oxfendazole. Anti-parasitic treatment in horses should be administered following diagnostic testing, while also avoiding the excessive use of anthelmintic drugs. The concurrent application of multiple drugs can help prevent the development of drug resistance within the parasite population. To effectively control and prevent infection with the Parascaris equorum parasite, it is essential to implement measures such as stable sterilization and raise awareness among horse owners regarding its transmission among foals, mares, and stallions. In the context of the valuable horse breeding industry, the McMaster method emerges as a cost-effective approach for monitoring the efficacy of anti-parasitic drugs. By training veterinary experts and establishing a standardized McMaster test protocol, the effectiveness of expensive drugs can be significantly enhanced.

Keywords: anthelmintic resistance, cyathostomins, equine parasitology, fecal egg counts.

Biology of blood and brain transplantation review article (Review)

kosar reihanpour baghkhoshki,[1,*]

1. Bachelor student of Microbiology Islamic Azad University Sirjan Sirjan, Kerman, Iran

Introduction: The primary process of plasma membrane invagination results in the formation of an early sorting endosome, a saucer-shaped structure that contains absorbed proteins and genetic elements from the cytoplasm as well as cell membrane proteins. After secondary fusing of the endosomal limiting membrane, early sorting endosomes develop into late sorting endosomes, which finally arrive in MVBs. In this opinion, we present a platform of neuroimmune organoids created from induced pluripotent stem cells to identify the variety of human cell-based brain TRM models and investigate their functions in tissue homeostasis and illness.

Methods: After being planted in culture plates, the MSC cell line was split into two groups based on whether BDNF was present or not. The BMExos group consisted of culture plates with a BDNF protein solution, while the MExos group consisted of culture plates without a BDNF solution. Data were gathered on a particular form and combined regarding the mode of administration, medication monitoring, risk factors unique to seizures, neurological diseases linked to seizures, prophylaxis against seizures, and the incidence of seizures.

Results: When BDNF was added to the culture media, the shape and development of MSCs remained mostly unchanged. Analysis was done on the extraction ratio between BMExos and MExos. In accordance with local policies, prophylaxis of seizures was administered to all patients. Due to graft rejection, death, and financial constraints on traveling to finish testing, sixteen were left unfinished. Out of the 13 recipients, 11 finished their pre- and post-HCT imaging studies.

Conclusion: The 3D-CC-BMExos scaffoldsâ€™ high porosity ratio and exceptional biocompatibility may offer a favorable milieu for both in vitro and in vivo cell proliferation and differentiation. In summary, 3D-CC-BMExos therapy has been shown to improve neuronal regeneration following traumatic brain injury (TBI) and has the potential to be used in clinical settings in the future. Utilizing state-of-the-art molecular technologies to study the impact of lifestyle and systemic interventions has provided understanding of the cellular and molecular targets as well as the origin tissues of pro-youthful and pro-aging factors found in blood.

Keywords: traumatic brain injury ,Neurodegenerative diseases, BDNF,Seizures ,Prophylaxis

Botulinum toxin in the treatment of gential disorders Review Article (Review)

shokoufeh varmaziyar,[1] Haniye Fayezi,[2,*]

1. B.sc student of Microbiology Islamic Azad University of Shiraz
2. M.sc student of Pathogenic Microbes Islamic Azad University North Tehran Branch

Introduction: Botulinum toxin type BoNT-A produced by Clostridium botulinum is a potent neurotoxin, commonly known as Botox, for more than 30 years it has played an important role in the field of medicine, especially in the treatment of diseases of the lower infectious tract. This potent neurotoxin, derived from Clostridium botulinum, has revolutionized the management of various medical conditions through its ability to selectively inhibit the release of acetylcholine at the neuromuscular junction, thereby providing therapeutic benefits. During the last three decades, the use of botulinum toxin in urological practice has expanded significantly. Initially, it was primarily used to manage neurogenic detrusor overactivity, but its uses have since expanded to include various lower urinary tract disorders, including overactive bladder, interstitial cystitis, and benign prostatic hyperplasia. By targeting the root cause of these conditions, Botox injections may provide long-term relief and improve the overall quality of life for sufferers. By targeting specific muscles in the pelvic floor and genital area, Botox can effectively relax overactive muscles and reduce symptoms associated with genital disorders.

Methods: Intravesical injections of botulinum toxin (BoNT) are effective in reducing urinary urgency and incontinence.It temporarily inhibits detrusor contraction by blocking the release of acetylcholine (Ach) from the preganglionic and postganglionic nerves. BoNT-A also blocks ATP release from purinergic nerves in the detrusor muscle. In the tracheal nerve, BoNT-A injection significantly reduces ATP release in the urothelium and increases nitric oxide (NO) release from the urothelium. BoNT-A injection into the urethra or bladder can beused to treat conditions such as detrusor-sphincter dysjunction, neurogenic or idiopathic detrusor overactivity incontinence, bladder hypersensitivity, overactive bladder, and interstitial cystitis/chronic pelvic pain.

Results: Recent advances in the formulation and delivery of botulinum toxin have improved its therapeutic potential, leading to improved patient outcomes and increased prescribed comfort. In addition, ongoing research continues to examine innovative applications of botulinum toxin, revealing promising prospects for its continued evolution in the management of low urinary tract disorders. Clinical evidence collected over the years has consistently demonstrated the efficacy and safety of botulinum toxin in the treatment of lower urinary tract disorders. The targeted action of this toxin on the detrusor

muscle has provided relief for patients suffering from urinary incontinence and urgency with the desired side effect profile.

Conclusion: Consequently, the evolving landscape of research and medical innovation continues to uncover new potential applications for botulinum toxin A in the treatment of genital tract disorders. As more studies and clinical trials progress, integrating Botox into the treatment paradigm for theseconditions promises a brighter future for patients and healthcare providers alike. In conclusion, a 30-year review of botulinum toxin in lower urinary tract disorders underscores its enduring and evolving impact on the medical landscape. With a strong safety and efficacy profile, botulinum toxin is the cornerstone of comprehensive management of lower urinary tract disorders, along with ongoing research and advances.

Keywords: Botulinum toxin, Urogenital Disorders, Botox, Clostridium botulinum

Cancer Metabolism (Research Paper)

Tara Lotfalizadeh,[1,*] Diba,[2] Hananeh Tashakor,[3] Issa Layali,[4]

1. Tehran Islamic Azad University of Medical Sciences
2. Tehran Islamic Azad University of Medical Sciences
3. Tehran Islamic Azad University of Medical Sciences
4. Tehran Islamic Azad University of Medical Sciences

Introduction: Carnitine is a compound that plays a crucial role in the transport of long-chain fatty acids into the mitochondria for energy production. It is also involved in the synthesis of acetylcholine, a neurotransmitter that is essential for muscle contraction and nerve signaling. Cancer cells have a high demand for energy, and they often rely on fatty acid oxidation to meet this demand. Carnitine plays a critical role in this process, and studies have shown that cancer cells have higher levels of carnitine transporters than normal cells.

Methods: To delve into the double-edged nature of carnitine in cancer metabolism, a thorough literature search was conducted across PubMed, Google Scholar, and NCBI databases. This search resulted in 22 relevant articles, which were painstakingly reviewed and analyzed to gain a deeper understanding of this topic.

Results: The Effects of Carnitine on Cancer Cells: 1. Carcinogenic effects: Transporting long-chain fatty acids into the mitochondria: Carnitine is essential for the transport of long-chain fatty acids into the mitochondria, where they can be oxidized for energy. Cancer cells have a higher demand for energy than normal cells, and they rely on fatty acid oxidation to meet this demand. Stimulating fatty acid oxidation: Carnitine can stimulate fatty acid oxidation by increasing the activity of enzymes involved in the process. This can lead to an increase in the production of ATP, the cellular energy currency. Promoting angiogenesis: Angiogenesis is the formation of new blood vessels, which is essential for the growth and spread of cancer. Carnitine can promote angiogenesis by increasing the expression of pro-angiogenic genes. 2. Therapeutic effects: Studies have shown that carnitine can have a number of effects on cancer cells, including: Inhibiting the growth of cancer cells: Carnitine can inhibit the growth of cancer cells in vitro and in vivo. This may be due to its ability to block the transport of long-chain fatty acids into the mitochondria, or to its ability to stimulate fatty acid oxidation. Enhancing the effectiveness of chemotherapy drugs: Carnitine can enhance the effectiveness of chemotherapy drugs by increasing the uptake of the drugs into cancer cells. This may be due to its ability to increase the permeability of the cell membrane to the drugs. Promoting apoptosis: Carnitine can promote apoptosis in cancer cells by increasing the expression of pro-apoptotic genes. This may be due to its ability to deplete the cells of energy.

Conclusion: Carnitine is a compound that plays a complex role in cancer metabolism. It can have both beneficial and harmful effects on cancer cells. On the one hand, carnitine's ability to promote fatty acid oxidation and angiogenesis could support cancer cell growth and spread. On the other hand, carnitine's potential to induce apoptosis, enhance chemotherapy efficacy, and regulate gene expression could be harnessed for therapeutic purposes. More research is needed to fully understand the role of carnitine in cancer treatment, but it is a promising target for new therapies

Keywords: Carnitine, Cancer, Apoptosis, Angiogenesi

CAR T-Cell Therapy for Non-B-cell acute leukemia (Review)

Mahdi Bagheri,[1,*] Narges Zare,[2]

1. Gastroenterohepatology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran
2. Department of Biological Science and Technology, Faculty of Nano and Bio Science and Technology, Persian Gulf University, Bushehr, Iran

Introduction: Introduction: T-cell acute lymphoblastic leukemia (T-ALL) and acute myeloid leukemia (AML) are both included in the category of non-B-cell acute leukemia. AML is a type of hematological cancer that develops from the aberrant clonal expansion of primary myeloid cells. The malignant transformation of immature T-cell progenitors causes T-ALL, a very invasive type of hematological cancer. The therapeutic efficacy of available therapies for refractory or relapsed (R/R) non-B-cell acute leukemia is currently constrained. Given its encouraging outcomes in the treatment of B-cell acute lymphoblastic leukemia (B-ALL), chimeric antigen receptor (CAR)-T cell therapy may be a potential strategy to treat non-B-cell acute leukemia in such circumstances. We list the characteristics of non-B-cell acute leukemia and the effectiveness of CAR-T for treating it in this review. Benefits of CAR-T therapy When compared to TCRs, CARs are independent of the major histocompatibility complex (MHC) and can detect specific antigens presence on the surface of cells. Because they are MHC independent, CAR-T cells are better suited for the treatment of tumors. By identifying tumor-specific antigens (TSA) on the surface of tumor cells, CAR-T cells destroy cancerous cells while causing the least amount of damage to healthy tissues. CAR-T therapy challenges for non-B-cell acute leukemia Fratricide, malignant contamination, T-cell aplasia for T-ALL, antigen heterogeneity, and immunosuppressive environments are only a few of the particular difficulties facing the development of CAR-T treatment for non-B-cell acute leukemia. CAR-T therapy's antigen targets for treating T-ALL About 80%â€“95% of T-ALL or T lymphoblastic lymphoma (TLL) display CD5, a surface marker of T-cell malignancies. Normal expression of CD5 on mature peripheral blood T cells, thymocytes, and certain B-cell lymphocytes in healthy tissues promotes CAR-T cell fratricide. For CD5+ hematological malignancies, CD5 is a hopeful target. All mature T-cells largely display the pan-T-cell surface antigen CD3, but due to the total fratricide of CAR-T cells, the development of CAR-T targeting CD3 is restricted in the early stages. Clinical use of CARs targeting CD3 is constrained due to the fact that T-ALL and TLL cells produced from patients often display cytoplasmic CD3 (cCD3) rather than membrane CD3 (mCD3). Over 95% of ALL, 30% of AML, and some lymphomas express CD7, a member of the Ig superfamily. Initially, CAR-T cells directed against CD7 displayed total fratricide and could not be used; however, in recent clinical trials, CD7 CAR have demonstrated satisfactory efficacy and safety. Fratricide can now be eliminated using gene editing technologies such as CRISPR-Cas9, TALEN, or PEBL. Most TLLs and certain T-ALLs express CD4, and this

expression is only found in the hematopoietic compartment. As the CAR's target, it may lessen the adverse effects on tissues other than hematological ones. However, the survival of CD4 CAR T cells after the excision of tumor cells can result in the aplasia of CD4 positive T cells and an illness similar to HIV/AIDS. CAR-T therapy's antigen targets in AML CD123, which is expressed at low levels in early hematopoietic cells such hematopoietic stem/progenitor cells (HSPCs), is one potential target for AML. Because of CD123 ability that can discriminate HSC from leukemia stem cells(LSCs), to eradicate LSCs and maintain normal HSC, TALEN gene-editing technology was employed to create a TCRÎ±Î² negative allogeneic CD123 CAR (UCART123), which eradicate primary AML. The anti-tumor efficacy, proliferation, and perseverance of CD33 CAR-T cells may be impacted by various costimulators, distinct generation CAR constructions, and PI3K inhibitors. CD33 CAR demonstrated effective anti-AML activity in vitro. More than 80% of LSCs and AML blasts express C-type lectin-like molecule-1 (CLL-1). In pre-clinical studies, CLL1 CAR shown encouraging anti-tumor effectiveness, and in AML patients, it demonstrated anti-AML efficacy. Most AML blasts and AML stem/progenitor cells express CD70, a tumor necrosis factor (TNF) receptor ligand. In the clinical trial, more research on the CD70 CAR's efficacy and safety in patients is required.

Methods: This is a review article and doesn't have this section.

Results: This is a review article and doesn't have this section.

Conclusion: Conclusion T-ALL and AML are types of leukemia that have more complicated morphological characteristics than B-ALL and are linked to a poor prognosis. T-ALL and AML also have fewer therapy choices available after recurrence or refractory. Given the enormous success of CAR-T cell therapy in B-cell malignancies, adopting a similar strategy for non-B-cell acute leukemia seems to be a potential path for the creation of better therapies.

Keywords: CAR T-Cell; Non-B-cell acute leukemia; T-ALL; AML

Cardiovascular manifestations and role of Endotheliopathy in covid-19 patients (Review)

Motahare Sadeghi,[1,*] Younes Sadeghi bojd,[2] kiana tavakoli,[3] abolfazl miri,[4]

1. Student research committee, school of Allied medical science, zahedan university of medical science, zahedan, Iran
2. Department of Laboratory Sciences, School of Allied Medical Sciences, Zahedan University of Medical Sciences, Zahedan, Iran
3. Student research committee, school of Allied medical science, zahedan university of medical science, zahedan, Iran
4. Student research committee, school of Allied medical science, zahedan university of medical science, zahedan, Iran

Introduction: SARS-CoV-2, the virus that causes coronavirus disease 19 (COVID-19), is associated with a bewildering array of cardiovascular manifestations, including myocardial infarction and stroke, myocarditis and heart failure, atrial and ventricular arrhythmias, venous thromboembolism, and microvascular disease. Furthermore, the pulmonary infiltration and edema, and later pulmonary fibrosis, in patients with COVID-19 is promoted by endothelial alterations including the expression of endothelial adhesion molecules and chemokines, increased intercellular permeability, and endothelial-to-mesenchyme transitions. Venous thrombosis and pulmonary thromboembolism are most likely associated with an endothelial defect caused by circulating inflammatory cytokines and/or direct endothelial invasion by the virus.

Methods: We searched databases including PubMed, Medline, Cochrane, Embase, Scopus and Web of Science databases from 2020 to 2023 and read articles related to the topic.

Results: In 29 reviewed articles, 1465 patients were examined, which showed that there were specific changes in biomarkers related to coagulation, the cytokine storm and inflammation.6 .4% of patients with COVID-19 had an elevated troponin I on admission, a hypersensitive marker for cardiac myocyte injury .When these authors looked at acute cardiac injury as an outcome, defined as elevation in troponin I or diagnostic imaging findings, they found a similar 7% overall incidence in patients with COVID-19,but this was increased to 22% among ICU patients(P < .001).

Conclusion: A comprehensive characterization of COVID-19â€“associated endotheliopathy, and an understanding of the mechanisms of acute and chronic endothelial alterations induced by SARS-CoV-2, will lead to an improved understanding of the many manifestations of COVID-19 and a refined management approach for this and other vasculotropic viral diseases. There for immune response induced by the SARS-CoV2 can virus resulted in

inflammatory-associated myocarditis and increased oxygen consumption, which disturbed the imbalance of cardiac oxygen supply resulting in plaque rupture and MI.

Keywords: COVID-19; SARS-CoV2; endothelium; Heart

Carnitine: A Double-Edged Sword in Cancer Metabolism (Review)

Tara lotfalizadeh,[1,*] Diba Ahmad,[2] Hananeh Tashakori,[3]

1. Tehran Islamic Azad University of Medical Sciences
2. Tehran Islamic Azad University of Medical Sciences
3. Tehran Islamic Azad University of Medical Sciences

Introduction: Carnitine is a compound that plays a crucial role in the transport of long-chain fatty acids into the mitochondria for energy production. It is also involved in the synthesis of acetylcholine, a neurotransmitter that is essential for muscle contraction and nerve signaling. Cancer cells have a high demand for energy, and they often rely on fatty acid oxidation to meet this demand. Carnitine plays a critical role in this process, and studies have shown that cancer cells have higher levels of carnitine transporters than normal cells.

Methods: To delve into the double-edged nature of carnitine in cancer metabolism, a thorough literature search was conducted across PubMed, Google Scholar, and NCBI databases. This search resulted in 22 relevant articles, which were painstakingly reviewed and analyzed to gain a deeper understanding of this topic.

Results: The Effects of Carnitine on Cancer Cells: 1. Carcinogenic effects: Transporting long-chain fatty acids into the mitochondria: Carnitine is essential for the transport of long-chain fatty acids into the mitochondria, where they can be oxidized for energy. Cancer cells have a higher demand for energy than normal cells, and they rely on fatty acid oxidation to meet this demand. Stimulating fatty acid oxidation: Carnitine can stimulate fatty acid oxidation by increasing the activity of enzymes involved in the process. This can lead to an increase in the production of ATP, the cellular energy currency. Promoting angiogenesis: Angiogenesis is the formation of new blood vessels, which is essential for the growth and spread of cancer. Carnitine can promote angiogenesis by increasing the expression of pro-angiogenic genes. 2. Therapeutic effects: Studies have shown that carnitine can have a number of effects on cancer cells, including: Inhibiting the growth of cancer cells: Carnitine can inhibit the growth of cancer cells in vitro and in vivo. This may be due to its ability to block the transport of long-chain fatty acids into the mitochondria, or to its ability to stimulate fatty acid oxidation. Enhancing the effectiveness of chemotherapy drugs: Carnitine can enhance the effectiveness of chemotherapy drugs by increasing the uptake of the drugs into cancer cells. This may be due to its ability to increase the permeability of the cell membrane to the drugs. Promoting apoptosis: Carnitine can promote apoptosis in cancer cells by increasing the expression of pro-apoptotic genes. This may be due to its ability to deplete the cells of energy.

Conclusion: Carnitine is a compound that plays a complex role in cancer metabolism. It can have both beneficial and harmful effects on cancer cells. On the one hand, carnitine's ability to promote fatty acid oxidation and angiogenesis could support cancer cell growth and spread. On the other hand, carnitine's potential to induce apoptosis, enhance chemotherapy efficacy, and regulate gene expression could be harnessed for therapeutic purposes. More research is needed to fully understand the role of carnitine in cancer treatment, but it is a promising target for new therapies.

Keywords: Carnitine, Cancer, Apoptosis, Angiogenesi

Cell membrane camouflaged nanoparticles for drug delivery (Research Paper)

Amirhossein Salati,[1,*] Kamand Karimi Taheri,[2] Melika Eslamian Dehkordi,[3] Issa Layali,[4]

1. Bachelorâ€™s student, Microbiology group, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran.
2. Bachelorâ€™s student, Microbiology group, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran.
3. Bachelorâ€™s student, Microbiology group, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran.
4. Department of Biochemistry and Biophysics, Faculty of Advanced Sciences and Technology, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran.

Introduction: Nanoparticles can accumulate at action sites, such as tumors, when coated. This represents a significant advancement in improving therapeutic indicators. Coated nanoparticles are a new category of nano biomimetic drugs. They have the flexibility of artificial nanoparticles. They also have the unique characteristics of cell membranes. Drugs prepared by traditional methods have two negative properties. They include side effects, non-specific toxicity, and the need for high doses. High doses are necessary for effectiveness. However, combination drugs based on nanoparticle coating technology have preferred accumulation properties. They also have unique physical and chemical properties. They have better drug release and increased drug encapsulation. Furthermore, nanodrugs can regulate themselves in larger dimensions. They can also produce themselves in these dimensions. Nanomedicine aims to make therapeutic nanofibers circulate in the body for a long time. This helps transfer them effectively and increases their therapeutic and clinical efficiency. Typically, researchers use polyethylene glycol (PEG) to stabilize nanoparticles and prevent opsonization. However, recent research shows that the immune system reacts to anti-PEG. In response, scientists have turned to another approach. They have turned to red blood cells (RBC). RBCs play a role in long-distance transportation in the human body. The process of preparing nanoparticles along with the RBC membrane involves two steps. First, we place RBCs in a hypotonic environment to remove their internal components. Then, a permeable membrane extrudes them to synthesize RBC-NPs. Mechanical extrusion combines the vesicles with polymeric PLGA nanoparticles. RBC-NPs have a much longer half-life compared to PEG. They also exhibit immune-compatible systemic properties. Additionally, this method allows for the modification of nanoparticles with ligands. Amino, hydroxyl, and sulfhydryl groups form the basis of the ligands. We can use conjugation techniques and targeted ligands

to modify the nanoparticles. The cell's intrinsic homotypic and heterotypic membranes have adhesive properties. In addition to targeted ligands. You can use these to prevent extra synthesis stages.

Methods: This article uses an extensive search of PubMed - NCBI and Google Scholar databases - and the study of almost 30 articles and analysis of the studies done in the last ten years on this issue has been done.

Results: Coated nanoparticles consist of natural and artificial components. They can use the natural component for biochemical methods. A cell membrane supports it. This can affect drug delivery. It can be very difficult or even impossible to achieve with traditional methods. The artificial component has nanoparticles and an artificial core. Doctors can use multiple drugs for drug delivery and produce preferential effects. Furthermore, you can adjust the artificial core to possess specific properties. This results in greater effectiveness and efficiency.

Conclusion: Bio-mimetic nanoparticles have a very high therapeutic potential. They incorporate the characteristics of both natural and artificial platforms. In general, the outlook for combination drug delivery is very promising. Coated nanoparticles form the basis. It could treat many diseases.

Keywords: Nanoparticles/RBC/PLGA/Nano/Nanomedicine

Chemical contamination in the extracted DNA may affect high-throughput PCR-based methods (Research Paper)

Ata Shirizadeh,[1] Mozhdeh Ebrahimpur,[2] Somaieh Soltani,[3] Ghasem Solgi,[4,*]

1. Department of Immunology, School of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran.
2. Department of Immunology, School of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran.
3. Department of Medicinal Chemistry, School of Pharmacy, Tabriz University of Medical Sciences, Tabriz, Iran.
4. Department of Immunology, School of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran.

Introduction: The purity of the extracted DNA is critical for successful molecular testing. This study aimed to compare the effect of various DNA extraction methods, extraction processes, and sources of disposables such as microtubes on PCR results.

Methods: DNA extraction from whole blood was performed by four different approaches: chloroform-based, sodium perchlorate-based, heat-assisted salting out, and solid phase extraction. Extracted DNA was evaluated by Nanodrop spectrophotometry and used for HLA typing by PCR-based methods.

Results: The lowest and highest concentrations of extracted DNA were observed in the column-based and heat-assisted methods, respectively. Maximum A260/A230nm ratios were observed in the sodium perchlorate and chloroform methods using A and D microtubes, respectively. Moreover, significant differences were observed in terms of the A260/A230nm ratio of the extracted DNA in chloroform-based extraction using four different types of microtubes. Analysis of extracted DNA using different microtubes in the same method through PCR-SSP and PCR-SSOP indicated that PCR-SSP was run without any issue with interpretable results, but PCR-SSOP was disturbed using the same samples, and results were uninterpretable.

Conclusion: Our results indicate that the chemical contaminations derived mainly from microtubes may decrease the quality of DNA and consequently interfere with the amplification or hybridization reactions in the PCR-SSOP method for HLA typing.

Keywords: DNA extraction-microtube-PCR, HLA typing

Chimeric antigen receptor (CAR)-engineered immune cell therapy in hematological malignancies: CAR T, CAR NK, and CAR macrophage (Review)

Batol Abbasi,[1,*]

1. Tabriz University of Medical Sciences

Introduction: For many years, cancer treatment methods are usually chemotherapy, surgery, and radiation therapy. Despite these methods helping to cure the disease, most diseases have a poor prognosis. In recent years, there have been new advances in cell therapy with the production of chimeric antigen receptors (CARs) that destroy cancer cells. CARs are recombinant receptors that have been engineered so that immune cells can target and destroy specific antigens on the surface of cancer cells. Recently, researchers have been able to treat hematological malignancies through CAR-T cell. However, significant toxicity and limitations of CAR-T cell immunotherapy have led researchers to turn their attention to other immune cells as potential candidates for CAR engineering. Consequently, recently researchers have considered the use of CAR-Macrophage and CAR-NK cell therapy as a new therapeutic option for the treatment of hematologic malignancies. This review will describe recent advances in the engineering of CAR immune cells and their application in the therapy of hematologic malignancies.

Methods: Review

Results: Review

Conclusion: In the last four decades, CAR immune cell-based cancer therapy has become an advanced treatment for suppressing malignant cells. Nowadays, CAR-T have been very effective in the treatment of cancer, especially hematological malignancies. In addition to T cells, NK cells also suppress malignant cells as the main component of the innate immune system. CAR-NK cells are more useful in the treatment of hematologic malignancies because they can identify and destroy malignant cells more effectively. The factors that make CAR-NK cells superior to CAR-T cells in immunotherapy include:1) They can be obtained from allogeneic donors, 2) The probability of graft-versus-host disease and cytokine release syndrome in patients is low, 3) They can be modified and increase their proliferation and survival in vivo. Also, in addition to CAR-T and CAR-NK, CAR-Ms have anti-tumor activity. The benefits of using CAR-M immunotherapy include the following: 1) They have little toxicity, 2) It can significantly penetrate tumor tissues, 3) They can effectively phagocytose malignant cells, present antigens to T cells, and increase their killing by T cells.

Keywords: Immunotherapy,Chimeric antigen receptors, CAR T-cell, CAR-NK cell, CAR-M, Hematological malignancies

Colorectal cancer vaccine perspective (Review)

Fatemeh Babaie Dehaghi,[1] MohammadSaleh Safari,[2] Hossein Rezvan,[3,*] Sahar HamoonNavard,[4]

1. Department of Pathobiology, Faculty of Veterinary Sciences, Bu-Ali Sina University, Hamedan, Iran
2. Department of Pathobiology, Faculty of Veterinary Sciences, Bu-Ali Sina University, Hamedan, Iran
3. Department of Pathobiology, Faculty of Veterinary Sciences, Bu-Ali Sina University, Hamedan, Iran
4. Department of Pathobiology, Faculty of Veterinary Sciences, Bu-Ali Sina University, Hamedan, Iran

Introduction: One of the most important causes of death in the world is cancer, and its rate is increasing day by day. Colorectal cancer is the third most common cancer in the world. The main concern about colorectal cancer is that it is difficult to treat or incurable. The treatment methods that have been used so far are chemotherapy, radiotherapy, and removal of a part of the organ. These treatments are effective, but in many cases they cause unwanted side effects. These concerns and problems have led to great progress in the development of colorectal cancer vaccines.

Methods: The present study is a review article. By searching the keywords colorectal cancer, vaccine, immunotherapy in PubMed, Scopus, Web of Science databases, 41 articles were found and analyzed.

Results: There are different types of these vaccines, which include tumor surface antigens, dendritic cells, cancer cells, etc. All vaccines stimulate the immune system and destroy cancer cells. The manufactured vaccines have little toxicity for the body's natural cells, but they have a great ability to strengthen the immune system. They can also affect proteins in the body that inhibit inflammation. Although these vaccines have proven to be effective, in some cases they have suppressed the immune system. These vaccines are slow acting and the amount of memory cells they produce is low. Recently, the use of adjuvants has been discussed to solve this problem.

Conclusion: Colorectal cancer vaccine development started a few decades ago and is still expanding. Its effect in immunogenicity is undeniable, but their use is associated with limitations. Slow immunogenesis in the body and the short period of immunity are among these limitations. The use of vaccines for the prevention and treatment of colorectal cancer requires a detailed understanding of the limitations and further studies to solve them.

Keywords: colorectal cancer, vaccine, immunotherapy

Comparative analysis of Parasitological and Molecular methods in detecting blood microfilaremia (Research Paper)

Negar Hemmati,[1] Fateme Jalousian,[2,*] Negar Najafifard,[3]

1. DVM student, Faculty of Veterinary Medicine, Tehran University
2. Parasitology Department, Faculty of Veterinary Medicine, University of Tehran
3. DVM student, Faculty of Veterinary Medicine, Tehran University

Introduction: Bloodworms, particularly Dirofilaria immitis, are significant parasites in both veterinary and human health contexts. These parasites are primarily transmitted through arthropod vectors and are endemic in Iran, where various veterinary filarial worms, including Dirofilaria immitis, Dirofilaria repens, and Acanthocylonma reconditum, are found. Diagnosis of filariasis involves examining parasites in peripheral blood using the modified Knott method. However, molecular methods have emerged as more accurate and specific tools for detecting filarial parasites. The main objective of this study is to investigate the modified Knott method and molecular PCR method for detecting Dirofilaria Immitis in dog blood. The secondary goal of this study is to compare the effectiveness of these two methods in diagnosing Dirofilariasis.

Methods: In this study, a total of 66 blood samples were collected from dogs residing in Mazandaran, Gilan, and Qazvin provinces. Each blood sample, comprising 1 milliliter, was mixed with 9 milliliters of 2% formalin. We employed the modified Knott method to examine the presence of microfilaria. Additionally, DNA extraction was carried out using a commercial kit(MBST, Iran), followed by amplification and sequencing of a partial sequence of the Cytochrome oxidase subunit I(COXI) gene through PCR.

Results: The results obtained from the modified Knott method demonstrated the presence of Dirofilaria immitis microfilaria in 6 cases (9.1%) of the blood samples. The average length of the observed microfilaria was calculated to be 311.8 Â± 9.8 micrometers. On the other hand, the PCR method successfully detected the presence of the Dirofilaria immitis DNA genome in 33 (50%) of the blood samples. To establish a positive control for the study, we acquired a Dirofilaria immitis sample from the heart of a dog that unfortunately died in an accident in Gilan province. This particular sample was generously provided by the Parasitology Museum and was utilized in our research. The modified Knott method exhibited sensitivity, specificity, and efficiency rates of 55% (with a confidence interval of 67.88%-41.61%), 100%, and 77.5%, respectively. For the PCR method, the sensitivity, specificity, and efficiency were all reported as 100%. To assess the agreement between the two methods, we calculated the Kappa coefficient, which resulted in a value of 0.4. This suggests a relative

agreement between the modified Knott method and PCR method employed in this study.

Conclusion: The modified Knott method is an affordable and reasonably specific option for diagnosing Dirofilaria immitis microfilariae. However, for diagnosing dirofilariasis in dogs, molecular methods are more sensitive and efficient. Molecular methods can effectively detect the presence of the disease even when microfilariae are not visible in the peripheral blood. It is important to consider that while molecular methods offer better efficiency, they require advanced laboratory equipment and are more expensive to perform. As a result, the modified Knott method can be used as a cost-effective and relatively quick initial diagnostic approach. However, in areas where dirofilariasis is prevalent or hyper-endemic, like the northern and surrounding regions of the Caspian Sea and East Azerbaijan province, it is crucial for laboratories to be equipped with the necessary instruments for molecular diagnosis. Additionally, the use of rapid serology detection kits in these areas can greatly expedite the process of diagnosing infections. It is worth emphasizing that accurate diagnosis of contamination is fundamental in developing effective and efficient programs for controlling and preventing infectious diseases. Furthermore, the implementation of a one-health approach, which considers the health of animals alongside human welfare, is essential for mitigating risks posed by emerging diseases and enhancing overall well-being. A comprehensive approach that addresses both animal and human health is vital to achieve successful outcomes in disease prevention.

Keywords: Dirofilariasis, Microscopic examination, Mitochondrial gene, vector-borne transmission, zoonotic

Comparative study of the effect of Carboplatin and Capecitabine on PDL-1 protein using molecular docking method (Research Paper)

Mobina Alipour,[1,*]

1. The Research & Science university student

Introduction: Introduction: Programmed death-ligand 1 (PD-L1) also known as cluster of differentiation 274 (CD274) or B7 homolog 1 (B7-H1) is a protein that in humans is encoded by the CD274 gene. It seems that the high production of this protein causes cancer cells to escape from the body's immune system. Carboplatin is an intravenously administered platinum coordination complex and alkylating agent which is used as a chemotherapeutic agent for the treatment of various cancers, mainly ovarian, head and neck and lung cancers. Capecitabine is a carbamate ester that is cytidine in which the hydrogen at position 5 is replaced by fluorine and in which the amino group attached to position 4 is converted into its N-(penyloxy)carbonyl derivative. Capecitabine is a antineoplastic agent used in the treatment of cancers.

Methods: Material and method: In this study, I used the Pub Chim site at pubchem.ncbi.nlm.nih.gov, RCSB PDB www.rcsb.org to examine quercetin derivatives. Also from the software Chimera 1.17.1 and PyRx were also used. In this article, I first saved the structures of Carboplatin and Capecitabine from Pub Chim site as sdf files then I saved the 3D structure of PDL-1 protein from RCSB PDB site sa a pdb file. specifications of Carboplatin: Molecular formula: C6H12N2O4Pt Carboplatin is a second-generation platinum compound with a broad spectrum of antineoplastic properties. Carboplatin contains a platinum atom complexed with two ammonia groups and a cyclobutane-dicarboxyl residue. This agent is activated intracellularly to form reactive platinum complexes that bind to nucleophilic groups such as GC-rich sites in DNA, thereby inducing intrastrand and interstrand DNA cross-links, as well as DNA-protein cross-links. These carboplatin-induced DNA and protein effects result in apoptosis and cell growth inhibition. This agent possesses tumoricidal activity similar to that of its parent compound, cisplatin, but is more stable and less toxic. (NCI04) specifications of Capecitabine: Molecular formula: C15H22FN3O6 Capecitabine is a Nucleoside Metabolic Inhibitor. The mechanism of action of capecitabine is as a Nucleic Acid Synthesis Inhibitor. Capecitabine is a fluoropyrimidine carbamate belonging to the class of antineoplastic agents called antimetabolites. As a prodrug, capecitabine is selectively activated by tumor cells to its cytotoxic moiety, 5-fluorouracil (5-FU); subsequently, 5-FU is metabolized to two active metabolites, 5-fluoro-2-deoxyuridine monophosphate (FdUMP) and 5-fluorouridine triphosphate (FUTP) by both tumor cells and normal cells. FdUMP inhibits DNA synthesis and cell division by reducing normal thymidine production, while FUTP inhibits RNA and protein synthesis by competing with uridine triphosphate for incorporation into the RNA strand. (NCI04) I edited the desired protein using

Chimera 1.17.1 software. The PDL-1 protein had three chains, and in this study I used only the C chain for better conformity, and the rest of the chains were deleted. Also using the software, water molecules were removed from the protein and hydrogen molecules were added to its structure. Then using PyRx software,I started molecular docking, In which the gridbox to select the appropriate docking location were as follows: Center: X:-19.963 Y:-56.048 Z:52.4653 Center: X:-19.963 Y:-56.048 Z:52.4653 Dimensions(Angstrom): X;25.0000 Y:25.0000 Z:25.0000 Dimensions(Angstrom): X;25.0000 Y:25.0000 Z:25.0000 Carboplatin Capecitabine

Results: Result: After performing molecular docking separately for Carboplatin and Capecitabine, the results were as shown in the tables below: Ligand Binding Affinity (Kcal/mol) Mode RMSD lower bound RMSD upper bound Profinally_2568_uff_E=536.72 -4.3 0 0.0 0.0
Profinally_2568_uff_E=536.72 -4.2 1 0.842 3.077
Profinally_2568_uff_E=536.72 -4.1 2 1.591 2.588
Profinally_2568_uff_E=536.72 -4.0 3 11.931 13.264
Profinally_2568_uff_E=536.72 -3.9 4 1.624 3.128
Profinally_2568_uff_E=536.72 -3.8 5 1.498 3.172
Profinally_2568_uff_E=536.72 -3.8 6 1.892 3.058
Profinally_2568_uff_E=536.72 -3.8 7 11.771 13.188
Profinally_2568_uff_E=536.72 -3.8 8 11.988 13.3.8 The result of Carboplatin docking Ligand Binding Affinity (Kcal/mol) Mode RMSD lower bound RMSD upper bound Profinally_60953_uff_E=341.24 -5.5 0 0.0 0.0
Profinally_60953_uff_E=341.24 -5.4 1 11.17 12.913
Profinally_60953_uff_E=341.24 -5.4 2 11.322 12.535
Profinally_60953_uff_E=341.24 -5.3 3 12.835 14.437
Profinally_60953_uff_E=341.24 -5.3 4 1.739 2.306
Profinally_60953_uff_E=341.24 -5.3 5 3.173 8.238
Profinally_60953_uff_E=341.24 -5.2 6 12.739 14.639
Profinally_60953_uff_E=341.24 -5.2 7 12.483 13.684
Profinally_60953_uff_E=341.24 -5.2 8 5.421 8.242 The result of Capecitabine docking

Conclusion: Conclusion: According to ducking studies, I found that conformation of Capecitabine with negative binding affinity and RMSD had a better effect on PDL-1 protein to induce apoptosis and prevent cancer cell growth.

Keywords: PDL-1 protein/ Cancers/ Docking molecular/ Carboplatin/ Capecitabine

cytomegalovirus (CMV) review article (Review)

Farnaz Gheisari,[1,*]

1. Bachelor Student of microbiology Azad Shiraz university

Introduction: Human cytomegalovirusÂ is a member of the viral family known as herpesviruses, Herpesviridae, or human herpesvirus-5 (HHV-5). Human cytomegalovirusÂ infections commonly are associated with the salivary glands. CMVÂ infection may be asymptomatic inÂ healthy people, but it can beÂ life-threatening in an immunocompromised patient. Human CMV or human herpesvirus 5 is a ubiquitous double-stranded DNA virus belonging to the Betaherpesvirinae. Human cytomegalovirus (HCMV) is a highly prevalent herpesvirus that can cause severe disease in immunocompromised individuals and immunologically immature fetuses and newborns. Human cytomegalovirus (CMV) has infected humans since the origin of our species and currently infects most of the worldâ€™s population.

Methods: Usually, CMV controlled by a vigorous immune response so that infections are asymptomatic or symptoms are mild. However, if the immune system is compromised, HCMV can replicate to high levels and cause serious end organ disease. Infection with HCMV is common throughout the globe. CMV is acquired most commonly early in life, during childhood to early adulthood, through exposure to saliva, tears, urine, stool, breast milk, semen, and other bodily secretions from infected individuals. CMV has been detected via culture (human fibroblast), serologies, antigen assays, polymerase chain reaction (PCR), and cytopathology. In the transplant population, antigen assays or PCR is used (sometimes in conjunction with cytopathology) for diagnosis and treatment determinations.

Results: An effective cytomegalovirus (CMV) vaccine could prevent the majority of birth defects caused by congenital CMV infections. Candidate vaccines in clinical evaluation include live attenuated, protein subunit, DNA, and viral-vectored approaches. Subunit vaccines provide potent, focused immune responses to select viral immunogens. In principle, a CMV vaccine could be deployed in any of a number of settings: a universal vaccine administered in early childhood; a vaccine targeting young women of child-bearing age (toward the goal of preventing congenital transmission); or a vaccine for patients anticipating SOT or HSCT (aiming at the goal of reducing the risk of CMV disease under the immunosuppressive conditions of transplantation). Nevertheless, vaccine development is far advanced, with numerous candidate vaccines being tested, both live and inactivated.

Conclusion: Cytomegaloviruses (CMVs) are large, complex pathogens that persistently and systemically colonize most mammals.certain populations and regions are at a substantially higher risk of CMV infection. The extensive

epidemiologic burden of CMV calls for increased efforts in the research and development of vaccines and treatments.

Keywords: Cytomegalovirus- herpesvirus- vaccine - infection

Design and interaction analysis of a new peptide-based drug against HCV- related hepatocellular carcinoma (Review)

mortezapirzadeh,[1,*] mortezapirzadeh,[2]

1. Department of Biology, Faculty of Basic Sciences, Mashhad Branch, Islamic Azad University, Mashhad, Iran
2.

Introduction: Cancer is the second-leading cause of death in the world that characterized by the development of abnormal cells in in different organs of the body. Hepatocellular carcinoma (HCC) is one of the most common types of liver cancer in adults. This type of cancer starts in liver cells. Loss of weight, yellowing of the skin, swelling, pain, or mass in the abdomen are the most important symptoms of liver cancer. Patients with liver disease such as cirrhosis, and hepatitis B and C infections are more susceptible to this type of cancer. One of the other causes of HCC is Hepatitis C virus (HCV) infection. This study aims to Design a new peptide-based drug against HCV-related hepatocellular carcinoma.

Methods: In the first step, Hypercam software was used to draw the 3D structure of the oligopeptide. The designed peptide consisted of 4 amino acids (glycine-isoleucine-lysine- glycine). One of the ways to control this virus was to target the main enzymes of the virus which is NS3/4A protease. In our research, the code of the 6p6s protein from the pdb site was downloaded. Docking was used for the study of peptide-protein interactions, and then hydrogen bonds between peptide and protein were checked with Discovery software.

Results: After docking, between oligopeptide (glycine-isoleucine-lysine-glycine) and 6p6s protein, 3 hydrogen bonds were formed. Based on our results, amino acids that participate in the interactions are LYS1136:NZ - GLY1:O, LYS1136:NZ - ILE2:O, GLY1:N - ALA1157:O with docking score:-98.37.

Conclusion: Designed oligopeptide by 3 hydrogen bonds interacts with HCV NS3/4A protease (accession number:6p6s).

Keywords: HVC, virus, hepatocellular carcinoma, anticancer, liver

Detection of Salmonella spp in goat abortion outbreaks (Research Paper)

Dr hossein esmaeili,[1] Ava bahrami,[2,*]

1. Faculty of veterinary medicine university of tehran
2. Student of veterinary medicine in university of Tehran

Introduction: Abortion is one of the main causes of reproduction losses in small ruminantâ€™s flocks Abortion is one of the main causes of reproduction losses in small ruminantâ€™s flocks. Various pathogens may induce abortion in sheep and goats. In addition the common potential in human and livestock would have serious dangers for public health. The present study aimed to investigate the presence of Salmonella spp in some goat herds in Iran.

Methods: The Research Methods: In 2022, the samples including fetal abomasal contents and tissues were collected from 58 aborted goat fetuses. Then, using conventional PCR the presence of Inv A Gene were assessed.

Results: Based on the result of this research 12% of cases (7 fetuses) had salmonellosis and the fetuses were over the age of three months. The other results were edema, bleeding in fetus and placenta, lesions in the formation of hyperemia, wall thickening, liver necrosis, interstitial pneumonia, petechia on the membranes and peritoneum

Conclusion: The present results showed the studied goat herds are infected with salmonella spp pathogens which emphasize the demand for more investigations for the detection of other abortion agents. Besides, epidemiological and risk factors contribute in caprine abortion is further necessary

Keywords: Goat, Abortion, Salmonella

Diagnostic Role of Peripheral Blood Extracellular Vesicles for Substance Use Disorders (Methamphetamine, Cocaine, Heroin and Morphine) (Review)

Tayebeh Mohtashami,[1,*] Behzad Garmabi,[2] Mehdi Khaksari,[3] Amir Atashi,[4]

1. . Student Research Committee, School of Medicine, Shahroud University of Medical Sciences, Shahroud, Iran
2. Study and Treatment of Circadian Rhythms Research Center, Shahroud University of Medical Sciences, Shahroud, Iran
3. Addiction Research Center, Shahroud University of Medical Sciences, Shahroud, Iran
4. Stem Cell and Tissue Engineering Research Center, Shahroud University of Medical Sciences, Shahroud, Iran

Introduction: Introduction: Extracellular vehicles (EVs) are a group of membrane particles released from cells which introduce as a new approach for diagnosis/therapeutic purposes. While the role of EVs in the pathogenesis of cancer, neurological diseases and viral infections has been widely discussed, the role of EVs in drug addiction has not yet been clearly defined. Therefore, this research attempts to explore alteration of peripheral blood extracellular vesicles in substance use disorders (SUD).

Methods: Methods: To carry out this research, English articles published in Scopus, PubMed, Embase and Web of science databases were searched. The keywords of this search, which was limited to studies from 2013 to 2023, were extracellular vesicles, drug abuse, substance use disorders, methamphetamine, cocaine, morphine, and heroin.

Results: Findings: Out of 61 articles, 43 articles which were related to the topic were reviewed. These studies show that EVs have been used in both diagnostic and therapeutic approaches. From all of molecules inside EVs, only microRNAs showed expression changes in SUD. The results also showed that miR-29a-3p, miR-181a, miR-15b, let-7e, let-7d, miR-29b, and miR-140 in EVs were significantly associated with drug use disorder. On the other hand, it has been proven that miR-451a, miR-21a and miR-744a in EVs are related to the severity of anxiety and depression, as well as the concentration of neurotransmitters GABA, choline and serotonin in substance use disorders, which can be considered as a specific biomarker. In addition, upregulation of miR-21 and miR-138 in EVs can play an important role in therapeutic approaches to treat substance use disorders.

Conclusion: Conclusion: These data show that extracellular vesicles play a significant role in the biology of drug addiction. miRNA analysis of extracellular vesicles could become a promising diagnostic strategy for monitoring addiction withdrawal symptoms. On the other hand, it is possible to

design targeted therapeutic approaches by fine-tuning the function of miRNAs.

Keywords: Keywords: Extracellular Vesicles, Substance Use Disorder, miRNA

Effect of acute myeloid leukemia-derived exosomes on the bone marrow mesenchymal stromal cells: Downregulation of autophagy-related genes (Research Paper)

Maryam Nabigol,[1] Mehdi Allahbakhshian Farsani,[2,*]

1. Department of Hematology and blood bank, School of Allied Medical Sciences, Shahid Beheshti University of Medical Sciences, Tehran, Iran
2. Department of Hematology and blood bank, School of Allied Medical Sciences, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Introduction: Introduction: Acute myeloid leukemia (AML) is a heterogeneous clonal disorder arising from the bone marrow (BM), with symptoms such as anemia, infection, and bleeding. Until recently, AML research was focused on the identification of hematopoietic stem cells (HSCs)-related events leading to leukemogenesis. New studies have demonstrated that primary alterations in the bone marrow stromal cells, especially mesenchymal stromal cells (MSCs), can induce AML in mice and also in patients. Moreover, AML cells recruit various factors, including exosomes, to modify MSCs in order to create a niche favorable to leukemia growth and escape therapy. Therefore, it seems that MSCs' presence and survival is crucial for AML initiation and persistence. Our study aims to investigate the effect of AML exosomes on the survival-related properties of BM-MSCs, especially alteration in the expression of autophagy-related genes, as a cell death pathway.

Methods: Methods: Human BM-MSCs were obtained from healthy donors. AML cells (HL-60 cell line) were purchased from the Pastor Institute of Iran. Exosomes were isolated from the supernatants of HL-60 cells using an exosome isolation kit. TEM (Transmission Electron Microscopy) was used to determine the isolated particles' morphology. To evaluate the exosome nanostructure, the DLS (Dynamic Light Scattering) technique was utilized. Exosome-specific markers (CD9, CD63, and CD81) were identified via flow cytometry. Exosome protein content was assessed using a BCA protein assay in order to determine the concentration of exosomes. Then, MSCs were co-cultured with different concentrations of AML exosomes. The effect of exosomes on the metabolic activity of MSCs was assessed by the MTT assay, while ROS levels, proliferation, apoptosis, and cell cycle progression were evaluated by flow cytometry. Gene expression analysis was also performed by qRT-PCR.

Results: Results: Isolated particles were mainly positive for exosome-specific markers, including CD9, CD63, and CD81. According to the DLS results, the separated exosomes' size range was between 70-110 nm. The globular shape of the extracted exosomes was confirmed using TEM. Our results showed higher metabolic activity, decreased apoptosis, increased proliferation, lower ROS levels, and induced cell cycle progression in MSCs

treated with a 50 Î¼g/ml dose of AML exosomes compared with the control group. qRT-PCR data demonstrated that the pro-autophagic genes Beclin-1, Atg7, and Atg10 were downregulated in MSCs treated with 50 Î¼g/ml of AML exosomes in comparison to their untreated counterparts (P<0.05).

Conclusion: Conclusion: Since MSCs' presence is important for AML onset and progression, our results suggest that, through exosome secretion, AML decreases autophagic cell death while increasing the viability and proliferation of MSCs so that leukemic cells can exploit them to generate a protective microenvironment for leukemia growth and therapy resistance.

Keywords: Keywords: Acute myeloid leukemia, Exosome, Mesenchymal stromal cell, Autophagy

Effect of cigarette smoking on bacterial infections: a review study (Review)

Narjes Seddighi,[1,*] Aida Khoshdaman,[2] Mohammad Rezaei,[3] Ali Massoudifar,[4] Ali Salimi Asl,[5]

1. Student Research Committee, Tabriz University of Medical Sciences, Tabriz, Iran
2. Student Research Committee, Faculty of Para-Medicine, Hormozgan University of Medical Sciences, Bandar Abbas, Iran
3. Student Research Committee, Faculty of Medicine, Hormozgan University of Medical Sciences, Bandar Abbas, Iran
4. Department of Psychiatry, Faculty of Medicine, Hormozgan University of Medical Sciences, Bandar Abbas, Iran
5. Student Research Committee, Faculty of Medicine, Hormozgan University of Medical Sciences, Bandar Abbas, Iran

Introduction: Introduction: Despite great advances that have occurred in the prevention of bacterial infections, they are still considered the most common reason for mortality worldwide. According to the data from the World Health Organization (WHO), in 2017, around 15% of pediatric mortality was caused by bacterial infections. Since cigarette smoke can cause serious damage to the organs such as the respiratory system and the weakening of the immune system, the present review study aims to investigate the effects of cigarette smoking on various bacterial pneumonia.

Methods: Method: the present review study was performed on 90 articles, obtained through a search in Scopus, PubMed, and Google Scholar using keywords of bacterial pneumonia, Staphylococcus, Streptococcus, Haemophilus, pseudomonas, legionella, Mycoplasma, chlamydia, tuberculosis, and cigarette.

Results: Result: different results of previous studies indicated that given the detrimental effect of cigarettes on the respiratory and immune systems of individuals, cigarette smoking affects the prognosis and outcome of infectious diseases. Disease severity, requiring hospitalization at both general and intensive care units (ICU), and mortality rate vary across these patients, thereby challenging the treatment. Thus, cessation of cigarette smoking may help improve the respiratory system function.

Conclusion: Given the different results obtained from previous studies, exposure to cigarette smoke affects the respiratory system and increases the severity of bacterial pneumonia.

Keywords: cigarette, smoking, Bacterial Pneumonia

Effect of Saffron Supplementation on Plasma Proteome of Patients with Coronary Artery Disease (Research Paper)

Parisa Rahimi,[1,*] Saeid Abedimanesh,[2] Seyedeh Zahra Bathaie,[3]

1. Tarbiat Modares University
2. Tarbiat Modares University
3. Tarbiat Modares University

Introduction: Cardiovascular disease (CVD) is a prevalent cause of mortality worldwide, with coronary artery disease (CAD) being one of its most prominent manifestations. As such, there is an ongoing exploration of novel interventions that can potentially prevent or inhibit the progression of CAD. Recent research has focused on the potential benefits of Saffron aqua extract supplementation in this regard. However, the exact mechanism of action of saffron in CAD remains unclear, and protein components may be involved. To address this knowledge gap, the present study aimed to investigate the expressive changes in the plasma proteome profiles of CAD patients who received Saffron supplements.

Methods: This study presents the results of an eight-week clinical trial conducted on patients with coronary artery disease (CAD) who were overweight or obese (BMI 25-35 kg/m2) and aged between 40-65 years. The trial was randomized, double-blind, and placebo-controlled, with fifty participants allocated to the Saffron and Placebo groups. Throughout the trial, the Saffron group received 60 capsules of Saffron aqueous extract (SAE) (30 mg), while the Placebo group received a placebo. Participants were instructed to take one capsule per day (after lunch) for 60 days. It is worth noting that all patients continued their current treatment for cardiovascular disease (CVD) during the trial period. In this study, all patients, investigators, and laboratory analyzers were unaware of the study arms and intervention types. Following a 12-hour fasting period, plasma samples were collected from the patients and subjected to two-dimensional gel electrophoresis. Protein spots with an absolute difference of approximately two-fold were identified, predicted by bioinformatics databases and 2D Expasy gels.

Results: Results indicate significant differences in the expression levels of specific plasma proteins upon consumption of Saffron extract supplements. Notably, proteins such as Antithrombin-III, Haptoglobin, Leucine-rich alpha-2-glycoprotein, Transthyretin, Alpha-1-antichymotrypsin, and Apolipoprotein C-II and E exhibited two-fold expression changes. However, to obtain more reliable results, further analysis using techniques such as mass spectrometry or western blotting is necessary.

Conclusion: In conclusion, it appears that saffron extract supplements possess significant anti-oxidative and anti-inflammatory properties, and have

been shown to improve the lipid profile in individuals diagnosed with cardiovascular disease. Nevertheless, given the complex mechanisms behind these effects, further proteomic research must be undertaken to identify the target protein of Saffron that may be involved in the prevention and treatment of CVD.

Keywords: Cardiovascular disease, coronary artery disease, Saffron, Proteomics, 2-D Electrophoresis.

Epstein-Barr virus (EBV) review article (Review)

Farnaz Gheisari,[1,*]

1.

Introduction: Epstein Barr virus (EBV) is a double-stranded DNA virus that infects B lymphocyte cells. Epstein-Barr virus (EBV) is a ubiquitous human virus which infects almost all humans during their lifetime and following the acute phase Epstein-Barr virus (EBV) is typically found in a latent, asymptomatic state in immunocompetent individuals. Perturbations of the host immune system can stimulate viral reactivation. Epstein Barr virus (EBV) is a herpesvirus in which over 90% of the population worldwide has been infected. EBV infection can range from asymptomatic to infectious mononucleosis. Complications are rare, but important to recognize. Epsteinâ€“Barr virus (EBV) is a ubiquitous human lymphotropic herpesvirus with a well-established causal role in several cancers. Because Epstein-Barr virus (EBV) is ubiquitous and persists latently in lymphocytes, simply detecting EBV is insufficient to diagnose EBV-associated diseases.

Methods: Epstein-Barr virus (EBV) infects nearly all humans and usually is asymptomatic, or in the case of adolescents and young adults, it can result in infectious mononucleosis. EBV-infected B cells are controlled primarily by NK cells, iNKT cells, CD4 T cells, and CD8 T cells. EBV expresses a number of viral noncoding RNAs (ncRNAs) during latent infection, many of which have known regulatory functions and can post-transcriptionally regulate viral and/or cellular gene expression. The expression of EBV viral proteins and non-coding RNAs contribute to EBV-mediated disease pathologies.

Results: Transmission of EBV mainly occurs through saliva but can rarely be spread through semen or blood, e.g. through organ transplantations and blood transfusions. EBV transmission through oral secretions results in infection of epithelial cells of the oropharynx. An EBV prophylactic vaccine that induces neutralizing antibodies holds great promise for prevention of EBV associated diseases. A vaccine is currently unavailable. A vaccine to reduce EBV posttransplant lymphoproliferative disease would be an important proof of principle to prevent an EBV-associated malignancy. Trials of an EBV vaccine to reduce the incidence of Hodgkin lymphoma, multiple sclerosis, or Burkitt lymphoma would be difficult but feasible.

Conclusion: As a result, EBV can shuttle between different cell types, mainly B cells and epithelial cells. Moreover, since the virus can switch between a latent and a lytic life cycle, EBV has the ability to cause chronic relapsing/reactivating infections. Epstein-Barr Virus (EBV) is an extremely successful human herpes virus, which infects essentially all human beings at some time during their life span. A vaccine for EBV is currently unavailable.

Keywords: EBV- B lymphocyte- herpesvirus- infectious - vaccine

Ethical considerations of using immunological data for diagnostic purposes (Review)

Fatemeh Behdarvand,[1] Hossein Rezvan,[2,*]

1. Department of Pathobiology, Faculty of veterinary Sceince, Bu-Ali Sina University, Hamedan, Iran
2. Department of Pathobiology, Faculty of veterinary Sceince, Bu-Ali Sina University, Hamedan, Iran

Introduction: Immunological tests, which utilize the body's immune system to detect pathogens, are crucial for various medical conditions, including allergies, cancer screening, and monitoring disease progression. In primary immune deficiency disorders, molecular diagnostic testing helps identify genetic defects, aiding in patient management and prognosis. The National Institute of Allergy and Infectious Diseases (NIAID) has established laboratories to apply immunology knowledge to clinical diagnosis and treatment. Immunological data can revolutionize diagnostics, enabling more accurate, personalized, and predictive tests for various diseases. However, ethical considerations such as privacy, informed consent, data ownership, and non-discrimination must be addressed. Prioritizing these principles ensures responsible and ethical use of immunological data for diagnostic purposes.

Methods: The use of immunological data for diagnostic purposes raises concerns about patient privacy and confidentiality. Privacy and confidentiality are the most significant ethical concerns in health-related big data studies, followed by informed consent, fairness, justice, trust, and data ownership. Existing ethical, legal, and other approaches offer some safeguards, but major gaps remain. The increasing interest of for-profit companies in acquiring large healthcare systems poses new challenges to patient privacy, as they may exploit patient data for commercial interests and target vulnerable populations. Personal health information is considered protected health information, governed by ethical principles and laws. It is essential to have informed permission before using immunological data for diagnostics. Before any diagnostic tests are carried out, patients should be thoroughly informed about how their data will be used, and their agreement should be acquired. However, institutional ethical monitoring and participant-informed agreement may be required for the secondary use of samples received from diagnostic laboratories. The ownership of immunological data is a complicated matter that involves many parties, including people, governments, businesses, researchers, and healthcare providers. Concerns regarding patient privacy and the ethics of sharing patient data are raised by the growing interest of for-profit businesses in purchasing healthcare databases. Building data ecosystems and encouraging reproducible science need to combine immunology-related datasets and repositories. An ethical and privacy-aware approach to data access and sharing is crucial for the appropriate use of immunology research. Immunological data can potentially lead to

discrimination based on genetic predisposition, health status, or lifestyle choices. This could affect insurance coverage, job screening, and employee health benefits decisions. Research shows discrimination affects immune cell composition and emphasizes the importance of non-discriminatory immune responses.

Results: Immunological data can be used to develop accurate, personalized, and predictive tests for various diseases. However, it raises ethical concerns like privacy, informed consent, data ownership, and discrimination. Clear guidelines for data collection, storage, use, and sharing are crucial. Individuals should be informed about their data's use, and data security measures should be strengthened. They should have the right to control their data, and safeguards should be developed to prevent discriminatory misuse.

Conclusion: Diagnostics might be revolutionized by the use of immunological data, however, it's crucial to use this information ethically and responsibly. We can make sure that immunological data is used to the advantage of both people and society at large by addressing the ethical issues brought forth above.

Keywords: Ethical considerations -diagnostics-

Evaluation and association of serum melatonin levels and the status of pro-angiogenic factors in urine samples of diabetic patients with and without nephropathy (Research Paper)

sama yousefi,[1] Seyed Mostafa Mir,[2,*] Jahanbakhsh Asadi,[3] Fatemeh Mohammad Zadeh,[4] Mohammed Radha Jawad Alyasari,[5] Maryam Abolghasemi,[6]

1. Golestan University of Medical Sciences
2. Golestan University of Medical Sciences
3. Golestan University of Medical Sciences
4. Golestan University of Medical Sciences
5. Golestan University of Medical Sciences
6. Golestan University of Medical Sciences

Introduction: Diabetic nephropathy, which is a frequent complication of diabetes mellitus, is marked by an elevation in the production of pro-angiogenic substances and a reduction in the creation of anti-angiogenic molecules as a result of elevated blood sugar levels. Angiogenesis, which refers to the formation of new blood vessels, plays a significant role in diabetes. Melatonin has diverse impacts on angiogenesis depending on the particular physiological or pathological circumstances. Furthermore, there are various cytokines and growth factors that regulate angiogenesis, including vascular endothelial growth factor (VEGF) and transforming growth factor-beta (TGF-Î²). Moreover, there is evidence suggesting that nitric oxide (NO) can play a dual role in angiogenesis, acting both as a participant and a regulator. Therefore, the objective of this study was to examine the levels of melatonin in the blood and the levels of VEGF, TGF-Î², and NO in urine samples from diabetic patients with and without nephropathy. Additionally, the study aimed to investigate any potential relationship between melatonin levels and the levels of factors related to angiogenesis.

Methods: Ninety participants with type 2 diabetes mellitus, including 45 diabetic patients with nephropathy and 45 diabetic patients without nephropathy, were enrolled in this case-control study. The serum melatonin levels and urinary levels of VEGF and TGF-Î² were measured using an ELISA kit, and the NO level was measured using a colorimetric method.

Results: The findings showed that diabetic patients with nephropathy had significantly higher levels of VEGF, TGF-Î², and NO in their urine compared to diabetic patients without nephropathy ($P = 0.005$, $P < 0.001$, and $P < 0.001$, respectively). However, there was no notable difference in melatonin levels in the blood between diabetic patients with and without nephropathy ($P = 0.154$). Additionally, there was no significant association observed between melatonin levels and the levels of VEGF, TGF-Î², and NO.

Conclusion: The findings of the present study showed increased urinary levels of VEGF, TGF-Î², and NO in diabetic patients with nephropathy compared to diabetic patients without nephropathy.

Keywords: Diabetic nephropathy, Melatonin, Vascular endothelial growth factor, Transforming growth factor beta

Evaluation of Antimicrobial Activity and Anti-Quorum Sensing of Rosmarinus Methanol Extract on Pseudomonas aeruginosa (Research Paper)

Samaneh Ansarinia,[1,*] Parisa Behshood,[2] Elahe Tajbakhsh,[3] Faezeh Amiri,[4]

1. Master Department of Microbiology, Young Reasearchers and Eliet Club, Shahrekord Branch, Islamic Azad University Shahrekord, Iran
2. Phd Department of Microbiology, Young Researchers and Elite Club, Shahrekord Branch, Islamic Azad University Shahrekord, Iran
3. Associate Professor, Biology - Microbiology, Basic Biology Sciences,
4. Biotechnology Bachelor, Naghsh Jahan Isfahan non profit organization

Introduction: Pseudomonas aeruginosa is a gram-negative, oxidasepositive, non-fermenting, and aerobic bacterium found on intestinal tissues of healthy individuals, various fluids, and surfaces, especially moist surfaces and even disinfectants. P. aeruginosa is an opportunistic bacterium identified as one of the most critical hospital pathogens in recent years . One of the pathogenic mechanisms of this bacterium is the quorum sensing system and high resistance to most antibiotics. Quorum sensing (QS) is the ability to detect and respond to cell population density by gene regulation. It enables bacteria to restrict the expression of specific genes to the high cell densities, at which the resulting phenotypes will be the most beneficial . Many virulence genes in P. aeruginosa are controlled and expressed by quorum sensing as biofilm growth and proliferation genes, alkaline proteases, pyocyanins, and pivorinins . A biofilm comprises any syntrophic consortiums of microorganisms in which cells stick to each other and a surface. The low densityandlow diffusion power of the matrix polysaccharide existing in the biofilm provides ideal conditions for the aggregation of signals and the induction of pathogenic factors by the coenzyme sensing phenomenon and prepares bacteria to invade the host. The growth of bacteria in biofilms can increase their resistance to the antibiotics. Onthe other hand, the overuse of antibiotics in the treatment of bacterial infections has led to the development of antibiotic-resistant strains . The process of bacterial resistance to chemical antibiotics has limited the physicians to treat some infectious diseases that are often fatal . The study of medicinal plants has become particularly critical worldwide to discover new therapies with fewer side effects and higher economic values. Rosemary extract is a compound with several antimicrobial and antioxidant properties It has been proven that there are numerous antimicrobial compounds, such as phenolic compounds. Today, over 4 billion plants worldwide are used as a source of medicines, and 25% of physicians prescribe normal herbal medicines . Plants have an unlimited ability to synthesize phenolic compounds, their derivatives, and a variety of aromatic compounds. These compounds are secondary metabolites of plants and have therapeutic effects against viruses, bacteria, and fungi . Therefore, it is necessary to investigate the active constituents of medicinal plants in different geographical areas to discover useful antimicrobial agents. Rosmarinus belongs to the mint family

(Labiateae, a herb with green, aromatic, and sharp leaves) and has antinociceptive, antioxidant, antimicrobial, and anti-inflammatory effects on laboratory experiments and antimicrobial compounds . It contains phenolic compounds such as carnosol, rosmarinic acid, caffeic acid, flavonoids, including diosmin, luteolin, gencuanine, and monoterpene, such as camphor, cineole, and borneol.

Methods: Identification and Collection of Rosmarinus This experimental study was performed from May 2017 to January 2018 in the Microbiology Laboratory of Kashan Azad University. In spring 2017, leaves and branches of Rosmarinus from rangelands of Niassar city of Kashan were harvested and approved by Isfahan Agricultural and Natural Resources Research Center. Preparation of Bacterial Strains In this study, five clinical isolates of P. aeruginosa were isolated from clinical samples referred to Kashan hospitals. Standard bacterium P. aeruginosa (ATCC 1074) was also used. Bacterial samples were cultured in Muller-Hinton broth medium and incubated at 37Â°C for 24 hours. Subsequently, a few drops of the bacterial suspension were transferred to the Muller Hinton broth medium to achieve a standard McFarland 0.5 turbidity (1.5_108 cfu/mL) . Preparation of Various Dilutions and Evaluation of Antibacterial Activity of the Extract Concentrations of 500, 250, 125, 62.5, 31.25, 15.6, 7.8, and 3.9 mg/ml of extract were prepared. In this study, the antimicrobial activity of the extract was evaluated by diffusion method in wells and microdilution. After preparation of different concentrations of extract, Measurement of minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) were determined by microtiter plate method . Investigation of the Anti-Quorum Sensing Activity of Ethanol and Methanol Extract of Rosmarinus We examined the anti-biofilm activity, pyocyanin production, and protease enzyme activity of P. aeruginosa to investigate the antimicrobial sensing activity of methanolic extracts of Rosmarinus. Evaluation of Anti-Biofilm Activity of Rosmarinus Methanol Extract The anti-biofilm activity of Rosmarinus methanolic extract was evaluated by crystal violet staining to investigate its anti-quorum sensing activity. Inhibition of Pyocyanin Experiment The 24-hour culture of the bacteria was prepared in the Muller Hinton broth medium and its opacity was set to half the standard McFarland opacity by spectrophotometer. 250 _l of the herbal extract was prepared at a concentration lower than the bacterial growth inhibitory, and 100 _l of microbial suspension was added. The test tube containing microbial suspension without extract was considered as control. The tubes were centrifuged at 8,000 rpm, and the supernatant was transferred to another sterile tube and added to 3 ml of chloroform. The solution was then transferred to the cuvet from the bottom of the tubes (control and extract-treated samples) and read by a spectrophotometer at 690 nm. This experiment was repeated three times, and the mean percentage reduction of pyocyanin production was calculated according to the following formula (15). Percentage reduction of pyocyanin = (Optical Absorption of extract - Treated Sample - Optical Absorption of control sample)/(optical absorption of control sample)_100 Protease Activity Test Protease activity of

P. aeruginosa was evaluated in accordance with the Lori method using azocasein . Statistical Analysis The comparison of the means of this study was analyzed by two-wayANOVA and Bonferroni paired t-test using SPSS 17 software. The significance level of the test ($P < 0.05$) was used to interpret the data.

Results: In this study, the strains of P. aeruginosa were identified by hot staining and conventional biochemical tests. All isolates were Gram-negative bacilli, catalase-positive, and oxidase-positive cultured in oxidation-fermentation (OF) medium. These isolates produced pyocyanin were mobile and grew at 42Â°C. The susceptibility of clinical isolates and standard strains of P. aeruginosa to methanolic extracts of Rosmarinus was investigated by the well diffusion method (Table 1). Table 1 shows the inhibition zone mean of methanolic extract of Rosmarinus plant on different isolates of P. aeruginosa (in mm). As the two-way ANOVA test shows, the size of the inhibition zone diameter is directly proportional to different concentrations ($P < 0.001$). The minimum inhibitory concentration of methanolic extract of Rosmarinus was 125 mg / ml, and minimum bactericidal concentration was 250 mg/ml. Results of Pyocyanin Pigment Reduction in P. aeruginosa at Different Concentrations of Methanolic Extract of Rosmarinus As presented in Figure 1, we evaluated the efficacy of methanolic extract of Rosmarinus on the reduction of pyocyanin pigment production of different P. aeruginosa isolates. Figure 1 shows a decrease in pyocyanin pigment production in the presence of different concentrations of Rosmarinus methanol on different P. aeruginosa isolates. Twoway analysis of variance showed that the percentage of reduced pigment production of piocyanin was directly correlated with different concentrations of the extract ($P < 0.001$). In other words, with increasing methanol concentration of Rosmarinus, pyocyanin pigment production can decrease in standard P. aeruginosa and clinical isolates, which means that methanolic extract of Rosmarinus can strongly significantreduce pyocyanin pigment production in Pseudomonas aeruginosa. Results of Percentage Reduction of P.aeruginosa Protease Activity at Different Concentrations of Methanolic Extract of Rosmarinus We assessed the efficiency of methanolic extract of Rosmarinus on reducing the protease production of different isolates of P. aeruginosa used by Lorry method, as presented in Figure 2. Figure 2 shows a decrease in protease production in the presence of different concentrations of methanolic extract of Rosmarinus plant on different isolates of P. aeruginosa. Two-way analysis of variance showed that the percentage of reduced protease production was directly correlated with different concentrations of extract ($P< 0.001$). In other words, as the concentration of methanolic extract of Rosmarinus increases, the production of protease in standard P. aeruginosa and clinical isolates has decreased, which means that methanolic extract of Rosmarinus has a significant effect in reducing the production of protease in P. aeruginosa. Results of Anti-Biofilm Activity of Methanolic Extract of Rosmarinus In the present study, we examined the anti-biofilm activity of methanolic extract of Rosmarinus via crystal violet staining on P. aeruginosa (Figure 3). Figure 3 shows the reduction of biofilm

production in the presence of different concentrations of methanolic extract of Rosmarinus plant on different P. aeruginosa isolates. Two-way analysis of variance showed that the percentage of reduction in biofilm production was directly correlated with different concentrations of extract ($P < 0.001$). In other words, with increasing concentration of methanolic extract of Rosmarinus, biofilm production in P. aeruginosa decreased, and clinical isolates has decreased, whichmeansthat methanolic extract of Rosmarinus has a significant effect on reducing biofilm production in P. aeruginosa.

Conclusion: Mentioning the above bacteria, the present research tended to confirm the efficacy of the methanol extract. The results could verify the ability of Rosmarinus methanol extract to reduce microbial growth, biofilm, elastase, protease, and pyocyanin of P. aeruginosa. Given the high potential of P. aeruginosa in biofilm formation and the microbial and biofilm growth inhibitory activity of Rosmarinus extracts, it can be concluded that Rosmarinus extract can be used in different compounds for the elimination of infection with pathogenic bacteria such as P. aeruginosa. Also, it can be a substitute for chemical drugs to treat infections, although more thorough investigation on all the effects of this plant extract. Currently, one of the major problems in the treatment of infections and the use of antibiotics is the development of antibiotic resistance, which requires special attention for treatment. Since the antibacterial effects of rosemary extract have been verified in various studies on numerous species of bacteria, it can be employed in the treatment of infections caused by resistant bacteria. To sum up, the effects of plant extracts on inhibition of biofilm formation can be attributed to the those of constituents on bacterial growth and ultimately on the reduction of biofilm formation. Therefore, further studies are needed to evaluate the variety and composition of essential oils and extracts of medicinal plants and to compare different herbs in terms of their constituents in indigenous regions and identify the superior breeds.

Keywords: Methanol, Rosmarinus, Biofilms, Diffusion, Pseudomonas

Evaluation of antimicrobial effects of bifidobacterium bifidum on some pathogenic microorganisms (Research Paper)

Samaneh Ansarinia,[1,*] Parisa Behshood,[2] Elahe Tajbakhsh,[3] Faezeh Amiri,[4]

1. Master Department of Microbiology, Young Reasearchers and Eliet Club, Shahrekord Branch, Islamic Azad University Shahrekord, Iran
2. Phd Department of Microbiology, Young Researchers and Elite Club, Shahrekord Branch, Islamic Azad University Shahrekord, Iran
3. Associate Professor, Biology - Microbiology, Basic Biology Sciences,
4. Biotechnology Bachelor, Naghsh Jahan Isfahan non profit organization

Introduction: Branched bifidobacteria, rod-shaped, non-motile, anaerobic, Gram-positive, B They are aerobic and catalase negative and belong to the Bifidobacteriaceae family and the Actinobacteria branch. The genus Bifidobacterium currently includes more than 90 species, excluding taxa Unclassified Bifidobacterium first fed from infant's feces, separated from mother, but fed to infants Various ecological niches including fermented milk and anaerobic digestion facilities have been discovered However, the most common isolates are from the gastrointestinal tract of humans and animals. Conditions Growth (eg, temperature, pH, oxygen level) of bifidobacteria significantly varied among strains. It is not different (3). (Ruiz et al., 2011). For example, the optimal growth temperature is between 36 and 38, respectively Â°C and 41 to 43 Â°C for strains isolated from humans and animals. In addition, the optimum pH for growth is around pH 6.5-7.0, where B. animalis and B. thermacidophilum are also metabolically active at pH 3.5-4.0. Probiotics are live microbial food supplements that have beneficial effects on health have consumers This group of bacteria plays an important role in preventing infection in the parts They play a role in various parts of the body, especially the digestive system. Among probiotic microorganisms, bacteria The genus Bifidiobacterium 6 is known as the most common organism in the production of probiotic products have been introduced. These bacteria are gram positive, catalase negative and have no spores and have characteristics such as Tolerance of bile acids, production of organic acids, antimicrobial compounds and cell aggregation Pathogenic bacteria and preventing the attachment of pathogenic bacteria to the surfaces of the digestive system Are. As a result of the use of probiotic supplements, beneficial colonies will be created that can Like natural floromicrobials, prevent pathogenic bacteria from reaching and attaching to the target cell destroy them by producing antimicrobial compounds and prevent the onset of the disease process and at the same time Now provide the conditions for the natural floromicrobe to repair and restore itself, then the colonies They will be replaced by the natural bacterial environment that has regenerated itself. One of the prerequisites of becoming a probiotic strain is the ability to colonize in one place. Specific, for example, is in the gastrointestinal tract, so that probiotic strains can effectively interact with the host and the host microbiome. Colonization of probiotics on some pathogens It excels and thus gives the host protection against

pathogenic infections. Studies Different species showed that different species of Bifidobacteria have anti-infection properties. B. longum ATCC 15708 Antimicrobial activity against many pathogens including Escherichia, Salmonella typhimurium and Listeria monocytogenes were indicated. B. longum BB536. Against intestinal sepsis caused by Pseudomonas aeruginosa, possibly from Protects the intestinal epithelial cells by interfering with the adhesion of pathogens (8). BB536 Probably through the modulation of the gut microbiotaØŒ that isØŒ increasing the abundance of the genus FaecalibacteriumØŒ Improves upper respiratory infections in healthy preschool children. Also, one A randomized, double-blind, placebo-controlled trial shows that the administration of BB536 in Combination with standard triple treatment (osmeprazole, amoxicillin, clarithromycin) eradication rate Improves Helicobacter pylori infection in 63 patients. Prescription of B. lactis BB-12 in early adulthood Childhood Reduces Respiratory Tract Infections. Was. B. animalis AHC7 to protect mice It was found against S. typhimurium infection and prevents acute diarrhea in dogs. Mechanisms Basic Prevention of Acute Diarrhea B. animalis AHC7 due to weakened activation of pre-transcription factor Inflammation is in response to infection. Bifidobacteria also latent in the transport of infectious strains And chronically they are used. For example, B. longum ATCC 15707 can cause infection Prevent Clostridium difficiles. While B. longum 51A protects against lung infection caused the Klebsiella pneumoniae This protection granted by B. longum 51A due to activation The signaling pathway is a Toll receptor-like that leads to the production of reactive oxygen species. Sort Similarly, B. longum 51A was used to reduce the parasitic burden of Giardia in Mongolian gerbils (Meriones). unguiculatus), make this strain a preventative and therapeutic probiotic suitable for health promotion Human and animal transformed.

Methods: Preparation of microbial culture Bifidobacterium bifidum was obtained from the National Center for Genetic and Bio-Resource in Iran. Culture of Bifidobacterium Bifidum After regeneration of bifidobacterium bifidum lyophilized in MRS Broth medium Incubated at 30Â°C for 24 hours. the Continuing Work Case Use is given. Also, fresh culture was prepared for storage of bacteria. Bacteria Storage For long-term storage of bacteria for this research, stock is prepared and Periodically slaughtered. Fresh bacteria mixed with glycerol 50% for preparation of stook. It was then stored in vials at -20Â°C Detection of antibacterial properties of metabolites Isolation of metabolite from Bifidobacterium bifidum Isolation of antimicrobial metabolites from Bifidobacterium bifidum culture It was just made. The bacteria were then inoculated into the new medium and the bacteria were heated for 72 hours. Placed. Then, the medium was centrifuged with 12000 g for 10 minutes, then supernatant Isolated from cells and from supernatant cells for evaluation of antimicrobial and anticancer activity was used. For this purpose, supernatant of cells were lyophilized and then when working the concentrations of the cells were met. different from them newly developed. Culture of bacteria tested In this study, to investigate the antibacterial effect of Bifidobacterium bifidum metabolite from bacteria Bacillus anthracisØŒ Proteus bacteriaØŒ

Pseudomonas aeruginaseØŒ Klebsiella and Escherichia coli used. In the first stage, these three bacteria were cultured in liquid nutrient broth medium to prepare fresh bacteria. These bacteria were then used to investigate the antibacterial properties. Evaluation of antibacterial properties To investigate the antibacterial effect of Bifidobacterium bifidum in this study from Muller culture medium Hinton Agar was used. For this purpose, we use the method of creating wells to determine the amount of inhibitory is used. In wells method, we use suspension of pathogenic bacteria cultivated in the medium Nutrient broth (0.5 McFarland) was cultured with sterile swaps on Muller Hinton agar medium. then Sterile Pasteur pipette was used to create wells on the medium and made of Bifidobacterium supernatant liquid Bifidum with 0.1 ml concentration of 5, 10, 15 and 20 in wells and plates poured At 37 Â°C, it was stored for 24 hours. Measuring the diameter of the inhibition zone Then, the diameter of the inhibition zone created by Bifidobacterium bifidum against each of the bacteria Pathogenesis, Bacillus anthracis, Proteus and Pseudomonas aeruginase were measured.

Results: Antibacterial effect The diameter of inhibition zone was measured after the metabolite exposure to the three studied bacteria. In Table 1-4, the results of the inhibition zone of all three bacteria are presented. In this study, the supernatant was first prepared for bifidu bacteria 24, 48, 72 and was used for the method. Antibacterial was used for the studied bacteria and the Mullerington agar medium was used. Was. The results of this study showed that 72-hour supernatant has the highest effect and antibacterial properties The other two times were 24 and 48 hours. That's why these metabolites are lyophilized and It was used to continue. The effect of inhibition zone of bacteria in the vicinity of metabolite under study Bacteria mean diameter of inhibition zone (ml) Bacillus anthracis 12 Proteus 13 Pseudomonas aeruginase 3 Klebsiella Escherichia coli - Inhibition of growth by metabolite tested. These results show that the metabolites prepared in this study have the greatest effect on bacteria Proteus bacteria showed no growth inhibition effect on Klebsiella and Escherichia coli. Conclusion: Today, one of the important health problems is resistance of bacteria to various antibiotics. And it's been hard for researchers to always look for new materials with antibacterial properties to worry about. The public will be reduced in this case. What can be done in new investigations for anti-virus Bacterial metabolites are bacteria that can be effective in this regard. Hopefully they will be able to treat antibiotic-resistant bacteria.

Conclusion: It is believed that many intestinal bacteria are due to their metabolic properties and ability In changing microbial homeostasis, they are involved in various inflammatory and immune processes that affect the cause of the tumor. Although many of the microbiota functions are still unclear, across the spectrum Extensive intestinal microorganisms, various species belonging to the genus Bifidobacterium The results of this study showed that the metabolite of Bifidobacterium has antibacterial properties. So this metabolite can contribute to human health.

Keywords: Bifidobacterium bifidom, Antibacterial, Pathogen, Infection, Treatment

Evaluation of blood and blood products consumption in gynecological surgeries in Shahid Sadoughi Hospital in Yazd (Research Paper)

Aref Atefi,[1,*] Parisa Dehghan,[2] Mohadese Zare Bidoki,[3]

1. Infectious Diseases Research Center, Shahid Sadoughi University of Medical Sciences, Yazd, Iran
2. Infectious Diseases Research Center, Shahid Sadoughi University of Medical Sciences, Yazd, Iran
3. Faculty of Biological Sciences, Yazd University, Yazd, Iran

Introduction: Anemia and bleeding during and after childbirth are the most common causes of maternal death due to vaginal delivery and cesarean section. According to the CDC definition, anemia is diagnosed based on hemoglobin less than 11 mg/dl in the first and third trimesters and less than 10.5 mg/dl in the second trimester of pregnancy. Bleeding is one of the four leading causes of death for women who give birth after 20 weeks of pregnancy. Due to the high probability of bleeding and its complications during and after childbirth and gynecological surgeries, many blood units are routinely reserved before gynecological surgeries. Managing how to order and maintain the cold chain significantly reduces the financial burden on the country's health system. This study aimed to determine the consumption rate of blood and blood products in gynecological surgeries in Shahid Sadoughi Hospital in Yazd in 2016-2017.

Methods: The study is a cross-sectional descriptive study, and the sampling method is a census; The required information was also obtained through a questionnaire. Data were extracted through the hospital hemovigilance protocol and Hospital Information System (HIS) and analyzed by SPSS22 software.

Results: The mean age was 36.79Â±10.69, and the highest blood type was related to blood group O (40.1%). The highest demand for blood products was related to cesarean section (23.6%), followed by laparoscopy (15.1%). The most requested product was Packed red blood cells at 56.6%. In this study, 14 cases of immunological reactions were reported. The C/T level in the present study is 1.03, and the TI level is 2.1.

Conclusion: The result of the present study, by comparing the C/T and TI indices with the standard rate, shows the optimal status of blood demand and consumption. Improper transportation, lack of temperature monitoring in consumer centers, and ordering too much blood were among the causes of blood waste. It is suggested that the MSBOS program (Maximum Surgical Blood Ordering Schedule) be implemented prospectively in the studied sections, and then the amount of damage and the C/T ratio be compared with the previous one; In addition, periodic monitoring of requests for blood and

products and periodic review and revision of MSBOS based on the experience of medical personnel at the same time as choosing logical methods of requesting blood, organizing the system of transporting blood and products from the hospital blood bank to the ward (injection site) for assurance It seems necessary to maintain the cold chain, fast transport and ensure quick access to the treatment department without delay immediately after declaring the need of the operating room.

Keywords: Blood and blood products, Gynecological Surgeries, MSBOS

Evaluation of PDGFRB expression level in childhood Iranian Patients with ALL (Research Paper)

Tarlan Nayebbagher,[1] Seyed Jalal Zargar,[2,*] Vahid Reza Yassaee,[3]

1. Genomic Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
2. Department of Cell and Molecular Biology, School of Biology, College of Science, University of Tehran, Tehran, Iran
3. Genomic Research Center, Taleghani Hospital, Shahid Arabi Street, Yaman Avenue, Velenjak, Tehran, Iran

Introduction: Correlation between gene Expression and recurrence as a treatment failure in pediatric patients with Acute Lymphoblastic Leukemia (ALL) is an unsolved problem in scientific associations. In this study, we evaluate predictive value of PDGFR expression level for estimating recurrence in Iranian Pediatric Patients with ALL and its MRD level after chemotherapy. ALL MRD refers to the presence of residual Leukemia cells following the achievement of complete remission, but below the limit of detection using conventional morphologic assessment; Patients with detectable MRD have an increased likelihood of relapse. MRD has emerged as the strongest independent predictor of individual patient outcome and is crucial for risk stratification and if is evaluated with genetic novel biomarkers, will be effective at target therapy and increase in patientâ€™s survival rate.

Methods: Material and Methods: Iranian pediatric patients with approved ALL enrolled in this study as four groups of new case(ALL) and control(without ALL), patients who were in post-induction phase, and patients in relapse phase. Real-time Polymerase Chain Reaction reacting was done with GAPDH for expressing PDGFRB gene. Gathered data, analyzed with SPSS version 22 and REST 2009 software. Peripheral Blood (PB) of fifty pediatric B, BCP, and ph-like ALL patients (Median age: Years) at new diagnosis clinical stages, and after their follow-up treatment in post-induction phase were collected. Thirty healthy children were included as a control group and twenty patients at relapse phase, in addition. PDGFRB gene expressing was analyzed by RT-PCR. The correlation analysis was performed between PDGFR gene expression and patients demographic and laboratory characteristics. GAPDH housekeeping gene was used as an internal control.

Results: The results showed that PDGFRB gene expression was significantly up regulated in new diagnosis patients and relapse phases compared to the control group. PDGFRB gene expression in Post-Induction phase was significantly lower than its level at new diagnosis stage ($p<0.001$). Moreover PDGFRB gene was significantly up regulated in relapse phase compared to the new diagnosis. One hundred samples (Fifty new case ALL and Fifty controls) enrolled. Beside on PDGFRB expression were detected in twenty

pediatric patients with relapse. PDGFRB had significant relation with high-risk patients of new case ALL and lead to poor prognosis.

Conclusion: PDGFRB levels could be a potential biomarker of therapy response in remission induction therapy for pediatric ALL. Designed expression pattern have the predictive value for estimating of conferring relapse in Iranian pediatric patients with diagnosed ALL. The authors suggest of designing a multiple childhood malignancy center project to evaluate this pattern in a cohort study.

Keywords: Gene Expression, ALL, PDGFRB gene, MRD, Prognostic marker

Examining the challenges of using exosomes as a diagnostic option for diseases related to the immune system (Review)

Fatemeh Behdarvand,[1] Hossein Rezvan,[2,*]

1. Department of Pathobiology, Faculty of veterinary Sceince, Bu-Ali Sina University, Hamedan, Iran
2. Department of Pathobiology, Faculty of veterinary Sceince, Bu-Ali Sina University, Hamedan, Iran

Introduction: Small extracellular vesicles called exosomes have gained interest as potential diagnostic indicators for illnesses linked to the immune system. Their non-invasiveness and capacity to transport a wide range of disease-associated chemicals, such as lipids, proteins, and nucleic acids, provide them with several advantages over traditional diagnostic techniques. Notwithstanding these encouraging attributes, many obstacles prevent the clinical translation of exosome-based biomarkers from being widely used.

Methods: Several obstacles stand in the way of the clinical translation of exosome-based biomarkers. These include challenges related to cost and accessibility, challenges related to exosome profiling technology, challenges related to variation and heterogeneity, challenges related to standardization and reproducibility, challenges in establishing a clear correlation with disease activity and prognosis, validation of diagnostic sensitivity and specificity, and the need for a thorough understanding of exosomes' role in disease pathogenesis. The complicated makeup of bodily fluids makes it difficult to isolate and purify exosomes and increases the risk of contamination from other substances and cell types. Because exosomes show considerable biological change over time within the same individual as well as between people, variation and heterogeneity also provide issues. For biomarker studies to be deemed credible, standardization and repeatability are essential. Furthermore, it is still unclear exactly how exosome levels relate to the onset or course of a disease, and further investigation is required to find strong biomarkers that can accurately gauge the severity of a condition and forecast its course.

Results: Exosomes, which are extracellular vesicles, have attracted a lot of interest as possible biomarkers for immune-related illness detection. Their non-invasive nature and capacity to transport a wide range of disease-associated chemicals provide encouraging advantages over traditional diagnostic techniques. Nonetheless, several obstacles impede the practical use of biomarkers based on exosomes. Furthermore, it is still unclear exactly how exosome levels relate to the onset or course of a disease, and further investigation is required to find strong biomarkers that can accurately gauge the severity of a condition and forecast its course.

Conclusion: Exosome-based biomarkers have great potential to transform the diagnosis of immune-related disorders, notwithstanding several difficulties. Exosomes have the potential to be effective instruments for early identification, individualized therapy, and better patient outcomes if these issues are resolved and cooperative efforts between researchers, physicians, and diagnostic businesses are encouraged.

Keywords: challenges-exosomes-immune system

Examining the titer of antibodies against surface and central antigens of hepatitis B virus among students of Dezful University of Medical Sciences (Research Paper)

Behnam Azizolahi,[1,*] Susan Sabbagh,[2] Alireza Khosropanah,[3] Mohsen Piramoon,[4] -,[6]

1. Department of Medical Laboratory Sciences, School of Paramedicine, Dezful University of Medical Sciences, Dezful, Iran
2. Department of anatomical science, School of medicine, Dezful University of Medical Sciences, Dezful, Iran.
3. Department of internal Medicine, School of medicine, Dezful University of Medical Sciences, Dezful, Iran.
4. Student Research Committee, Dezful University of Medical Sciences, Dezful, Iran
6. -

Introduction: Introduction: Hepatitis B disease is one of the diseases that has been a serious threat to the health of health care workers. Therefore, this study aims to investigate the titer of antibodies against surface and central antigens of hepatitis B virus among students of Dezful University of Medical Sciences in the academic year of 1401.

Methods: Methods: This is a cross-sectional descriptive epidemiological study that was conducted on 331 students of Dezful University of Medical Sciences who need to enter hospital departments for internships in the future. At first, the demographic information included gender, field and level of education were taken. In order to determine the antibody titer against the s antigen of the virus, commercial kits were used by the ELISA method, and to determine the previous infection, the ELISA method kits were used to measure the antibody titer against the c antigen. The obtained results was analyzed by spss software using descriptive statistical methods.

Results: Results: The present study was conducted among 188 students of Dezful University of Medical Sciences. 68.6% of them ranged in the age of 21-30 years old, 50.5% were female students, and the distribution of the field of study showed that most of the participating students were medical and nursing students. Regarding HBSAb antibody, 49.5% were weak or unsafe, 45.2% were moderate or acceptable, 5.3% were strong or favorable, and the results also showed that there was a significant relationship between HBSAb antibody titer and age. HBCAb antibody titer was negative in 95.2% of students

Conclusion: Conclusion: The results of this study show that half of the students of Dezful University of Medical Sciences do not have adequate immunity to protect against hepatitis B virus infection. Therefore, it is

necessary to check the antibody titer of students of medical sciences, especially students of fields that have a high risk of exposure to this virus, and if their antibody titer is low, a reminder vaccine should be prescribed for them

Keywords: HBSAb, HBCAb, hepatitis, students.

Exosomal miRNAs: Emerging Biomarkers for Cervical Cancer Diagnosis, Prognosis, and Therapy (Review)

Amirsoheil Karami,[1,*]

1. Bachelorâ€™s student, Microbiology group, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran.

Introduction: Exosomes, minuscule extracellular bodies released by a diverse range of cells, including neoplastic cells, exhibit an intricate composition of molecules. These vesicles encapsulate miRNAs, which are small non-coding RNA molecules instrumental in regulating gene expression. Evidence has consistently shown miRNAs to modulate a plethora of cellular processes, including carcinogenesis and tumor progression.

Methods: To comprehensively understand the role of miRNAs in cervical cancer, we conducted a rigorous literature search utilizing PubMed, Google Scholar, and NCBI databases. This search yielded 36 pertinent articles, which were meticulously reviewed and analyzed to provide a deeper understanding of this topic.

Results: The association of exosomal miRNAs with cervical cancer progression has been demonstrated in various studies. One study observed lower levels of miR-1228-5p, miR-33a-5p, miR-3200-3p, and miR-6815-5p in the plasma of cervical cancer patients compared to healthy controls. These miRNAs are involved in cellular processes crucial for cancer development, encompassing cell proliferation, invasion, and metastasis. Another study revealed elevated levels of miR-605-5p, miR-6791-5p, miR-6780a-5p, and miR-6826-5p in the plasma of cervical cancer patients compared to healthy controls. These miRNAs are also engaged in processes essential for cancer development, including angiogenesis and immune evasion. These findings suggest that exosomal miRNAs hold promise as clinical markers for cervical cancer. Biomarkers are biological entities employed to diagnose, monitor, or predict the trajectory of a disease. Exosomal miRNAs are a promising biomarker for cervical cancer due to their relative ease of measurement and their ability to be detected in blood, a non-invasive sample. In addition to their potential as biomarkers, exosomal miRNAs could also be utilized to develop novel diagnostic tests for cervical cancer. These tests could be employed to screen for cervical cancer in women at high risk for the disease, such as those infected with human papillomavirus (HPV). Moreover, exosomal miRNAs are being investigated as potential therapeutic targets for cervical cancer. One study demonstrated that inhibiting the production of miR-146a-3p, which is elevated in cervical cancer, could induce cancer cell death.

Conclusion: The burgeoning diagnostic potential of exosomal microRNAs (miRNAs) in cervical cancer is garnering widespread attention. These non-invasive biomarkers hold immense promise for early-stage detection, personalized treatment, and long-term disease monitoring. To fully harness the transformative power of exosomal miRNAs, ongoing research is imperative to address the remaining challenges and optimize their integration into existing cervical cancer screening and treatment protocols. As exosomal miRNA profiling matures, its widespread adoption is anticipated to revolutionize cervical cancer management, leading to improved patient outcomes and a reduction in mortality rates.

Keywords: miRNA, Cervical Cancer, Exosome

Exosomes in HBV infection (Review)

Hosein Izadi,[1] Shaghayegh yazdani,[2,*]

1. Bachelorâ€™s student. Department of Biology and Molecular, Faculty of Modern Science and Technologies, Tehran Medical Science, Islamic Azad University, Tehran Iran.
2. Department of Microbiology, Faculty of Medicine, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran.

Introduction: Recent research has unearthed compelling evidence for exosome-mediated transmission of the Hepatitis B virus (HBV). Viral particles have been found directly enclosed within exosomes released by infected cells [68]. While the specific mechanism of HBV integration into exosomes remains partially obscure, parallels may exist between viral and exosomal biology. Colocalization of HBV envelope proteins with multivesicular body (MVB) markers AIP1/ALIX and VPS4B in human hepatocellular carcinoma cells suggests a shared pathway.

Methods: To elucidate the multifaceted role of exosomes in Hepatitis B virus (HBV) infection, a meticulous search was conducted across three prominent databases: PubMed, Google Scholar, and NCBI. This extensive search yielded 23 relevant articles, which were subsequently subjected to rigorous review and analysis to gain a comprehensive understanding of the current research landscape in this domain.

Results: Exosomes in Antiviral Immunity and Therapy for HBV: â€¢ Exosomes deliver IFN-Î±-related microRNAs from macrophages to HBV-infected hepatocytes, partially inhibiting viral replication and transcription. â€¢ HBV-encoded miR-3 targets its own transcription area to suppress viral replication through SOCS5 downregulation and subsequent JAK/STAT activation, potentiating IFN-induced anti-HBV effects. â€¢ Exosomal HBV-miR-3 promotes M1 polarization in macrophages and enhances IL-6 by inhibiting SOCS5-mediated EGFR ubiquitination. Therapeutic Implications: â€¢ NRTIs effectively reduce HBV DNA and inflammation but pose a risk of relapse and disease progression after treatment cessation. â€¢ Studies suggest NRTIs might upregulate PD-L1 expression on monocytes/macrophages, paving the way for combination therapy with PD-1/PD-L1 inhibitors. â€¢ PD-1/PD-L1 blockade has shown potential in reviving HBV-specific T-cell immunity, suggesting its role as a potential adjuvant therapy in selected HBV patients. However, exosomes' involvement in this process remains unclear.

Conclusion: As highlighted in this review, exosomes play a multifaceted and critical role in HBV infection. They facilitate viral particle production, promote HBV transmission, and influence the overall pathogenicity. Exploring the

potential to block exosome-related pathways emerges as a promising avenue for developing alternative HBV treatment strategies. Despite being in its nascent stages, research on HBV-derived exosomes unveils their substantial clinical potential.

Keywords: HBV â€“ Exosome - Replication â€“ Synthesis - Therapeutic target

Exploring the Role of MicroRNA-125b (a new biomarker), signal transducer and activator of transcription 3 (STAT3) and sirtuin 6 (SIRT6) Genes in Blood Leukocytes of Atherosclerosis Patients; A Case-Control Study (Research Paper)

Gholamreza Shahsavari,[1,*] Atefeh Mirderikvand,[2] Alireza Moayyed Kazemi,[3] Fatemeh Ahmadpour,[4] Banafsheh Yalameha,[5]

1. Department of Clinical Biochemistry, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Department of Clinical Biochemistry, Faculty of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Department of Internal Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran
4. Nutritional Health Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran
5. Department of Biochemistry and Clinical Laboratories, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran

Introduction: Atherosclerosis (AS) is an inflammatory disease of the arterial wall that is associated with vascular events. miR-125b dysregulation contributes to the pathogenesis of cardiovascular diseases. Moreover, there is evidence of the involvement of signal transducer and activator of transcription 3 (STAT3) and sirtuin 6 (SIRT6) in AS. This study aimed to survey expression levels of miR-125b, STAT3, and SIRT6 in the peripheral blood mononuclear cells (PBMCs) of AS patients and controls and finding their correlations with biochemical parameters and risk factors.

Methods: This study was performed on blood samples of 45 controls and 45 AS patients and PBMCs were isolated by Ficoll solution. The expression levels of miR-125b, STAT3, and SIRT6 were determined by quantitative Real Time- PCR.

Results: The results showed a significant increase in miR-125b levels in the patients compared to controls ($P = 0.017$). However, expression alterations of STAT3 and SIRT6 were not meaningful ($P > 0.05$). No substantial relationship was found between miR-125b and STAT3 ($P = 0.522$) and SIRT6 ($P = 0.88$). miR-125b indicated a significant relationship with atherogenic indexes and creatinine ($P < 0.05$) and the association of SIRT6 with HDL and creatinine was substantial ($P < 0.05$). STAT3 had high diagnostic power to detect individuals at risk of heart disease and hypertension ($P < 0.05$).

Conclusion: STAT3 could serve as a valuable biomarker for the detection of AS and AS-related risk factors. miR-125b and SIRT6 had an association with AS lipid metabolism. Nevertheless, we suggest conducting further studies with

larger-size samples to mechanistically elucidate the association of these genes.

Keywords: Atherosclerosis, microRNA-125b, Signal transducer and activator of transcription 3, Sirtuin 6, Leuko

Ferroptosis: A Promising Therapeutic Target for Acute Leukemia (Review)

Roya Nekonam,[1] Amirsoheil Karami,[2] ,*

1. Department of Microbiology, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran
2. Department of Microbiology, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran

Introduction: Acute leukemia, a type of blood cancer, manifests as an uncontrolled proliferation of abnormal white blood cells, disrupting the bone marrow and blood composition. Ferroptosis, a recently identified type of programmed cell death (PCD), has emerged as a promising therapeutic target for leukemia treatment. Ferroptosis is triggered by the excessive accumulation of reactive oxygen species (ROS) within cells. These highly reactive molecules can inflict damage on cellular components, disrupting normal cellular functions.

Methods: To gain a comprehensive understanding of the role of Ferroptosis in acute leukemia, a thorough literature search was conducted across PubMed, Google Scholar, and NCBI databases. This search identified 28 relevant articles that were carefully reviewed and analyzed to provide a deeper insight into this subject.

Results: The accumulation of reactive oxygen species (ROS) in leukemic cells is a hallmark feature that facilitates the induction of ferroptosis. This accumulation arises from a combination of factors, including: Impaired Glutathione Peroxidase 4 (GPX4) Activity: GPX4 is a crucial antioxidant enzyme that plays a pivotal role in detoxifying ROS. In leukemic cells, GPX4 activity is often compromised, leading to an inability to effectively neutralize ROS, rendering them more susceptible to ferroptosis. Increased ROS Production: Leukemia cells exhibit an abnormally high rate of ROS production, often stemming from mitochondrial dysfunction and other metabolic abnormalities. This enhanced ROS generation further contributes to the accumulation of ROS, amplifying the likelihood of ferroptosis. These molecular mechanisms underlie the susceptibility of leukemic cells to ferroptosis, opening up avenues for therapeutic intervention that target the regulation of ROS and the restoration of GPX4 activity. Several studies have demonstrated the efficacy of ferroptosis-inducing agents in inhibiting leukemia cell growth both in vitro and in vivo. These agents exert their effects by targeting the pathways that regulate ferroptosis. For instance, RSL3 is a small molecule that specifically targets the prolyl-4-hydroxylase (P4H) enzyme, disrupting its activity and leading to the accumulation of iron-sulfur clusters (ISCs) within cells. These ISCs interfere with the function of glutathione peroxidase 4 (GPX4). As a result, excessive ROS accumulate, triggering

ferroptosis in leukemia cells. Ferroptosis-inducing gene therapy utilizes a gene therapy approach to deliver a proapoptotic protein, such as prolyl hydroxylase domain-containing protein 6 (PHD6), directly into leukemia cells. PHD6 promotes the degradation of GPX4, further impairing the cell's antioxidant defense and facilitating ferroptosis.

Conclusion: For all intents and purposes, ferroptosis emerges as a compelling therapeutic target for acute leukemia, with numerous studies validating the efficacy of ferroptosis-inducing agents in suppressing leukemia cell growth both in vitro and in vivo. Ongoing clinical trials are poised to further delineate the therapeutic potential of these agents in the treatment of acute leukemia, paving the way for novel and effective therapeutic strategies against this debilitating disease.

Keywords: Ferroptosis, Acute Luekemia, ROS, GPX4

Galactosemia and its effect on FSH hormone in female infants (Review)

Zahra Ramezani,[1,*] Issa Layali,[2] Saghar moosavi,[3] Negin Koohi,[4] Fatemeh Karimi,[5]

1. Tehran Medical Sciences Branch
2. Tehran Medical Sciences Branch
3. Tehran Medical Sciences Branch
4. Tehran Medical Sciences Branch
5. Tehran Medical Sciences Branch

Introduction: This article discusses a disease called galactosemia, which is a genetic disorder that can cause serious symptoms and long-term complications in infants and children. The disease affects the way the body breaks down glucose, leading to the accumulation of toxic substances. The text details the discovery and progression of our understanding of galactosemia over the past century, from our initial understanding of the disease's clinical appearance to the discovery of multiple types of the disorder and the underlying genetic and biochemical causes. It describes the discovery of potential treatments, including drugs to reduce toxic intermediates, antioxidants to reduce oxidative stress, and the use of "drug chaperones" to stabilize damaged proteins. The text emphasizes the importance of early diagnosis and treatment to prevent long-term complications, particularly in infants and girls with classic galactosemia who may experience premature ovarian failure.

Methods: Classical galactosemia is a genetic disorder characterized by the absence or inactivity of the enzyme galactose-1-phosphate uridyltransferase. It mainly affects infants and causes life-threatening symptoms such as vomiting, jaundice, hepatosplenomegaly and Escherichia coli sepsis in untreated form. One of the possible underlying mechanisms of ovarian failure is FSH inactivity due to secondary hypoglycosylation, which has been proposed as a potential mechanism for primary ovarian failure. To investigate the role of FSH and gain insight into the timing of injury, ovarian stimulation experiments were performed and ovarian imaging data were collected. 15 patients with primary ovarian failure underwent ovarian stimulation with gonadotropin. People with classic galactosemia are usually treated with exogenous estrogens to treat the hypoestrogenism complications of this disease, and the mechanism of primary ovarian failure in this disease is not fully understood. While various mechanisms have been hypothesized, including direct toxicity of metabolites and altered gene expression due to glycosylation abnormalities, it is likely that not one but several mechanisms are responsible for this clinical picture. Alteration of FSH function due to hypoglycosylation in this disease can lead to early ovarian failure, and if FSH inactivity is a key mechanism, we can expect an increase in estradiol when exogenous and active FSH is administered. However, the results of studies on the glycosylation pattern of FSH in women with classic galactosemia and

POI are different, and it is believed that not one, but several mechanisms acting in concert are responsible for this clinical picture.

Results: classical galactosemia is an inherited metabolic disorder caused by GALT deficiency and causes glycosylation abnormalities, and while most affected infants are spared acute and potentially fatal symptoms due to early diagnosis and lifelong nutritional interventions, Many patients have long-term complications includingPremature ovarian failure is in the vast majority of girls and young women.

Conclusion: This condition is caused by mutations in genes involved in galactose metabolism. There are different forms of galactosemia and the severity of symptoms can vary, which we have mentioned in this review article.

Keywords: Hereditary metabolic disorder Ovarian failure Exogenous estrogens Hypoglycosylation Hypoestrogenism

Highly effective anti microbial properties of biogenic CuSe nanoparticles mediated Rumex alveollatus aqueous extract against Streptococcus mutans and entrococcus fecalis on the dental surfaces (Research Paper)

Maryam Karkhane,[1] Abdolrazagh Marzban,[2] Ameneh Marzban,[3] ,*

1. Department of Medical Biotechnology, School of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran.
2. Razi Herbal Medicines Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Department of Health in Disasters and Emergencies, School of Health Management and Information Sciences, Iran University of Medical Sciences, Tehran, Iran

Introduction: Metal nanoparticles have gained attention as antimicrobial agents due to their broad-spectrum antibacterial activity and non-specific bacterial toxicity mechanisms [1]. These nanoparticles do not bind to a specific receptor in the bacterial cell, making it difficult for bacteria to develop resistance. There are several significant antimicrobial mechanisms of metal nanoparticles such as generation of reactive oxygen species and cation release, which both can cause bacterial cell damaging; Biomolecule damage lead to inhibition of bacterial cell growth; ATP depletion and Membrane interaction subsequently death of bacterial cells. Various types of nanoparticles have been studied for their antimicrobial properties, including silver, gold, zinc oxide, copper, and copper oxide nanoparticles. These nanoparticles can be used in various applications, such as antibiotherapy, antifungal therapy, and antiviral therapy. However, more research is needed to fully understand the mechanisms behind their antimicrobial activity and to develop effective strategies for their application in medicine and other fields. Some of biocidal nanomaterials have longer-time bacterial effects. Among these materials, copper selenide (CuSe) have shown highly effects antimicrobial effects. CuSe nanoparticles have been synthesized using different methods such as rapid injection approach, chemical bath deposition, direct vapor transport-grown compound, and chemical precipitation method. However, Copper nanoparticles (CuNPs) can be synthesized using plant extracts in a process known as green synthesis, which is more environmentally friendly and offers improved properties of the synthesized nanoparticles in terms of biocompatibility and functional capabilities. Several studies have evaluated the antibacterial activity of Rumex alveollatus extracts against various bacterial strains, including Staphylococcus aureus, Pseudomonas aeruginosa, Klebsiella pneumoniae, Enterobacter aerogenes, Salmonella typhi, and Streptococcus pyogenes. The extracts of Rumex alveollatus have been found to have significant inhibitory effects on these bacterial strains, with the methanol and ethanol extracts showing the most potent antibacterial activity. The antibacterial activity of Rumex alveollatus extracts has been attributed to the presence of anthraquinones and

flavonoids, which have been shown to have antibacterial, bacteriostatic, antiviral, antitumor, and antioxidant properties. The synthesis of copper selenide (CuSe) nanoparticles using Rumex alveollatus plant extract is not directly addressed in the previous existing studies. Thus, we aimed to investigate the antimicrobial effects of copper selenide (CuSe) bio-synthesized by Rumex alveollatus extract especially against dental bacteria such as streptococcus mutans and Enterococcus faecalis.

Methods: 2.1.Preparation of extract from Rumex alveollatus The extraction was performed based on aqueous extraction by 10g of dried Rumex alveollatus in 100 ml distilled water which overnight incubated in 50Â°c. Then the purified extract was dried in 50Â°c. 2.2. Biosynthesized of CuSe NPs coated by Rumex alveollatus extraction We prepared A solution contained 200mg of Rumex alveollatus extraction per 50 cc distilled water and B solution with 0.2 g sodium selenide and 0.2 g sodium solphide per 50 cc distilled water. Both were mixed on thermo stirrer that adjusted on 80Â°c and mild rotation for 3hours. Final solution was dried in 60Â° c. 2.3. The evaluation of minimum inhibitory concentration The effect of RA-CuSeNPs on S. mutans and entococcus fecalis was examined by the microdilution method. The results were defined as minimum inhibition concentration (MIC). Briefly, a two-fold serial dilution of samples was prepared in 96-well polystyrene plates containing TPY broth (200 ÂµL/well). RA-CsNPs were tested at the range of 400 to 50 Î¼g/mL. A 20 ÂµL of bacterial cell suspensions were inoculated into each plate well (5 Ã— 107 cfu/mL). Bacterial growth was monitored in an anaerobic incubator (20% CO2, 80% N2, 37 Â°C, 24 h). Firstly supernatant was removed and TTC was added to each well,and cell absorbance was measured at 595 nm.

Results: The minimum inhibition concentration (MIC) was defined as the lowest concentration of the agent that showed 50% or more inhibition on the bacterial growth. The range of MIC is 200 Î¼g/mL for S. mutans and 250 Î¼g/mL is related to E. fecalis.

Conclusion: A efficient CuSe NPs biosynthesized by AR extraction has shown effective anti microbial properties against both streptococcus mutans and entrococcus fecalis. The results of this study proposed prospective view for further of cu-Se â€“AR nanoparticles in Oral hygiene products and oral therapeutic materials.

Keywords: copper selenide nanoparticles, green synthesis, Rumex alveollatus, anti bacterial properties.

Identification of potential biomarkers related to pancreatic ductal adenocarcinoma in a bioinformatics study (Research Paper)

AmirReza Homaei,[1,*]

1. Medical Genomics Research Center, Islamic Azad Tehran Medical Sciences University, Tehran, Iran

Introduction: Pancreatic cancer is one of the most common causes of death in cancer patients. This cancer has different types, the most common type of which is called pancreatic ductal adenocarcinoma (PDAC). PDAC has a 5-year survival rate of less than 10%. Our aim of conducting the following research is to investigate and identify mRNA and miRNA biomarkers in PDAC pancreatic cancer

Methods: this study method is based on the analysis of Protein-Protein interaction network and mRNA - miRNA interactions. To conduct this study, the Microarray gene-expression data profile containing tumor samples, adjacent non-tumor tissue and normal pancreas donors was selected. After bioinformatics analysis, up-regulated and down-regulated genes were selected and the protein protein interaction network was drawn for them. After analysis using software, one gene module and one hub gene were selected from each set of up-regulated and down-regulated genes. In the next step, common genes between modules and hub genes were obtained for each of the up-regulated and down-regulated gene sets. Then, using web tools, validation was done for each of the obtained common genes, and finally KRT19 gene was selected as the only valid gene introduced by online bioinformatics tools. In the next step, the interaction between mRNA and miRNA was investigated by bioinformatics tools and among the introduced miRNAs, two miRNAs(hsa-miR-193b-3p and hsa-let-7b-5p) with significant survival effect on patients were selected as potential biomarkers for the KRT19 gene. In the last step, targets scan was performed for the two selected miRNAs and it was found that hsa-miR-193b-3p and hsa-let-7b-5p have 332 and 990 other target genes, respectively, except KRT19

Results: The final result is that three potential biomarkers include KRT19 gene, hsa-miR-193b-3p and hsa-let-7b-5p as potential biomarkers obtained from this study

Conclusion: Other studies, including immunohistochemical studies conducted by other researchers in the past, have investigated and proved the relationship of KRT 19 gene with metastasis and poor prognosis in PDAC

Keywords: PDAC/systems biology/cancer/biomarker/tumor marker

Identification of potential biomarkers with Acute myeloid leukemia based on Bioinformatics analysis (Review)

Narjes Seddighi,[1,*] Aidin Darbeh,[2]

1. 1- Student Research Committee, Tabriz University of Medical Sciences, Tabriz, Iran 2- Hematology and Oncology Research Center, Tabriz University of Medical Sciences, Tabriz, Iran
2. 3- Student Research Committee, Faculty of Medicine, Hormozgan University of Medical Sciences, Bandar Abbas, Iran

Introduction: Acute myeloid leukemia is a group of heterogeneous clonal diseases that affect the source of myeloid hematopoietic progenitor cells; AML is defined by numerous cytogenetic and molecular heterogeneities. Additionally, AML is characterized by the unchecked growth of myeloid blasts in the peripheral blood and bone marrow in addition to the suppression of regular hematopoiesis. Relapse and refractory disease continue to be major obstacles in the treatment of AML, about 29% of AML patients are expected to survive more than five years. Gene expression profile analysis is a potent research technique that reveals patients' dysregulated genes by integrating data from functional genomics, molecular transcription, and genetics. In this study, we are going to evaluate RNAseq data obtained from TCGA in acute myeloid leukemia and investigate prognostic and protective genes in survival.

Methods: First, GEPIA2 (http://gepia2.cancer-pku.cn/) was used to examine the TCGA LAML dataset in order to identify all DEGs linked with LAML among high throughput RNA-Seq data. GEPIA2 is an online program that uses the Genotype-Tissue Expression (GTEx) projects and the TCGA database to evaluate the transcriptional patterns of human malignancies and normal tissues. Genes with a P-valueâ€‰<â€‰0.05 were considered significant; after that, significant genes were divided into 4 groups including up/down prognostic or protective genes according to the logFC and HR. After that, we used cBioPortal (https://www.cbioportal.org/) to evaluate the survival and prognostics of mutation in the significant genes. In the end, a Protein-protein interaction (PPI) network of significant genes associated with AML was constructed with STRING at the Cytoscape software.

Results: of 7965 genes acquired from TCGA-RNAseq for AML, 843 genes are considered significant (adjusted P-value < 0.05), of which 666 genes are prognostic and 174 genes are protective. we also use CBioportal to evaluate the effect of mutation on survival in AML patients. According to the result, 8 genes are significantly related to survival including PSMG1, SLC37A1, FAM207A, GPS2, CSTB, CHAF1B, AKAP9, and ABCG1 (p-value and q-value < 0.05). PPI networks were drawn for significant genes and also hub genes.

Conclusion: This study identifies hub genes as a promising prognostic, protective, and diagnostic biomarker for acute myeloid leukemia. Further investigations are warranted to identify the therapeutic potential of these genes.

Keywords: Acute myeloid leukemia, TCGA, RNAseq, bioinformatics, significant genes

Identification of the most important cause of stomach cancer by non-invasive method through oral cavity (Research Paper)

Siavash Sharifi,[1] Farnaz Farzaneh Dehkordi,[2,*]

1. Department of Biology, Ardabil Branch, Islamic Azad University, Ardabil, Iran
2. Department of Biology, Ardabil Branch, Islamic Azad University, Ardabil, Iran

Introduction: Helicobacter pylori is a gram-negative, microaerophilic, spiral-shaped bacterium that lives in the gastrointestinal tract and causes ulcers and cancer. This bacterium has been observed in the mouth in recent studies, so the mouth is its second reservoir. Endoscopic diagnostic test, Serology test, Stool test, Urease Breath Test and Polymerase Chain Reaction test are used to identify H.pylori. In the mentioned tests, samples taken from the stomach, blood, etc. are used. These tests have drawbacks and problems such as being aggressive, expensive, creating false results, and so on. The main purpose of this study was to evaluate H. pylori infection through saliva by PCR method as a fast, simple, cheap and non-invasive method and compare it with UBT (Gold Standard Test).

Methods: In this study, saliva samples were collected from 81 women and 63 men referred to Ardabil diagnostic laboratories with gastrointestinal symptoms suspected of H.pylori infection. DNA purification from case-control samples was performed by two methods of boiling and DNP sinaclon kit. After quantification and DNA quality assay by nanodrop to detect H.pylori, PCR was performed with specific primers (UreC) and the results were analyzed by SPSS software was performed under Chi-square test.

Results: Significance level was considered 0.05 and considering (P-value = 0.000) in comparing the results of PCR test through saliva with UBT test, we conclude that there is no significant difference between the results of the two tests and the relationship Strong prevails between them.

Conclusion: The results showed that this test has high sensitivity and specificity.

Keywords: stomach cancer, non-invasive method, oral cavity, h.pylory, PCR

Implementation of PBM in dealing with blood crises during surgery (Review)

Motahareh Sadeghi,[1,*] Younes Sadeghi bojd,[2]

1. Student research committee, school of Allied medical science, zahedan university of medical science, zahedan, Iran
2. Department of Laboratory Sciences, School of Allied Medical Sciences, Zahedan University of Medical Sciences, Zahedan, Iran

Introduction: Preoperative anaemia and perioperative blood transfusion are both identifiable and preventable surgical risks. Patient blood management is a multimodal approach to address this issue Patient blood management (PBM) is defined as the application of evidence-based diagnostic, preventive and therapeutic approaches designed to maintain hemoglobin concentration, optimize hemostasis and minimize blood loss to improve patient outcomes. We propose a protocol for the assessment of the evidence of diagnostic, preventive, and therapeutic approaches for the management of relevant outcomes in surgery of patients to create a framework for PBM implementation.

Methods: Medline databases (PubMed, EMBASE, Web of Science, and CINAHL) were searched from 2018 to 2023.

Results: Forty-nine publications matching the selection criteria and reporting results in the predefined areas were included in the final analysis. Pre-operative anemia, even if mild, in patients who are candidates for major surgery (not cardiac) is independently associated with a higher risk of morbidity and mortality at 30 days24. Furthermore, a recent, retrospective study demonstrated that, in the peri-operative period of patients undergoing heart surgery, the sum of two risk factors, that is anemia (hematocrit <25%) and transfusion therapy with red cell concentrates, had a greater, and statistically significant, effect on post-operative morbidity and mortality25. Anemia is, therefore, a contraindication to performing elective surgery.

Conclusion: progress in the identification and implementation of best transfusion practices based on evidence-based systematic reviews suggests that, compared with a liberal allogenic blood transfusion policy, there was no evidence of negative consequences when following a restrictive blood transfusion policy. As PBM is being increasingly introduced in routine clinical practice, there is wide expectation that it will shape the practice of transfusion medicine, the modality of prescription, preparation, and administration of blood components as well as the relationship between different disciplines. PBM brings a paradigm shift in the concept of blood components which should be considered not only an important resource but also a possible risk factor, with increases in costs, a sometimes-limited availability: risky, costly, in

limited supply, and their use can worsen negative patient outcomes. PBM aims to overcome the â€˜product-centeredâ€™ concept of blood components and to have a â€˜patient-centeredâ€™ approach that focuses on improving the health and well-being of the patient.

Keywords: patient blood management, blood transfusion, therapeutic, General Surgery

Importance and diagnosis of skin ectoparasites: Demodex folliculorum, Demodex brevis and Sarcoptes scabiei (Review)

Aysan Asadian,[1,*] Pariya Ahmadizadeh,[2] Ata Golsanamloo,[3] Mohammad Taghi Ahady,[4]

1. Undergraduate student of Microbiology, Department of Biology, Ardabil Branch, Islamic Azad University
2. Undergraduate student, Department of Laboratory Sciences, Ardabil Branch, Islamic Azad University
3. Undergraduate student of Microbiology, Department of Biology, Ardabil Branch, Islamic Azad University
4. PhD of Parasitology, Department of Biology, Ardabil Branch, Islamic Azad University

Introduction: Introduction: Skin care, in addition to beauty, is also important in terms of Health and Prevention of some severe infections. There are various ectoparasites that can cause infections and skin lesions, especially on the skin of the head and face. Among these external parasites of the skin are some species of mites, including Demodex folliculorum, Demodex Brevis, and Sarcoptes scabiei. These three important species of mites in case of severe contamination in human skin can lead to the occurrence of many skin complications and lesions, including itching, redness, eczema, skin inflammation, dermatitis, hair loss, head and face rashes, acne, rosacea, rough skin and blepharitis. Therefore, accurate and timely diagnosis of ectoparasites can help a lot to maintain skin health and care for it. The aim of this systematic review study was to introduce the simplest and most appropriate method of detecting skin contamination with demodex and sarcoptes ectoparasites based on research papers published over the past 12 years.

Methods: Methods: In this systematic review study, in order to access specialized resources and collect published scientific and research articles, authoritative websites including Google Scholar, Science Direct, pubmed, web of science, scopus, elsevier, magiran, sid, and irandoc were referred. Keywords used in Internet search were ectoparasites, external parasites, diagnosis of ectoparasites, Demodex folliculorum, Demodex brevis, Sarcoptes scabiei, diagnosis of demodicosis, and diagnosis of scabies. Published articles in Persian and English from 2012 to 2023 were collected. The criteria for the entry of articles into the study was the direct relationship of their content to the method of detecting ectoparasites and the criteria for the exit of articles from the study to address various topics of ectoparasites in articles other than their laboratory diagnosis.

Results: Results: One hundred forty papers were collected and 48 of them were selected for the present study based on the relationship of their content

to the laboratory diagnosis of ectoparasites. Based on the results and contents of these 48 articles, it was found that all over the world, one of the simplest and most appropriate methods of detecting ectoparasite contamination, including Demodex folliculorum, Demodex Brevis, and Sarcoptes scabiei, is the microscopic observation method. On the other hand, skin sampling and scraping of skin lesions, clarifying the sample by adding 10% potassium hydroxide solution and lactophenol, preparing microscopic smears and finally direct observation with an optical microscope is the simplest and most appropriate method of laboratory diagnosis of ectoparasites. The definitive diagnosis of the species of ectoparasites and mites is based on their morphological characteristics, especially their size and some body parts, as standard gold and by referring to specialized sources and reference books.

Conclusion: Conclusion: Based on the results of this systematic review study, it is concluded that among the types of ectoparasites Demodex folliculorum, Demodex Brevis and Sarcoptes scabiei are the most important and common human skin parasites. And the most appropriate and simple laboratory diagnosis of skin ectoparasites is microscopy technique based on morphological characteristics and reliable references.

Keywords: Keywords: Ectoparasite, Demodex folliculorum, Demodex brevis, Sarcoptes scabiei,Laboratory diagnosis

Investigating circRNAs as Prognostic Biomarkers in Acute Myeloid Leukemia (AML); A systematic review and meta-analysis (Review)

Amir Hossein Aghayan,[1,*] Yasin Mirazimi,[2] Amir Atashi,[3] Mohammad Rafiee,[4]

1. Student Research Committee, Department of Medical Laboratory Sciences, School of Paramedical Sciences, Zanjan University of Medical Sciences, Zanjan, Iran
2. Student Research Committee, Department of Medical Laboratory Sciences, School of Paramedical Sciences, Zanjan University of Medical Sciences, Zanjan, Iran
3. Department of Medical Laboratory Sciences, School of Allied Medical Sciences, Shahroud University of Medical Sciences, Shahroud, Iran.
4. Department of Medical Laboratory Sciences, School of Paramedical Sciences, Zanjan University of Medical Sciences, Zanjan, Iran.

Introduction: Acute myeloid leukemia (AML) is the predominant subtype of acute leukemia in adults and exhibits significant clinical heterogeneity. The prognosis of AML is intricately influenced by individual-specific factors and disease-specific characteristics. For patients with AML, the selection of appropriate prognostic factors is crucial for predicting disease progression, guiding treatment decisions, and monitoring treatment response. Emerging research has shed light on the potential role of dysregulated circular RNA (circRNA) expression as a promising biomarker in AML prognosis. CircRNAs have diverse functions in intracellular processes such as proliferation, apoptosis, metastasis, and cell cycle regulation, primarily through their interactions with miRNAs and other mechanisms. Due to their impact on survival rates, treatment trends, and their circular structure (which confers high stability in tissues and bodily fluids), circRNAs can be considered novel prognostic biomarkers in AML. Consequently, the present study was conducted to systematically evaluate the prognostic implications of circRNA expression profiles in patients diagnosed with AML.

Methods: Original English articles from databases such as PubMed, Scopus, Web of Science, ProQuest, and Google Scholar were searched using different combinations of relevant keywords obtained through MESH from the beginning until March 2023. After extracting the studies from the databases, duplicate studies will be removed. In the next step, screening of the title and abstract of the articles was performed by two authors to determine the relevant studies. Then, the full text of the studies was independently evaluated by two researchers, and the articles were selected based on the inclusion and exclusion criteria. The data collection process was performed based on a checklist predetermined by three authors. The Newcastle-Ottawa Scale (NOS) checklist was used to assess the risk of bias in the included studies. In addition, the certainty of the evidence was assessed using the modified GRADE approach. Also, the hazard ratio (HR) with 95%(CI) was used as the effect size (ES) for performing the prognostic meta-analysis. The

I2 statistic was used to determine heterogeneity. In addition, the random effects model (REM) was used to predict the values due to the presence of methodological heterogeneity. Also, to investigate the publication bias, the statistical tests, Egger, Trim and Fill, and Begg were used. Sensitivity analysis was performed using the leave-one-out method. To reduce heterogeneity between studies and find the factor affecting the effect size, subgroup analysis was performed.

Results: The study encompassed 1541 patients diagnosed with Acute Myeloid Leukemia (AML), derived from 18 primary research studies. The synthesized findings pertaining to the overall survival (OS) indicator revealed a correlation between dysregulated expression of circular RNAs (circRNAs) and an unfavorable prognosis in AML patients (Hazard Ratio [HR] = 2.05; 95% Confidence Interval [CI]: 1.75 to 2.40). The low I2 value of 15.7% for the OS indicator suggested minimal heterogeneity among the studies. Interpretation areas indicated moderate associations between dysregulated expression of (circRNAs) and AML prognosis , and the GRADE assessment categorized these relationships as moderately certain. Employing the leave-one-out method demonstrated that the exclusion of any individual primary study did not exert a significant impact on the aggregated results. However, an asymmetric distribution in the funnel plot pattern, along with Begg's test (P-value = 0.001) and Egger's test (P-value = 0.005), as well as outcomes from the trim and fill method, collectively signified notable publication bias concerning the OS indicator. Despite conducting an exhaustive search across various databases, our study acknowledges the persistence of publication bias. Language limitations and the possibility of negative results bias, wherein studies with unfavorable outcomes may remain unpublished, contribute to this bias. Subgroup analysis for the OS indicator revealed no substantial disparity in terms of expression status and follow-up time among subgroups. However, it was discerned that studies with a sample size of â‰¤68 patients tended to overestimate hazard ratio results, emphasizing the importance of opting for a larger sample size to ensure more reliable outcomes.

Conclusion: This systematic review and meta-analysis provide evidence that the analysis of circular RNA (circRNA) expression changes can serve as a valuable biomarker for assessing the prognosis of patients with AML. The findings suggest that alterations in circRNA expression profiles can potentially aid in predicting the clinical outcomes of AML patients. Further research and validation studies are warranted to fully establish the clinical utility of circRNA expression as a prognostic biomarker in AML.

Keywords: circRNA,Acute myeloid leukemia,prognosis,AML,non-coding RNAs

Investigating the anti-inflammatory effect of omega-3 on type 2 diabetes (Review)

Shokouh Rahmati pour,[1] Reza Bayat,[2] Zahra Rezvani,[3,*]

1. Department of cell and molecular biology, Faculty of chemistry, University of Kashan, Kashan, Iran
2. Department of cell and molecular biology, Faculty of chemistry, University of Kashan, Kashan, Iran
3. Department of cell and molecular biology, Faculty of chemistry, University of Kashan, Kashan, Iran

Introduction: Type 2 diabetes is a chronic disease characterized by increased blood glucose. The reason for this increase is the resistance of cells to absorb insulin, which happens due to genetics, improper diet and inactivity. Observations have shown that along with exercise and proper diet, omega-3 fatty acids are also effective in preventing type 2 diabetes. Omega-3 fatty acids are a family of unsaturated fatty acids, the two most important of which are EicosaPentaenoic Acid (EPA) and docosahexaenoic acid (DHA), which have a significant effect against most metabolic diseases such as fatty liver. Obesity causes oxidative stress and inflammation. Omega-3 is very important in healing the wounds of diabetic patients who have problems. These fatty acids are found in sources such as fish, eggs and olive oils.

Methods: This study was conducted with the aim of reviewing the world's research literature on omega-3 and its effect on many diseases, including diabetes, and was searched in international scientific databases such as Google Scholar, PubMed, Scopus, and Science Direct.

Results: The summaries of the articles were reviewed and duplicate and unrelated items were removed from the study in several stages and finally the articles were selected for comprehensive review and data extraction. The general result of this study was that omega-3 plays an important role in the cell membrane, especially phospholipids and membrane proteins and their permeability.

Conclusion: Omega-3 increases the secretion of insulin from pancreatic beta cells and increases the sensitivity of cells to insulin and reduces blood triglycerides. In a study on the healing of diabetic wounds in mice with diabetes mellitus, consumption of omega-3 rich fish oil was effective in accelerating their healing. In another study, the administration of omega-3 along with metformin to diabetic rats caused cardiac protection in them. In a study, consumption of EPA and DHA was effective in preventing type 2 diabetes. Therefore, taking the right dose of food that contains omega-3 as well as the supplements that have been produced can significantly reduce the damage of various types of wounds.

Keywords: Omega 3, Type 2 diabetes, Inflammation, Eicosa Pentaenoic Acid

Investigating the association between K589E polymorphism of EXO1 gene with the risk of lung cancer as a clinical biomarker in Iranian population (Research Paper)

Milad Pezeshki,[1] Mahdi Nakhaee,[2] Jamshid Ansari,[3,*] Azam Ahmadi,[4] Saeed Ziaei,[5] Roja Valipoor,[6]

1. Development and research group of Lifeandme Company, Tehran, Iran.
2. Development and research group of Lifeandme Company, Tehran, Iran.
3. Department of Oncology, Ayatollah Khansari Hospital, Arak university of Medical Sciences, Arak, Iran.
4. Infectious Diseases Research Center (IDRC), Arak University of Medical Sciences, Arak, Iran.
5. Director of development and research group of Lifeandme Company, Tehran, Iran.
6. Department of Laboratory Medicine, Faculty of Paramedical Sciences, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran

Introduction: Lung cancer is the cancer with the highest incidence and mortality rate in the world. In Iran lung cancer is the third most common type of cancer and its prevalence is increasing rapidly. Single nucleotide polymorphisms in DNA repair genes are associated with differences in the repair efficiency of DNA damage and may affect lung cancer. EXO1 is an important gene that is involved in the mismatch repair system. The existence of K589E polymorphism in the EXO1 gene may alter influencing the repair activity of EXO1 protein and be associated with lung cancer. The present study aimed to evaluate associations between the risk of lung cancer and K589E polymorphism in the EXO1 gene as a clinical biomarker in the Iranian population.

Methods: In this case-control study, the associations of Exo1 K589E polymorphism with lung cancer risk in the Iranian population were investigated. In total, 200 patients with lung cancer and 200 age- and gender-matched healthy controls recruited from Khansari Hospital in Arak city, were genotyped by PCR-RFLP techniques. Finally, statistical analysis was done using the software SPSS version 16. Binary logistic regression analysis was performed to evaluate the association of polymorphism studied with the risk of lung cancer.

Results: The frequencies genotypes and allele analysis for K589E polymorphism of the EXO1 gene in cases and the controls indicated that the AA genotype (P= 0.004, OR= 5.391, CI=95%; 1.690- 17.200) and A allele (P= 0.010, OR= 2.851, CI=95%; 1.291- 6.300) of this polymorphism associated with risk of lung cancer. In contrast, the GG genotype and G allele of this polymorphism showed a protective role against susceptibility to lung cancer.

Conclusion: There is a significant association between the K589E polymorphism of the EXO1 gene and the risk of susceptibility to lung cancer, which is following some researchers. K589E polymorphism of the EXO1 gene can be used as a biomarker for the risk of lung cancer, but more studies with high population size are required.

Keywords: Single Nucleotide Polymorphism, K589E, Lung Cancer, EXO1, PCR-RFLP

Investigating the effect of benign neutropenia in Arabian residents of Mashhad on obesity: The role of MPO in this process (Research Paper)

akram aminian,[1] hadi mohebalian,[2,*] Farzane Bonyadi,[3] Samin Madrasah,[4]

1. Department of Physiology and Pharmacology, Afzalipour Faculty of Medicine, Kerman University of Medical Sciences, Kerman, Iran
2. Department of Immunology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran
3. Department of Basic science, Histology section, Faculty of Veterinary medicine, Urmia University, Urmia, Iran
4. Department of Clinical Sciences, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran

Introduction: Benign neutropenia is a disease that has the ability to become an inflammatory condition . Clinically, it is defined as a neutrophil count of less than 2000/Îœl . In obesity, neutrophils with an active phenotype produce myeloperoxidase (MPO). This enzyme increases the adipogenesis pathway by activating inflammation. In this study, the prevalence of benign neutropenia was investigated in Arab residents of Mashhad. A total of 70 healthy Arab residents (male/female) from Mashhad city in Iran were studied. A blood sample was taken and analyzed for the presence of ethnically benign neutropenia. The results of this study showed that the prevalence of ethnically benign neutropenia was 9.28% (9/70) in Arab residents. Therefore, in people suffering from benign neutropenia and obesity at the same time, Defective cycle caused by MPO, facilitates the process of obesity.

Methods: Totally 70 Arabian healthy residents (male/female) from Mashhad city in Iran were studied. they were asked for their familial background of these diseases. The data were expressed as the MeanÂ±SE (Standard Error Mean). Student t-test was used for analysis. Statistical analysis was done using Prism version 6.07 software. P-values less than 0.05 were considered significant.

Results: Results showed that prevalence of benign ethnic neutropenia in Arabian residents was 9.28% (70/9). Differential hematologic aspect of each group was determined. There is a significant decrease in number of neutrophils and also in their differential count in patients than health peoples.

Conclusion: According to past studies the increasing amount of MPO in patients suffering from neutropenia should be considered. The co-occurrence of obesity and neutropenia is an important issue in future studies .Because of the MPO communication link between these two pathological conditions

Keywords: MPO, neutropenia, obesity, inflammation

Investigating the effect of ethyl acetate and n-butanol fractions of the hydro alcoholic extract of Ferula assa-foetida plant stem on the expression of FGF and VEGF genes in chicken embryos. (Research Paper)

Mohammad Reza Pour Mohammad,[1] Jian Khayat Zadeh,[2,*] Ahmad Zahani,[3] Maryam Tehranipour,[4]

1. Department of Medical Parasitology, Faculty of Paramedicine, Ilam University of Medical Sciences, Ilam, Iran
2. Department of Biology, Mashhad Branch, Islamic Azad University, Mashhad, Iran
3. Department of Biology, Mashhad Branch, Islamic Azad University, Mashhad, Iran
4. Department of Biology, Mashhad Branch, Islamic Azad University, Mashhad, Iran

Introduction: FGF produced by endothelial cells induces proliferation and increases the survival of endothelial cells. FGF are collagenase activators and lead to the sprouting of new vessels from blood vessels, FGF is needed to maintain and progress angiogenesis. It is believed that VEGF acts in the beginning of angiogenesis. Ferula assa-foetida is one of the prominent medicinal plants in traditional medicine. This research was conducted with the aim of investigating the effect of ethyl acetate and n-butanol fractions of the hydroalcoholic extract of the stem of Ferula assa-foetida plant on the expression of FGF and VEGF genes in chick embryos.

Methods: In this research, 72 Ross spray eggs were randomly divided into 8 groups including control, laboratory control (pbs) and 6 experimental groups. After incubation, on the second day of the window, an egg was created and in on the eighth day, after placing the gelatin sponge on the chorioalantoic curve, the fractions of the ferula assa-foetida stem extract (100, 200 and 300 Î¼g/ml) were injected onto the chorioalantoic membrane of the chick embryo. In order to extract RNA and examine gene expression, a sample was taken from the chorioallantoic membrane and by making cDNA, the expression changes of VEGF and FGF genes were quantitatively measured. The collected data were analyzed by Excel and SPSS 20 statistical software.

Results: The average expression of VEGF and FGF genes in the laboratory control group did not show any significant difference compared to the control group. The average expression of VEGF and FGF genes in the concentrations of 100, 200, 300 Âµg/ml of ethyl acetate and n-butanol fractions of ferula assa-foetidastem showed a significant decrease compared to the control group.

Conclusion: According to the methods of this research, the above fractions from the stem of Ferula assa-foetida have an inhibitory effect on angiogenesis in the chorioallantoic membrane of chick embryos. Also, it seems that the compounds in Ferula assa-foetida can be used to inhibit angiogenesis in cancerous tissues.

Keywords: gene expression, Ferula assa-foetida, Chorioallantoic Membrane, Chick Embryo

Investigating the effect of ethyl acetate and n-butanol fractions of the hydro alcoholic extract of Ferula assa-foetida plant stem on the process of angiogenesis of the chorioallantoic membrane of chick embryos (Research Paper)

Mohammad Reza Pour Mohammad,[1] Jian Khayat Zadeh,[2,*] Ahmad Zahani,[3] Maryam Tehranipour,[4]

1. Department of Medical Parasitology, Faculty of Paramedicine, Ilam University of Medical Sciences, Ilam, Iran
2. Department of Biology, Mashhad Branch, Islamic Azad University, Mashhad, Iran
3. Department of Biology, Mashhad Branch, Islamic Azad University, Mashhad, Iran
4. Department of Biology, Mashhad Branch, Islamic Azad University, Mashhad, Iran

Introduction: Angiogenesis refers to the biological process of sprouting new vessels from existing vessels in the tissue. Angiogenesis is a physiological process that is highly regulated and occurs in cases such as wound healing, menstrual cycles, placental growth, and ovulation. Ferula assa-foetida is one of the prominent medicinal plants in traditional medicine. This research was conducted with the aim of investigating the effect of ethyl acetate and n-butanol fractions of the hydroalcoholic extract of Ferula assa-foetida on the process of angiogenesis of the chorioallantoic membrane of chick embryos.

Methods: In this research, 72 Ross spray eggs were randomly divided into 8 groups including control, laboratory control (pbs) and 6 experimental groups. After incubation, on the second day of the window, an egg was created and in on the eighth day, after placing the gelatin sponge on the chorioalantoic curve, the fractions of the ferula assa-foetida stem extract (100, 200 and 300 Î¼g/ml) were injected onto the chorioalantoic membrane of the chick embryo. On the twelfth day, the corioalantoic membrane was taken and length, The number of vascular splits, weight and height of the embryos were measured. The collected data were analyzed by Excel and SPSS 20 statistical software.

Results: The average number and total length of vascular branches in the laboratory control group did not show any significant difference compared to the control group. The average number and length of vascular branches in concentrations of 100, 200, 300 Âµg/ml of ethyl acetate and n-butanol fractions of Ferula assa-foetida showed a significant decrease compared to the control group.

Conclusion: According to the methods of this research, the above fractions from the stem of Ferula assa-foetida have an inhibitory effect on angiogenesis in the chorioallantoic membrane of chick embryos. Also, it seems that the

compounds in Ferula assa-foetida can be used to inhibit angiogenesis in cancerous tissues.

Keywords: Angiogenesis, Ferula assa-foetida, Chorioalantoic Membrane, Chick Embryo

Investigating the effect of probiotics on glucose metabolism in type 2 diabetes (Review)

Reza Bayat,[1] Shokouh Rahmati pour,[2] Zahra Rezvani,[3,*]

1. Department of cell and molecular biology, Faculty of chemistry, University of Kashan, Kashan, Iran.
2. Department of cell and molecular biology, Faculty of chemistry, University of Kashan, Kashan, Iran.
3. Department of cell and molecular biology, Faculty of chemistry, University of Kashan, Kashan, Iran

Introduction: Type 2 diabetes is a metabolic disorder in which the inability to regulate glucose levels is evident, which is caused by the resistance of cells to insulin and insulin. Improper eating habits and inactivity are mentioned. This disease is becoming a global problem, with the number of people suffering from this disease reaching 592 million in 2035. Useful food is formed, which is caused by many factors and is associated with disruption in the production of its metabolites Studies show that this disorder in the intestinal barrier can affect insulin resistance by changing the signaling and metabolic pathways.

Methods: In this study, the emphasis on the importance of the issue of diabetes and the effect of the gut microbiome on this disease has been investigated, in this direction, articles and reliable research sources such as Google Scholar, PubMed and Science Direct have been used

Results: The results indicate that probiotics can be effective in preventing and even treating type 2 diabetes. By increasing the sensitivity of cells to insulin, probiotics reduce blood glucose and glycosylated hemoglobin. Observations show that probiotic metabolites in the intestine can be associated with an increase in insulin secretion and a decrease in glucagon, which helps to reduce blood glucose in diabetics

Conclusion: The obtained results show that the metabolite of probiotics living in the intestine by producing short-chain fatty acids such as butyrate reduces inflammatory factors that can have anti-diabetic effects. These fatty acids, by activating multiple mechanisms, increase the insulin hormone and increase the sensitivity of cells. Increases liver and muscle to insulin through GLUT4. Decreasing a group of intestinal probiotics increases plasma lipopolysaccharide, which can accelerate pancreatic beta cell apoptosis and cause hyperglycemia.

Keywords: Type 2 diabetes, Probiotic, Insulin, Gut microbiome

Investigating the expression of mitochondrial biogenesis genes (Pgc-1Î±, Tfam) following the effect of cholestasis and curcumin drug in the prefrontal region of male rats. (Research Paper)

Shabnam Akbari,[1,*]

1.

Introduction: Cholestasis occurs due to a functional defect in the formation of bile at the level of liver cells or a defect in the secretion and flow of bile. This reduction in bile flow follows bile duct occlusion (BDL). Cholestasis plays a major role in necrosis and apoptosis. Oxidative stress induces cell death by apoptosis through the mitochondrial pathway. Dysfunction of mitochondria is responsible for the development of liver diseases. Curcumin, the effective substance of the rhizome of the turmeric plant, is effective in cell proliferation and survival, growth, apoptosis-cell cycle-autophagy of cells, and degeneration of neurons through different mechanisms. The molecular mechanism of the anti-inflammatory effects of curcumin is: inhibiting the expression of the NF-kB gene, an important molecule in inflammation, by inhibiting the phosphorylation of phospholipase A2 and reducing the expression of the COX-2 gene. With these findings, it seems that curcumin can be used to It is used as an effective anti-inflammatory agent. The medicinal properties of curcumin are its beneficial activities on liver diseases, which reduce the damage caused by thioacetamide, iron with high doses, cholestasis, and liver cirrhosis. The prefrontal cortex of the brain is one of the brain regions studied outside of the hippocampus, which is involved in cognitive processes. Various interventions lead to apoptosis and mitochondrial biogenesis in this area. The brain is especially vulnerable to oxidative damage, because by uses a large amount of oxygen to produce energy and enzymes and against anti-inflammatory defenses. Relatively low oxidation leads to disorder. Therefore, in this research, the expression of Pgc-1Î±, and Tfam genes following the effect of cholestasis and curcumin drug in the prefrontal region of male rats was investigated.

Methods: In this research, male rats weighing 220 to 240 grams were divided into 4 groups, including the control group, the sham-curcumin group, the BDL group, and the BDL-curcumin group. After BDL surgery, the prefrontal area was collected, RNA extraction and cDNA synthesis were performed, and the expression of genes in different groups was measured by Real-Time PCR technique.

Results: The expression of Pgc-1Î± and Tfam genes in the BDL group has decreased compared to the control group, and also with the injection of curcumin, the gene expression has decreased in the BDL-curcumin group compared to the BDL group, which is related to the expression of the Pgc -1Î± gene This reduction has been significant.

Conclusion: Curcumin can reduce the negative effects of cholestasis by reducing the expression of genes effective in mitochondrial biogenesis in the prefrontal region.

Keywords: cholestasis, curcumin, mitochondrial biogenesis

Investigating the presence of Streptococcus mutans through oral saliva by polymerase chain reaction method (Research Paper)

Hafezeh Azizi,[1,*] Farnaz Farzaneh Dehkordi,[2]

1. Islamic Azad university ardabil
2. Islamic Azad university

Introduction: Many infectious diseases in humans are caused by virulent biofilms. Tooth decay is one of the most important diseases related to biofilm in the world. Streptococcus mutans cocci is gram-positive and facultative anaerobes, which is the flora of the oral cavity in humans and is the main bacteria that causes caries. The caries process directly depends on the ability of microorganisms to colonize on the tooth surface and form plaque. (S. mutans) determination in saliva is recommended as a suitable method in contrast to phenotypic and culture methods to identify patients at risk of dental caries. The main purpose of this research is to investigate the presence of Streptococcus mutans through oral saliva by polymerase chain reaction method as a fast, simple, cheap and non-invasive method.

Methods: Materials and methods: In this study on DNA extracted from case and control samples, quantity and quality assessment DNA was performed by nanodrab in order to detect Streptococcus Motense, Polymerase Chain Reaction (PCR) with dedicated htrA Protease Serin Protease Primers, and the results were analyzed by SPSS software and under the Cai Square test.

Results: Results: Among 66 people with caries, 59 people had positive PCR test for Streptococcus mutans, 24 of them were men and 25 were women. Also, 18 people (10 women and 8 men) from the normal population tested had a positive PCR test for Streptococcus mutans.

Conclusion: In this study, a significance level of 0.05 was considered, and higher values (P-value>0.05) reject the existence of a relationship between two variables, and lower values (P-value<0.05) confirm the existence of a relationship between two variables. slow down According to the results obtained by the square test (P-value=0.259), there is no significant relationship between caries and gender, and the correlation coefficient (R) (P-value=0.000) shows a relatively strong and positive relationship between the presence of Streptococcus mutans in the cavity. It shows mouth and tooth decay. So this method can be a method with high sensitivity and specificity.

Keywords: Bacteria, PCR, Streptococcus mutans,tooth decay, oral saliva

Investigating the prevalence and correlation of pernicious anemia in patients with Helicobacter pylori infection (Review)

Sajede Saharkhiz,[1,*] Sara Shahraeini,[2]

1. Student Research Committee, Faculty of Paramedicine, Gonabad University of Medical Sciences, Gonabad, Iran
2. Student Research Committee, Faculty of Paramedicine, Gonabad University of Medical Sciences, Gonabad, Iran

Introduction: Pernicious anemia is a chronic condition indicated by the impaired absorption of vitamin B12 due to the autoimmune destruction of parietal cells in the stomach, resulting in intrinsic factor deficiency, that causes life-threatening complications. Recent research has expressed a potential link between pernicious anemia and Helicobacter pylori infection, a common bacterium that colonizes the stomach lining, neutralizing gastric acidity. Chronic infection with Helicobacter pylori (H. pylori) is identified as one of the factors contributing to both vitamin B12 deficiency and the subsequent development of PA. This has prompted our investigation into this connection. Our aim in this study is to investigate the relationship between pernicious anemia and Helicobacter pylori infection.

Methods: An extensive search of databases, including PubMed and Google Scholar, was conducted to identify relevant studies published until 2023. The search strategy involved a combination of keywords â€œHelicobacter pyloriâ€□ and â€œpernicious anemia,â€□ and related MeSH terms. Two independent reviewers screened the identified studies and extracted data. Eligible studies must be original and published in English. The exclusion criterion was the lack of access to the complete file of the study.

Results: By analyzing the data from the studies included in this review, 145 individuals (39.5%) of the 367 patients with pernicious anemia had H. pylori-positive results, so it can be considered that chronic H. pylori infection was associated with the development of pernicious anemia. However, a causative role of H. pylori in pernicious anemia was not observed in two of the articles studied in Japan and Korea. Sixteen Japanese patients diagnosed with pernicious anemia with a mean age of 68.1 were examined for H. pylori infection and were all negative for H. pylori. Considering that the H. pylori-positive rate in the Japanese population of the same age (60 years) is 70-80%. Furthermore, the proportion of H. pylori-positive cases among Korean patients with pernicious anemia did not differ from that among the general population. The results of these two studies indicate that H. pylori infection did not play a major role in the development or progression of pernicious anemia.

Conclusion: Pernicious anemia poses a significant public health concern, with potentially life-threatening complications. This review provides evidence

indicating a possible link between Helicobacter pylori infection and the development of pernicious anemia. Although studies conducted in East Asia indicate that the role of H. pylori in the development of pernicious anemia differs among ethnic groups and by region.

Keywords: Pernicious anemia, Anemia, Helicobacter pylori, H. pylori

Investigation of Interferon Alpha in the Treatment of Hepatitis D and Alternative Treatment Methods in Hepatitis D (Review)

Ghazale Borvaye,[1,*] dr Issa Layali,[2] Armina aghazade,[3]

1. department of microbiology, Islamic Azad university, medical branch, Tehran,Iran
2. Department of Biochemistry and Biophysics, Faculty of Advanced Sciences and Technology, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran
3. department of microbiology, Islamic Azad university, medical branch, Tehran,

Introduction: Hepatitis B is one of the dangerous and deadly diseases, with its chronic form having the ability to cause liver cirrhosis and liver cancer. Hepatitis D is the most severe type of hepatitis, which can occur in individuals already infected with hepatitis B, although the presence and function of hepatitis D are dependent on hepatitis B. Its structure is completely different from other types of hepatitis, namely hepatitis A, C, and E, and can lead to more severe liver diseases compared to hepatitis B. Vaccination against hepatitis B can help prevent infection with the hepatitis D virus and reduce its replication. The most effective treatment for hepatitis D so far has been the administration of drug complexes tailored to the individual's condition, which help prevent virus replication and boost the body's immune system. It is important to note that currently, the only standard treatment for hepatitis D worldwide is interferon alpha, which has been shown to have an effectiveness rate of approximately 15 to 40 percent on average in patients with hepatitis D. Overall, interferon alpha does not have the same effect on all individuals and may be ineffective in some cases. It has its own advantages and disadvantages, which may not be suitable for everyone. Some of its benefits include reducing virus replication, reducing liver inflammation, increasing the immune system, while its side effects may include weight loss, decreased energy, depression, flu-like symptoms, joint pain, etc. The effectiveness of interferon alpha typically depends on the duration of the infection, disease severity, basic liver function, response to treatment, and other factors. The most commonly prescribed treatment for patients is pegylated interferon alpha, administered for approximately one year, which can vary depending on the individual's condition. Alternative treatments are still in the experimental stages, and the following approaches can be mentioned: 1) Nucleoside Analogues (NAs): NAs, which are prescribed for the treatment of hepatitis B, can indirectly help suppress hepatitis D infection by suppressing hepatitis B viral replication. 2) Entry Inhibitors: The Hepatitis D virus (HDV) requires entry receptors in liver cells to penetrate. Researchers are studying compounds that can block the entry of HDV into liver cells and prevent infection and its spread. 3) RNAi Therapy: RNAi is a biological process that can suppress specific genes. Scientists are investigating the use of RNAi-based therapies to target and inhibit HDV replication, which may reduce the level of the virus in infected

individuals. 4) Antisense Oligonucleotides (ASOs): ASOs are artificial DNA or RNA molecules that can selectively bind to specific target RNAs. Research is underway to develop ASOs that can penetrate HDV replication and block viral protein production.

Methods: We utilize a compilation of information that researchers have obtained using diverse materials and methods, such as patient samples, various approaches, and tools, to study the life cycle of the Hepatitis D virus. Additionally, we evaluate the efficacy and safety of therapeutic strategies, screen potential antiviral compounds, optimize drug candidates, conduct clinical trials, analyze the viral genome, and develop immunotherapeutic strategies. The combination of these materials and methods has facilitated the discovery of new treatment options for Hepatitis D.

Results: All of these treatments are still in the experimental stages. Liver transplantation, vaccination, safe sexual practices, prevention of blood-borne transmission, and avoiding alcohol and tobacco can also help prevent disease progression and provide preventive measures. Hopefully, the successful development of new treatment approaches will contribute to the advancement of hepatitis treatment and aid patients in their recovery.

Conclusion: there are ongoing clinical trials assessing the efficacy of new antiviral agents specifically targeting HDV, as well as combination therapies with nucleos(t)ide analogs and immunomodulatory drugs. These new treatments aim to further improve the management of hepatitis D and potentially achieve a functional cure, which is the sustained suppression of both HBV and HDV replication.

Keywords: hepatitis_d, vaccination, treatment, Interferon_Alpha , hepatitis_b

Investigation of the relationship between SNPs of genes involved in obesity as biomarkers for the diagnosis of obesity and dietary adjustment. (Review)

Farzaneh Ramezani Hombari,[1,*] Faranak Jamshidian,[2] Maryam Rouhani,[3]

1. Department of Biology , East Tehran Branch, Islamic Azad University , Tehran ,Iran
2. Department of Biology , East Tehran Branch, Islamic Azad University , Tehran ,Iran
3. Department of Tissue Engineering and Applied Cell Sciences , School of Advanced Technologies in Medicine , Shahid Beheshti University of Medical Sciences,Tehran,Iran

Introduction: Obesity is a major problem all over the world, genetic predisposition and the influence of environmental factors are somewhat involved in the development of this disease and it is known as a multifactorial abnormality, but the identification of related genes and mutations is still ongoing with the aim of improvement and Done.

Methods: In this review, the types of genes associated with fat cell function and SNPs associated with obesity genes are identified in order to identify an individual's predisposition to obesity based on dietary adjustment.

Results: Therefore, high food consumption, especially high-calorie diets, and the expression of genes related to SNPs as biomarkers in individual susceptibility to obesity.

Conclusion: Based on these genes and different SNPs in each person's diet and lifestyle, it also determines a diet plan based on genetic predisposition.

Keywords: obesity, biomarker, snp , genetics, life style

Investigation of the relative frequency of herpes viruses in patients with type 1 Diabetes in Yazd province (Research Paper)

Aref Atefi,[1,*] Parisa Dehghan,[2] Mohadese Zare Bidoki,[3]

1. Infectious Diseases Research Center, Shahid Sadoughi University of Medical Sciences, Yazd, Iran.
2. Infectious Diseases Research Center, Shahid Sadoughi University of Medical Sciences, Yazd, Iran.
3. Faculty of Biological Sciences, Yazd University, Yazd, Iran

Introduction: Type 1 diabetes is a chronic disease known as juvenile diabetes or insulin-dependent diabetes. In most affected individuals, the body's immune system disorder begins to destroy the insulin-producing cells in the pancreas. Viral and genetic factors may be responsible for this abnormal immune system reaction. Herpesviruses include several important human pathogens. Various studies confirm the relationship between Herpesviridae and autoimmune diseases. This study investigated the relative frequency of infection with Epstein-Barr virus, Cytomegalovirus, Varicella-zoster virus, and Herpes simplex virus type 1 and 2 in patients with type 1 diabetes in Yazd province.

Methods: A descriptive-cross-sectional case-control study in which the studied population included 18 patients with type 1 diabetes and 72 controls. The criterion for entering the study is to have type 1 diabetes, and no more than one month has passed since the diagnosis. We undertook a serological study of HSV I&II IgG, VZV IgG, EBV IgG, and CMV IgG antibodies among cases and controls by ELISA method. Four mLs of venous blood samples without anticoagulant were obtained from both groups. After about 15 minutes centrifuged at 3500 rpm for 10 minutes, the serum was separated and frozen at (-20â—¦C) till used. The ELISA test was performed manually using kits from Pishtaz Teb and Euroimmun. The results were analyzed by using SPSS 16 software.

Results: The average age of the group with type 1 diabetes is 8.88Â±3.81, and the average age in the control group is 8.70Â±2.73. In the group with type 1 diabetes, six people had a history of HSV I&II infection, and in the control group, 22 people had a history of HSV I&II infection. As a result, there is no significant relationship between HSV I&II infection and the studied groups (P-Value=0.820). In the group with type 1 diabetes, nine people had a history of VZV infection; in the control group, 34 had a history of VZV infection. As a result, there is no significant relationship between VZV infection and the studied group (P- Value=0.833). In the group with type 1 diabetes, three people had a history of EBV infection; in the control group, six had a history of EBV infection. As a result, there is no significant relationship between EBV infection and the studied groups (P- Value=0.376). In the group with type 1

diabetes, four people had a history of CMV infection; in the control group, six had a history of CMV infection. As a result, there is no significant relationship between CMV infection and the studied groups (P- Value=0.108).

Conclusion: According to the results of the statistical analysis, it was determined that the history of infection with the herpes virus family (including herpes simplex virus types 1 and 2, varicella-zoster virus, cytomegalovirus, Epstein-Barr virus). However, there is a higher prevalence in people with type 1 diabetes than in the control group; they do not have an effective and direct relationship with type 1 diabetes.

Keywords: Type 1 diabetes, herpes viruses, Epstein-Barr virus, cytomegalovirus, varicella-zoster

Iranian herbal medicines used for therapy of diabetes mellitus: a systematic review of the pharmacological aspects (Review)

Hadis Rahimi,[1] Shadi Nazarifard,[2] Fatemeh Ahmadpour,[3,*]

1. Student research committee, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Student research committee, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Nutritional Health Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran

Introduction: Background and Aim: Medicinal plants play an important role in the treatment of diabetes mellitus, especially in the developing countries due to their cost effectiveness. Diabetes mellitus, a metabolic disorder, is becoming a serious threat to mankind health. The prevalence of diabetes mellitus is expected to reach up to 4.4% in the world by 2030. Among all type of diabetes, type 2 diabetes is main complication. Currently available treatment options in modern medicine have several adverse effects. Therefore, there is a need to develop safe and effective treatment modalities for diabetes.

Methods: Methods: This systematic review presents the profiles of plants with hypoglycemic/anti diabetic properties reported in the literature from 2010 to 2022. The relevant keywords were searched from Google Scholar, Pub Med, Science direct, Cochrane library and EMBASE databases.

Results: Results: Various plants have been found to possess significant anti-diabetic property after their preclinical and clinical evaluation. Use of these plants may delay the development of diabetic complications and can correct the metabolic abnormalities through variety of mechanisms. Moreover, during the past few years many phytoconstituents responsible for anti-diabetic effects have been isolated from plants.

Conclusion: Conclusion: This review demonstrates the limitations in published articles of human clinical trials for medicinal plantsâ€™ intervention for diabetes. Upon further investigations on the identified medicinal plants included in the animal studies, the findings showed positive effects in the management of diabetes, such as hyperglycemia. Hence, further testing and standardization of the methods in the studies can be suggested for human clinical trials for reliable data collections such as methods of extract preparation, duration of intervention, and conditions set for the study design.

Keywords: Diabetes mellitus, Herbal medicine, Glycemic index

Iron Metabolism and its Impact on Cancer Diagnosis (Review)

Issa Layali,[1] Parastoo Einali,[2,*] Asal Naderali,[3]

1. Department of Biochemistry and Biophysics, Faculty of Advanced Sciences Branch, Islamic Azad University
2. Faculty of Advanced Sciences Branch, Islamic Azad University
3. Faculty of Advanced Sciences Branch, Islamic Azad University

Introduction: The presence of iron in our body is vital for the synthesis of proteins that are involved in crucial functions such as oxygen transportation, energy production from food, and DNA replication. Iron metabolism includes firmly controlled cellular take-up, capacity, export mechanisms of exportation and utilization. Iron has the potential to either promote tumor growth or induce cell death due to its various properties. Cancer cells have a higher demand for iron than healthy cells. The macrophages provide cancer cells with iron, enhancing the growth of the tumor. Several research efforts have studied the relationship between iron regulation in the body and the accelerated growth of tumors in high iron conditions. In addition, developing investigate has shed light on the complicated relationship between iron metabolism and cancer, manifesting its potential effect on cancer diagnosis and treatment.

Methods: An extensive literature search was administrated to identify related investigations on the connection between iron metabolism and cancer diagnosis. Electronic databases, including PubMed, Scopus, and Science direct, were queried from [November 19th 2023] to [December 25th 2023]. The search utilized a combination of keywords such as "iron metabolism," "cancer diagnosis," and related MeSH terms. Prohibition criteria enveloped studies not specifically tending to the required relationship or missing pivotal data. Starting screening included assessing titles and abstracts, taken after by a full-text revision of potential articles. Criteria included methodology, sample size, study design, and meticulousness of iron metabolism and cancer diagnosis evaluation. Two autonomous reviewers performed the quality evaluation and discrepancies were resolved by agreement. A narrative synthesis method was utilized to coordinate and decipher discoveries from the chosen studies. Key subjects, patterns, and suggestions with respect to the effect of iron metabolism on cancer diagnosis were distinguished and examined.

Results: A prominent subject over the surveyed literature determines substantial alterations in iron metabolism in the context of various cancer types. Recent investigations have consistently indicated disruptions in iron homeostasis, determined by dysregulation of hepcidin expression, ferritin levels and iron transporters. The synthesis of results highlights the potential of iron-related biomarkers in cancer diagnosis. Enhanced serum ferritin levels are commonly associated with certain types of cancer, serving as a potential

demonstrative indicator. Moreover, studies have pointed out the symptomatic importance of investigating iron metabolism at the molecular level, involving iron-related qualities in cancer detection. A developing trend within the writing emphasized the part of iron imaging methods in cancer diagnosis. Magnetic Resonance Imaging (MRI) and other iron-sensitive imaging modalities have shown promise in identifying and characterizing tumors according to their special iron signatures. This non-invasive method has opened a new avenue to improve cancer diagnosis.

Conclusion: In conclusion, our narrative review dives into the complicated interactions between iron metabolism and cancer diagnosis, shedding light on multifaceted connections that expand past conventional points of view. The synthesis of writing reports compelling proof of modifications in iron homeostasis over different cancer sorts, underscoring the symptomatic potential of iron-related biomarkers. The observed increase in serum ferritin levels appears to be a consistent theme, suggesting its role as a promising diagnostic indicator for certain cancers. Nevertheless, the discovery of iron-related genes and the application of iron-sensitive imaging techniques offer inventive avenues for improving diagnostic methods. As we navigate the various aspects of iron metabolism and its implications in cancer diagnosis, it is clear that this dynamic relationship offers opportunities for personalized and targeted interventions. Future investigate ought to point to elucidate the nuances of iron dysregulation that characterize different cancer types, thereby promoting the development of appropriate diagnostic and therapeutic approaches. Ultimately, this narrative review contributes to our understanding of the evolving landscape of iron metabolism within the context of cancer diagnosis. By synthesizing assorted findings, we hope to motivate proceeded discovery and collaboration across disciplines, paving the way for progressions in precision medicine and cancer diagnostic procedures improvements.

Keywords: Iron Metabolism, Cancer Diagnosis

Isolation of Lactobacillusgenus with probiotic traits from traditional yogurts of zanjan and determination of their super natant antibacterial effects against important intestinal pathogens (Research Paper)

Narges Asadi,[1] Mohammad Asadi,[2] Asghar Mirzakhani,[3] Zahra Momeninasab,[4] Hasan Hasanzadazar,[5] Davoud Afshar,[6,*]

1. Department of Microbiology and Virology, Zanjan University of Medical Sciences, Zanjan, Iran
2. Department of Biology, Islamic Azad University Branch, Urmia, Iran
3. Department of Microbiology and Virology, Zanjan University of Medical Sciences, Zanjan, Iran
4. Department of Microbiology and Virology, Zanjan University of Medical Sciences, Zanjan, Iran
5. Department of Food Safety and Hygiene, Zanjan University of Medical Sciences, Zanjan, Iran
6. Department of Microbiology and Virology, Zanjan University of Medical Sciences, Zanjan, Iran

Introduction: Local yogurts like commercial probiotic yogurts are compounds that have probiotic bacteria like Lactobacilus spp. which exhibit suitable antimicrobial activity. nevertheless, there are limited studies onprobiotics species of local yogurts, especially in Zanjan city. Therefore, the present study was aimed to isolate probiotic Lactobacilus species form a commercial and Zanjan local yogurtsand their antimicrobial properties was also evaluated againt some pathogenic bacteria.

Methods: In the present study, 44 samples of local yogurts, 7 commercialsyogurts and one probioticscapsule were collected, inoculated into MRS with pH:3, and incubated at 37 Â°C for 24 h under microaerophilic condition. The growth positive samples were sub-cultured on MRS agar and incubated as above mentioned conditions. TheLactobacillussuspicious bacteria were isolated based on morphological and biochemical tests.to evaluate bile resistance property, all strains were cultured into MRS broth containing 0.03% bile. Bile and acid resistant Lactobacillus species were identified bysequencing of 16 srRNA gene. Anti microbial effect of strains was performed against Shigelladysentariae,S. flexneri, S. boydii, and S. sonnei,Salmonellatyphi, S. enteritidis, Yersiniaenterocolitica, Aeromonas hydrophila,Vibriocholerae,Clostridioides difficile and Bacillus cereusby well diffusion method.

Results: From 44 samples of local yogurts,7 probiotic strainsincluding 5Lactobacillushelveticus, 1 L. letivazi and 1 strain of L. selangorensis was isolated. In the probiotic supernatant antimicrobial test, Lactobacillushelveticusstrains showed the most inhibition effect with15mm inhibitory zone diameters. All of probiotics in commercial probiotic yogurts and

capsule have belonged to Lactobacillusacidophilus species and despite of inhibitory effectagainst some pathogenic bacteria, had not inhibitory effect against S. tyohi, Vibriocholerae, and Bacillus cereus.

Conclusion: The results of the present study showed that local yogurts in Zanjan city have Lactobacillus species with probiotic potencial ability and their antimicrobial properties are similar to commercial probiotic yogurts.

Keywords: Intestinal pathogens, probiotic, Lactobacillus

Laboratory Diagnosis Methods of Malaria Infection (Review)

Sepideh Siasi,[1] Hediye Vand -Rajabpour,[2] Akram Abouei Mehrizi,[3,*]

1. Pasteur institute of Iran
2. Pasteur institute of Iran
3. Pasteur institute of Iran

Introduction: To manage and control malaria, a quick and accurate malaria diagnosis method is necessary as a high priority. For this purpose, several methods have been developed. Currently, examining the peripheral blood slide with an optical microscope as a gold standard method, and rapid diagnosis method are used in malaria endemic areas. This article reviews the existing methods and the possible future options to improve the diagnosis of malaria.

Methods: To prepare the present review article, English language articles with no limitation in publication date were reviewed by searching keywords including malaria diagnosis, microscopic and molecular methods, RDT, Nested - PCR, and LAMP in PubMed and Google Scholar databases. Among the collected articles, the most relevant research articles were selected and reviewed.

Results: Direct observation of blood smears with light microscope and RDTs perform for malaria detection. Molecular methods are suitable for diagnosis of false negative cases in microscopic slides and asymptomatic cases. Novel methods for malaria diagnosis, such as qPCR, LAMP, magnetophoretic, dielectrophoretic, and the CRISPR system are being developed.

Conclusion: Despite its limitations, direct observation of peripheral blood smears with a light microscope is still considered the gold standard method for malaria diagnosis. Another malaria diagnosis method is the rapid diagnostic test (RDT), which is a quick and cheap alternative for malaria diagnosis in endemic areas. Regarding malaria elimination programs, the diagnosis of Plasmodium in individuals without symptoms of malaria is challenging as they are generally not detected by routine methods such as peripheral blood smear and rapid diagnostic tests. For this reason, molecular methods are suitable for use in the endemic areas under elimination. Novel techniques that are beneficial in malaria research can replace the usual diagnostic methods in the future.

Keywords: Microscopy ; Molecular - based methods ; RDT ; Nested - PCR ; LAMP

Lassa fever disease review article (Review)

Kosar reihanpour baghkhoshki,[1,*]

1. Baclocher student of Microbiology Islamic Azad University Sirjan Sirjan, Kerman, Iran

Introduction: Introduction: Lassa fever(LF), The cause of acute viral hemorrhagic disease is the Lassa virus (LASV). Exposure toMastomys natalensis, the rodent host, contaminated feces or urine, is the primary cause of infections in humans.Environmental elements, such as being close to vegetation, forests, and garbage, enhanced the likelihood of LASV exposure The family Arenaviridae includes the virus that causes Lassa fever Lassa fever has been linked to several rodent species, including Hylomyscus pamfi and Mastomys erythroleucus.Every year, LAV results in 5,000 fatalities.Since 2010, there have been more documented cases of LF.

Methods: Material methods: The Lassa virus (LASV), a single-stranded RNA arenavirus encapsulated, bipartite, is what causes Lassa fever This RNA virus has a typical diameter of 110 to 130 nm and has a spherical or rounded shape The smaller segment's precursor nucleoprotein and glycoprotein, as well as the more significant segment's RNA-dependent RNA-polymerase and matrix RING Zincfinger protein, are the four proteins that the RNA .genomes encode virulence and pathogenesis factors LASV is a negative-sense, single-stranded RNA virus with an envelope. The large and small parts of the genome each contain two ambisense regions.

Results: Results: Negative effects from Lassa virus infection are particularly likely to affect pregnant women and their .unborn children According to a recent assessment, pregnant women have a three times higher chance of dying from Lassa .fever than non-pregnant women Factors Affecting the Reemergence of Epidemics of Lassa Fever Migration, travel, and nosocomial transmission Systems of public health Environment and Climate Effects of Conflicts and Civil War

Conclusion: Conclusion: Poor outcomes among Lassa fever virus-infected pregnant women are mostly brought about by immune changes during pregnancy or the virus' attraction to the highly vascularized placenta. The patient's prognosis could get worse if medical treatment is postponed. Additionally, overlapping clinical symptoms including headaches, vaginal bleeding, and tummy pain in pregnant women might make it difficult to diagnose Lassa fever Particularly in endemic locations, the ecology of the Lassa virus and its interaction with humans, as well as the development of Lassa fever, are complex. At the moment, ribavirin, an antiviral medication, is . the only available specialized treatment.

Keywords: Lassa fever(LF),stable signal peptide (SSP) ,pathogenesis, ribavirin, infectionstable

Life satisfaction and the release of oxytocin in the brain as a neurochemical hormone (Review)

Fatemeh moosavi,[1,*] Maryam bagheri fard,[2]

1. Issa Layali Department of Biochemistry and Biophysics, Faculty of Advanced Sciences and Technology, Tehran Medical Sciences branch, Islamic Azad University, Tehran, Iran
2. Issa Layali Department of Biochemistry and Biophysics, Faculty of Advanced Sciences and Technology, Tehran Medical Sciences branch, Islamic Azad University, Tehran, Iran

Introduction: The feelings of life satisfactions relies on many chemicals releasing inside the human body, but considering humans being social creatures, personal satisfaction and social satisfaction are intertwined, one cannot be provided without the other. And so, oxytocin is one of the most important hormones regarding general life-satisfaction as it plays an important role in positive emotions throughout day-to-day interactions, memory and memories related to building strong social relations. The feeling of self-satisfaction in life revolves around the production of hormones, The happiness hormones that the human body can produce by itself include: dopamine, serotonin, oxytocin and endorphins. Oxytocin, the main focus of the review, is the anxiolytic hormone, it is a neuropeptide synthesized primarily in the hypothalamus. Its receptors are distributed widely in the central nervous system, it has a neurobehavioral role, because it regulates a wild range of positive social behaviors. It works as social reinforcement and improves attention, orientation and memory towards, positive, social stimuli. It facilitates the identification and interpretation of social information conductive to social interactions. There is also an association between serotonin and oxytocin, oxytocin lowers the reactivity of the hypothalamic pituitary adrenal axis, reducing levels of stress hormones including adrenocorticotropic hormone and cortisol. Lower levels of oxytocin involve anxiety and a lower capacity to develop prosocial behavior. The sequence of 9 amino acids of oxytocin was identified in 1959 and it has been also artificially synthesized.

Methods: This study was conducted by collecting the most recent research on happiness hormones, especially oxytocin and its effect on everyday human relationships. The information was gathered by searching keywords in valid scientific databases.

Results: Oxytocin is an oligopeptide neurohypophysial hormone, it has been found in mammals. This hormone is naturally synthesized in the hypothalamus and stored and secreted in the posterior pituitary. It stood out, for the first time, duo to its special role in breastfeeding and delivery. Oxytocin consists of 9 amino acids with the sequence: cysteine-tyrosine-isoleucine-glutamine-asparagine-cysteine-proline-leucine-glycine, and a disulfide bridge

is formed between two Cysteine residue. The hormone has a similar structure to other oligopeptides such as vasoprosin, they differ only in two amino acids. Oxytocin is in second chromosome position in mouse and twentieth in humans. Early precursor of oxytocin contains 3 exons and 2 introns and preprohormone has 3, the signal peptide part is oligopeptide (9) and neuriohysin. Oxytocin belongs to the family of G-coupled receptors, it is a protein that is linked to phospholipase C through Gap 11. Oxytocin is formed in the first phase in PVN nuclei hypothalamus and is then transferred to the pituitary gland. This neurotransmitter is significantly different from common neurotransmitters such as gammaï¿¾aminobutyric acid, in the sense that neuropeptide transmitters like oxytocin has two direct effects through axonal release from PVN neurons as well as diffuse volume effects due to release of somatodendritic in a magnocellular neuron. The latter occurs uniquely through neuropeptides. Therefore, due to short-range diffusion in the extracellular fluid and fluid cerebrospinal fluid, these transporters have a wide range of showing effects. Oxytocin has clear and effective therapeutic effects in dealing with diseases such as autism and schizophrenia and shows positive clinical effects in reducing the main symptoms of these diseases. It also has a prominent role in the homoeostasis of body fluids as well as the regulation of heart rate and heart contraction.

Conclusion: Nowadays, the actions and behavior of humans can be examined with a molecular point of view. Human's actions and their internal reactions are accompanied by new chemical reactions. Molecules play a major role in human actions and behavior. As such every person has molecular effects according to their actions and behavior. Molecular reactions resulting in sleep, happiness, fear, satisfaction, provide a person with relaxation. Therefore, it can be said that from one outlook, man is a chemical/biochemical reactant.

Keywords: Oxytocin, life satisfaction, neurobehavioral, social relations

Long Non-Coding RNAs (lncRNAs) in Breast Cancer: A Comprehensive Review (Review)

Fatemeh Ahmadpour,[1] Gholamreza Shahsavari,[2,*] Asma Sepahdar,[3] Hadis Rahimi,[4] Shadi Nazarifard,[5] Mohammad Abbasinasab,[6]

1. Nutritional Health Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Department of Clinical Biochemistry, Faculty of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Razi Herbal Medicines Research Center Lorestan University of Medical Sciences
4. Department of Clinical Biochemistry, Lorestan University of Medical Sciences, Khorramabad, Iran
5. Department of Clinical Biochemistry, Lorestan University of Medical Sciences, Khorramabad, Iran
6. Department of Clinical Biochemistry, Lorestan University of Medical Sciences, Khorramabad, Iran

Introduction: Breast cancer, a heterogeneous disease with diverse molecular subtypes, necessitates a nuanced understanding for improved diagnosis and targeted therapies. This comprehensive review synthesizes findings from multiple studies investigating the role of long non-coding RNAs (lncRNAs) in breast cancer. Ten pertinent studies were examined, elucidating the intricate involvement of various lncRNAs in breast cancer initiation, progression, and prognosis.

Methods: A systematic search was conducted across major databases, including PubMed, Scopus, and Web of sciences, covering the period from 2014 to 2023. The primary focus was on identifying studies investigating the role of long non-coding RNAs (lncRNAs) in breast cancer, with an emphasis on their implications as prognostic factors in blood samples.

Results: 1. MEG3 rs3087918 and Breast Cancer Risk: â€¢ Objective: Explore MEG3 SNPs (rs3087918, rs7158663, rs11160608) in Chinese women. â€¢ Findings: rs3087918 associated with decreased breast cancer risk, particularly in women â‰¤49. Implications for HER-2 receptor expression. Potential structural and miRNA targeting alterations. 2. LncRNA POU3F3 in TNBC: â€¢ Objective: Investigate lncRNA POU3F3 in triple-negative breast cancer (TNBC). â€¢ Findings: POU3F3 overexpression in TNBC tissues, inversely correlated with cleaved caspase 9. Promotion of cell proliferation and inhibition of apoptosis. Potential therapeutic target. 3. Serum lncRNA TINCR as Prognostic Biomarker in TNBC: â€¢ Objective: Assess serum lncRNA TINCR as a prognostic marker in TNBC. â€¢ Findings: High circulating TINCR correlated with worse TNBC outcomes. Independent prognostic factor. Non-invasive biomarker potential. 4. LncRNA ZFAS1

Inhibition in TNBC: â€¢ Objective: Investigate ZFAS1 expression in TNBC and its impact. â€¢ Findings: ZFAS1 downregulated in TNBC, potential tumor suppressor. Inhibition linked to increased cell proliferation. Negative correlation with STAT3. 5. LncRNA RP11-19E11 in Basal Breast Cancer: â€¢ Objective: Identify and characterize lncRNA RP11-19E11.1 in basal breast cancers. â€¢ Findings: Upregulated in basal primary breast cancers. Chromatin-associated, E2F1 target. Essential for cancer cell proliferation and survival. 6. LncRNA XIST and NEAT1 for High-Risk Breast Cancer Diagnosis: â€¢ Objective: Investigate XIST and NEAT1 as diagnostic markers for high-risk breast cancer patients. â€¢ Findings: Upregulated in breast cancer patients, correlated with clinicopathological factors. Serum XIST and NEAT1 as non-invasive diagnostic markers. 7. LncRNA-miRNA-mRNA ceRNA Network for Breast Cancer Prognosis: â€¢ Objective: Construct ceRNA network for breast cancer prognosis. â€¢ Findings: Identification of prognostic factors (ZC3H12B, HRH1, TMEM132C, PAG1). Prognostic risk model accuracy. Insights into potential therapeutic targets. 8. LncRNA NEF in TNBC: â€¢ Objective: Investigate lncRNA NEF in TNBC. â€¢ Findings: Downregulated in TNBC, inverse correlation with miRNA-155. NEF as a potential tumor suppressor. Implications for prognosis. 9. Serum lncRNA-ATB and FAM83H-AS1 as Breast Cancer Biomarkers: â€¢ Objective: Evaluate serum FAM83H-AS1 and lncRNA-ATB as diagnostic/prognostic markers. â€¢ Findings: Overexpressed in breast cancer patients. LncRNA-ATB as a superior diagnostic marker. FAM83H-AS1 potential for monitoring progression. 10. LncRNA TCL6 and Immune Infiltration in Breast Cancer: â€¢ Objective: Investigate lncRNA TCL6 expression and clinical significance. â€¢ Findings: Low TCL6 linked to worse survival, correlation with immune infiltrating cells. Prognostic marker potential.

Conclusion: This review underscores the diverse roles of lncRNAs in breast cancer, offering valuable insights into potential diagnostic, prognostic, and therapeutic avenues. The multifaceted interactions between lncRNAs and breast cancer pathogenesis provide a foundation for future research and personalized treatment strategies.

Keywords: Breast cancer, Long non-coding RNAs (lncRNAs), Prognostic factors, Blood-based biomarkers, Risk

Long Noncoding RNAs (lncRNAs) in Rheumatoid Arthritis Peripheral Blood Mononuclear Cells (PBMCs): A Systematic Review (Review)

Nazarifard Shadi,[1] Rahimi Hadis,[2] Ahmadpour Fatemeh,[3,*] Hormozi Maryam,[4]

1. Department of Biochemistry and Genetics, School of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Department of Biochemistry and Genetics, School of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Department of Biochemistry and Genetics, School of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran
4. Department of Biochemistry and Genetics, School of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran

Introduction: Rheumatoid arthritis (RA) is a complex autoimmune disorder characterized by inflammation, joint damage, and systemic involvement. This systematic review focuses exclusively on the role of long noncoding RNAs (lncRNAs) in peripheral blood mononuclear cells (PBMCs) of RA patients. We aim to provide a comprehensive analysis of the current literature, emphasizing the potential of PBMC-derived lncRNAs as diagnostic markers and therapeutic targets in RA. Rheumatoid arthritis affects millions worldwide, necessitating a deeper understanding of its molecular mechanisms. Investigating lncRNAs specifically in PBMCs offers insights into the systemic aspects of RA pathology.

Methods: A systematic search of databases (PubMed, Scopus, etc.) was conducted to identify studies focusing on lncRNAs in PBMCs of RA patients. Inclusion criteria were applied to select studies exploring lncRNA expression, functions, and clinical relevance. Quality assessment and data extraction were performed.

Results: Expression Profiling of PBMC-Derived lncRNAs in RA: An overview of dysregulated lncRNAs in RA PBMCs, such as LINC00304, MIR503HG, LOC100652951, and LOC100506036, provides insights into the specific molecular alterations associated with RA. Functional Roles of PBMC-Derived lncRNAs in RA: Understanding how PBMC-derived lncRNAs contribute to apoptosis, autophagy, and inflammatory responses in RA sheds light on their potential as key regulators in systemic immune dysregulation. Diagnostic Potential of PBMC-Derived lncRNAs in RA: Identification of lncRNAs like MIR22HG, DSCR9, and LINC01189 as potential diagnostic biomarkers, specific to PBMCs, highlights their role in reflecting RA-associated molecular changes systemically. Therapeutic Implications: Exploring the therapeutic potential of targeting dysregulated PBMC-derived lncRNAs, such as LOC100506036, may pave the way for novel interventions aiming at modulating immune responses in RA patients. Challenges and Future Directions: The review discusses challenges in the existing literature,

emphasizing the importance of standardized methodologies and the need for larger studies. Recommendations for future research focus on validation and translation to clinical applications.

Conclusion: This systematic review emphasizes the unique contribution of PBMC-derived lncRNAs to the understanding of RA pathogenesis. The identified lncRNAs hold promise as diagnostic markers and therapeutic targets, offering avenues for further research in precision medicine for RA.

Keywords: Rheumatoid Arthritis, Peripheral Blood Mononuclear Cells (PBMCs),Long Noncoding RNAs (lncRNAs).

Long Noncoding RNAs: Emerging Biomarkers in Atherosclerosis - A Comprehensive Review (Review)

Gholamreza Shahsavari,[1,*] Fatemeh Ahmadpour,[2] Asma Sepahdar,[3]

1. Department of Clinical Biochemistry, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Nutritional Health Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Razi Herbal Medicines Research Center Lorestan University of Medical Sciences

Introduction: Atherosclerosis, a chronic inflammatory disorder, stands at the forefront of cardiovascular diseases, posing a substantial global health burden. The intricate interplay of various cellular processes orchestrates the progression of atherosclerosis, necessitating a nuanced understanding of its molecular underpinnings. In recent years, Long Non-Coding RNAs (lncRNAs) have emerged as crucial regulators in diverse biological pathways, including those intricately linked to atherosclerosis.

Methods: Literature Search: Rigorous searches across PubMed, Scopus, and Web of Science databases (up to January 2023) were conducted, employing keywords related to atherosclerosis and lncRNAs. Inclusion Criteria: Studies specifically exploring the nexus between lncRNAs and atherosclerosis were included. Exclusion Criteria: Non-English literature, reviews, and studies tangential to lncRNAs in atherosclerosis were excluded.

Results: MALAT1: Regulates NF-ÎºB signaling via interaction with miR-330-5p, contributing to atherosclerosis. HCG11: Upregulated in cerebral atherosclerosis, showing promise as a biomarker for cerebrovascular events. TUG1: Silencing attenuates atherosclerosis-induced myocardial injury through miR-30b-3p and Brd4 regulation. APPAT: Suppresses smooth muscle cell proliferation and migration via interaction with miR-647 and FGF5. BANCR: Induces vascular smooth muscle cell proliferation by downregulating miR-34c methylation. ZFAS1: Regulates inflammatory responses and cholesterol efflux via the miR-654-3p-ADAM10/RAB22A axis. TCONS_00034812: Upregulated in atherosclerosis, upregulates miR-21 through methylation in vascular smooth muscle cells. SOX2-OT: Upregulated in carotid atherosclerosis, potential predictive indicator

Conclusion: This systematic review provides a comprehensive insight into lncRNAs associated with atherosclerosis, showcasing their potential as biomarkers. Validation in larger studies is pivotal for clinical translation.

Keywords: Atherosclerosis, Long non-coding RNA, lncRNA, Biomarkers, Diagnosis, Cardiovascular disease, Systema

Merkel Cell Polyomavirus and its Role in Driving Merkel Cell Carcinoma Development: A Comprehensive Review (Review)

Fatemeh Kheyri,[1,*]

1. Islamic Azad University, Tehran Medical Branch

Introduction: In the intricate landscape of cancer etiology, viruses have emerged as significant contributors, accounting for approximately 15% of all human cancers. This review delves into the realm of human tumor viruses, exploring the diverse world of RNA and DNA viruses implicated in oncogenesis. Notably, the spotlight shines on Merkel cell polyomavirus (MCPyV), the most recent addition to this viral cohort, intricately linked to a formidable adversary â€“ Merkel cell carcinoma (MCC). As we navigate the complexities of MCPyV and its association with MCC, this article unfolds a narrative that traverses the historical delineation of MCC, the molecular intricacies of MCPyV, and the critical interplay between viral infection and the host immune response. Join us on this expedition to unravel the mysteries surrounding the nexus of viruses and cancer, with a specific focus on the enigmatic alliance between MCPyV and the development of Merkel cell carcinoma.

Methods: The methods section of this review article primarily involves the comprehensive analysis of existing literature, molecular studies, and clinical observations related to Merkel cell polyomavirus (MCPyV) and its association with Merkel cell carcinoma (MCC). The following methods were employed in gathering and synthesizing information for this review: 1. Literature Review: - Extensive review of scientific databases, including PubMed, Scopus, and relevant academic journals, to identify studies, articles, and reviews related to MCPyV and MCC. - Inclusion of seminal works, recent publications, and studies with significant contributions to the understanding of MCPyV, MCC, and their interplay. 2. Data Collection and Analysis: - Compilation of data regarding the epidemiology, clinical features, and mortality statistics of MCC. - In-depth analysis of molecular characteristics, genome structure, and protein expression of MCPyV, with a focus on the early and late transcriptional units. 3. Virological Studies: - Investigation of virological aspects, including the identification and characterization of MCPyV as a naked double-stranded DNA virus. - Evaluation of the viral genome structure, transcriptional units, and protein products to elucidate their role in viral replication and association with MCC. 4. Clinical Observations studies: - Exploration of clinical observations related to MCC, including disease incidence, mortality rates, and comparisons with other well-known cancers. 5. Host-Pathogen Interaction Studies: - In-depth analysis of studies exploring the interaction between MCPyV and the host immune system, emphasizing the role of immune responses in MCC tumorigenesis. 6. Integration of Additional Evidence: - Incorporation of additional evidence, such as cases of spontaneous tumor regression and the presence of tumor-reactive T cells, to support the

involvement of the immune system in MCPyV-driven MCC tumor development. By employing these methods, this review aims to provide a comprehensive and up-to-date synthesis of knowledge surrounding MCPyV and its intricate relationship with the development of Merkel cell carcinoma.

Results: This review highlights the important role of Merkel cell polyomavirus (MCPyV) in Merkel cell carcinoma (MCC), a rare and aggressive skin cancer. Key findings include the association of MCPyV with MCC, the high mortality rate of MCC, the unique molecular characteristics of MCPyV, the virological complexity of MCPyV in tumorigenesis, the serological dynamics and immune response to MCPyV, the role of the host immune response in MCC tumorigenesis, and the supportive evidence for immune involvement in MCPyV-associated MCC. These results contribute to a better understanding of MCPyV and MCC and can guide further research and advancements in treatment.

Conclusion: This review highlights the strong connection between viruses and cancer, with around 15% of human cancers being caused by viruses. Merkel cell polyomavirus (MCPyV) is a significant factor in the development of Merkel cell carcinoma (MCC), a rare and aggressive skin cancer, being associated with approximately 80% of MCC cases. Understanding MCPyV is crucial due to its clinical significance. The virus has unique genomic characteristics and plays a complex role in viral replication and interaction with host cells. Early exposure to MCPyV in childhood is linked to the development of MCC, and the host immune response plays a pivotal role in the disease. Research on MCPyV and its interaction with the immune system holds promise for future diagnostic and therapeutic advancements in treating Merkel cell carcinoma.

Keywords: Merkel cell polyomavirus, Merkel cell carcinoma, MCPyV genome, MCPyV Seroprevalence patterns

Mesenchymal stem cells and natural killer cells interaction mechanisms and potential clinical applications (Review)

Batol Abbasi,[1] Karim Shamsasenjan,[2,*]

1. Tabriz University of Medical Sciences
2. Tabriz University of Medical Sciences

Introduction: Natural killer (NK) cells are a member of the body's innate immune system, which have anti-tumor and anti-viral roles [1]. NK cells in leukemia patients who are candidates for hematopoietic stem cell transplantation (HSCT) play an important role in the graft-versus-leukemia (GVL) response [2]. Following HSCT, NK cells are the first population of lymphocytes that recover after HSCT, which helps improve transplantation, reduce rates of leukemia relapse, and reduce GVHD [3, 4]. However, some studies have shown that transplanted NK cells may lead to GVHD by producing pro-inflammatory cytokines (IFN-Î³, TNF-a) that directly cause cell damage or indirectly by increasing the activity of transplanted T cells [3]. Mesenchymal stem cells (MSCs) are multipotent and non-hematopoietic stem cells that can differentiate into mesenchymal and non-mesenchymal tissues [5]. There are many reports that MSCs can affect the immune system by interacting with myeloid and lymphoid cells [6]. It has recently been shown that they can inhibit activity B cells [7,8,9], T cells [8,9,10,11], NK cells [12], dendritic cells [13, 14], and macrophages [9] through direct cell-to-cell interaction and secretion of soluble factors including prostaglandin E2 (PGE2), indoleamineâ€□2,3â€□dioxygenase (IDO), and transforming growth factorâ€□beta (TGFâ€□Î²) [15,16,17,18]. MSCs due to regulate the immune system can reduce GVHD in allogeneic HSCT [19, 20]. They can escape the immune system by the lack or low expression levels of stimulatory molecules [21], and also they can survive for a long time in an allogeneic environment [22]. Therefore, their allogeneic cell products can be used for therapeutic applications to regulate the immune system in autoimmune diseases, transplantation, and tissue regeneration [23]. This review investigates how MSC could affect NK cell phenotype, proliferation, and activity. We also show signaling two cells in contact with each other and therapeutic applications of MSC on NK cell-related diseases.

Methods: Review

Results: Review

Conclusion: Over the past few years, many researchers have focused on the moderating effect of MSC on the immune system. The researchers showed MSC modulate the function of immune system cells, including NK cells. Some studies have shown that MSC suppresses NK cell function, while a few studies show that MSC enhances NK cell function. This discrepancy in the

effect of MSC on NK cells could depend on co-culture conditions such as incubation time, MSC:NK cell ratio, pre-stimulated NK cell conditions. However, most studies indicate that MSC suppresses NK cell function. Today due to the effect of MSC on NK cell function, it has been considered as a therapeutic tool for the therapy of many diseases, including autoimmune diseases, and prevents transplant rejection and GVHD.

Keywords: Natural killer cell, Mesenchymal stem cells, Immunomodulation, Signaling, Therapeutic

Metabolic engineering for drug discovery and development (Research Paper)

Howra valinejad,[1,*] Issa layali,[2] Erfan kashefi,[3] Sajad cheraghali,[4]

1. Department of Microbiology ,Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran
2. Department of Biochemistry and Biophysics, Faculty of Advanced Sciences and Technology, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran
3. Department of Microbiology ,Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran
4. Department of Microbiology ,Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran

Introduction: Metabolic engineering, emerging in the early 1980s, stands at the forefront of manipulating biological systems via genetic alterations. This paper emphasizes recent strides, particularly the synergy between genetic engineering and biosynthetic chemistry, influencing the exploration of natural-product drugs. While natural products offer a bounty of successful drug leads, they often present challenges related to pharmacokinetics, production costs, and yield limitations from native hosts. Addressing these challenges involves innovative methodologies like organic chemistry, combinatorial synthesis, and leveraging enzymes, both in vitro and potentially within cellular environments. The balancing act of gene expression within heterologous pathways and the native metabolic milieu remains a core challenge in utilizing metabolic engineering for drug development

Methods: To comprehend the effects of metabolic engineering techniques, this study employed an integrative approach. Genetic manipulation, biosynthetic chemistry, and combinatorial synthesis were the primary methodologies utilized. Enzymatic processes were explored for in vitro functionalization of complex molecules, while the potential for cell-based combinatorial synthesis was also investigated. Introducing genes into biosynthetic pathways of heterologous hosts was a core aspect, demanding meticulous gene regulation to circumvent impediments in product synthesis and metabolic pathway bottlenecks.

Results: The convergence of genetic manipulation and redirection of metabolic pathways has not only facilitated the identification and understanding of biosynthetic pathways but also provided opportunities to streamline drug development pipelines. This has the potential to reduce the time and costs associated with bringing new drugs to market, offering hope for more accessible and affordable therapeutics, especially in regions where drug affordability remains a significant barrier.

Conclusion: Metabolic engineering has revolutionized drug discovery and development, particularly in the realm of natural-product drugs. The integration of genetic engineering and biosynthetic chemistry has significantly advanced our ability to harness natural compounds for therapeutic purposes. Despite the challenges related to optimizing pharmacological properties and production costs of natural products, metabolic engineering offers promising solutions.

Keywords: metabolic engineering drug discovery Biochemistry product natural product natural drug

Metarhizium robertsii: A Versatile Fungus for Bioremediation and Plant Growth Promotion (Review)

Seyed Ali Sadr Tabatabaee,[1] Maliheh Entezari,[2,*]

1. Bachelorâ€™s student, Microbiology group, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran.
2. Farhikhtegan Medical Convergence sciences Research Center , Farhikhtegan Hospital Tehran Medical sciences ,Islamic Azad University,Tehran,Iran

Introduction: Metarhizium robertsii is a fascinating fungus with diverse capabilities that make it a valuable asset in bioremediation and plant growth promotion. This species of fungus belongs to the genus Metarhizium, which is known for its insect-pathogenic and endophytic properties. However, recent research has unveiled the remarkable potential of M. robertsii in addressing environmental challenges and enhancing agricultural productivity. In this manuscript, we will explore the numerous attributes of M. robertsii, its mechanisms of action, and its applications in bioremediation and plant growth promotion. One of the most significant findings regarding M. robertsii is its ability to tolerate and remediate mercury pollution. Mercury contamination poses a serious threat to public health and ecosystems worldwide. M. robertsii has demonstrated its capacity to degrade methylmercury, a highly toxic form of mercury, and reduce divalent mercury, effectively decreasing the accumulation of mercury in plants and promoting their growth. The fungus achieves this through the activity of specific enzymes: methylmercury demethylase (MMD) and mercury ion reductase (MIR). These enzymes play a crucial role in the demethylation of methylmercury and the reduction of divalent mercury to volatile elemental mercury. The ability of M. robertsii to remove mercury from both soil and water makes it a promising candidate for bioremediation efforts.

Methods: This article uses an extensive search of PubMed - NCBI and Google Scholar databases - and the study of almost 20 articles and an analysis of the studies done in the last ten years on this issue.

Results: The molecular mechanisms underlying M. robertsii's mercury tolerance have been investigated extensively. The MMD enzyme is responsible for the demethylation of methylmercury, converting it into less toxic forms. Through genetic engineering, researchers have enhanced the expression of MMD in M. robertsii, resulting in improved bioremediation capabilities. Similarly, the MIR enzyme facilitates the reduction of divalent mercury to elemental mercury, which can then be volatilized. Overexpression of MIR in M. robertsii has also been shown to enhance its ability to remediate mercury-contaminated environments. Additionally, the presence of MIR

homologs in various fungi suggests that the tolerance to divalent mercury is widespread in fungal species. In addition to its bioremediation potential, M. robertsii has been found to promote plant growth. The fungus forms symbiotic relationships with plants, particularly rice, and influences various aspects of plant physiology. When exposed to M. robertsii, rice plants exhibit enhanced growth characteristics, including increased height and above-ground biomass. The fungus also modulates the expression of plant defense genes and phytohormone content, leading to improved resistance against phytopathogens. These findings suggest that M. robertsii can act as a growth-promoting agent, potentially contributing to increased agricultural productivity. The unique properties and capabilities of M. robertsii have led to investigations into its potential for genetic engineering. Researchers have successfully overexpressed key enzymes involved in mercury tolerance, such as MMD and MIR, resulting in improved bioremediation capabilities. This genetic engineering approach holds promise for further enhancing the fungus's ability to remediate mercury-contaminated environments. Additionally, the identification of genes responsible for plant growth promotion and nutrient selection opens up avenues for genetic manipulation, potentially leading to the development of more efficient biofertilizers and biocontrol agents. While the research on M. robertsii has provided valuable insights, there are still many challenges and questions that need to be addressed. Further studies are needed to elucidate the specific mechanisms by which M. robertsii interacts with plants and modulates their growth and defense responses. Understanding the genetic regulation of these interactions and the underlying signaling pathways will be crucial for harnessing the full potential of M. robertsii in agriculture and environmental remediation. Additionally, field trials and long-term monitoring are necessary to assess the efficacy and sustainability of M. robertsii-based interventions.

Conclusion: Metarhizium robertsii is a versatile fungus with immense potential in bioremediation and plant growth promotion. Its ability to tolerate and remediate mercury pollution, as well as its capacity to enhance plant growth and defense, make it a valuable asset in addressing environmental challenges and improving agricultural productivity. The molecular mechanisms underlying M. robertsii's mercury tolerance and its interactions with plants provide a foundation for further research and potential applications. With continued investigations and advancements in genetic engineering, M. robertsii has the potential to become a powerful tool in managing environmental pollution and promoting sustainable agriculture.

Keywords: Metarhizium robertsii/MMD enzyme/Mercury

Metformin as a Potential Therapeutic Agent in Breast Cancer: Targeting miR-125a Methylation and Epigenetic Regulation (Research Paper)

Fatemeh Ahmadpour1,[1] Somayeh Igder2,[2] Ali Reza Eftekhari Moghadam3,[3] Bahman Moradipoodeh4,[4] Ghorban Mohammadzadeh,[5,*]

1. Nutritional Health Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Cellular and Molecular Research Center, Medical Basic Sciences Research Institute, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
3. Department of Anatomical Science, Faculty of Medicine, Baqiyatallah University of Medical Sciences, Tehran, Iran
4. Department of Laboratory Sciences, Lahijan Branch, Islamic Azad University, Lahijan, Iran
5. Department of Clinical Biochemistry, Faculty of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Introduction: Breast cancer, a prevalent malignancy, has been on the rise. Molecular subtypes, including HER2-positive, pose significant challenges in treatment. Repurposing metformin as an anti-cancer agent has gained interest, particularly due to its potential impact on miRNA regulation. This study aimed to explore metformin's effects on miR-125a promoter methylation in breast cancer and its underlying mechanisms.

Methods: The human cell line SK-RB3, known for strong HER2 expression, was treated with varying concentrations of metformin, and cell viability was assessed using the MTT assay. Subsequent analyses explored the methylation status of the miR-125a promoter through DNA extraction and Methylation Specific PCR (MSP). Real-time PCR was employed to evaluate gene expression, and immunocytochemical staining was conducted to assess the presence of HER2 protein and Vimentin protein with Immunofluorescence test. Furthermore, in silico studies identified miR-125a-5p-regulated genes and their association with tumor pathways.

Results: Results indicated a dose-dependent reduction in cell viability, with IC50 values of 65 mM (48 hr) and 25 mM (72 hr). Metformin induced hypomethylation of the miR-125a promoter, resulting in a twofold increase in miR-125a expression. Additionally, it downregulated the expression of DNMT1, a DNA methyltransferase, and HER2, a key protein implicated in breast cancer. Furthermore, metformin exhibited an inhibitory effect on Vimentin, suggesting potential interference with epithelial-mesenchymal transition (EMT) processes.

Conclusion: This study highlights metformin's potential as an anti-cancer agent in breast cancer treatment, shedding light on its mechanisms involving miR-125a promoter methylation and its impact on key proteins like HER2 and

Vimentin. Further research is warranted to fully elucidate its therapeutic benefits.

Keywords: Metformin, Breast Cancer, miR-125a, Methylation, HER2, DNMT1, Epigenetics

Microsatellite Instability, An Important Molecular Hallmark for Colorectal Cancer (Review)

Mahoora Rahimi,[1] Fatemeh Keyfi,[2,*]

1. Department of Medical Genetics and Molecular Medicine, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
2. Department of Medical Laboratory Sciences, Varastegan Institute for Medical Sciences, Mashhad, Iran

Introduction: The second deadliest and one of the most prevalent kinds of cancer is colorectal cancer (CRC), a diverse disease marked by a slow buildup of genetic and epigenetic alterations. Even though CRC is one of the most deadly types of cancer in the world, it is also one of the most treatable if caught early. Most colorectal cancers (CRCs) start as precursor lesions like adenoma and progress to adenocarcinoma. The identification of three distinct molecular carcinogenesis pathways: No.1 chromosomal instability No.2 microsatellite instability (MSI) No3. CpG island methylator phenotype account for about 85%, 15%, and 17% of cases, respectively. Most other malignancies as well as sporadic colon, stomach, and sporadic endometrial cancers have MSI. microsatellite instability is present in 15â€“25% of colorectal cancer cases. In CRC, determining the MSI status has therapeutic and prognostic significance. Additionally, tumor identification and categorization employ MSI detection as a diagnostic tool. Given the significance of this matter, we decided to compile and publish a summary of data about the diagnostic and therapeutic aspects of MSI to aid in the diagnosis of CRC.

Methods: In this research, from the 36 primary articles searched in online databases such as PubMed and Google Scholar during the last 5 years (2018-2023), according to the inclusion and exclusion criteria of the study (which was the English language and the time frame of the articles), the final 14 articles Related to the two main keywords colorectal cancer and microsatellite instability were selected and analyzed.

Results: Short repeating DNA sequences, known as microsatellites or Short Tandem Repeats (STRs), makeup approximately 3% of the human genome. Mutations in these sequences occur often. A genetic disorder called microsatellite instability (MSI) is brought on by a flaw in the DNA mismatch repair machinery. Errors that arise during DNA replication and recombination are often corrected by this system. The repair process is carried out by the proteins MutS and MutL in prokaryotes, and by their homologs, MSH2, MSH3, MSH6, MLH1, MLH2, and MLH3 in eukaryotes. MSI can be directly identified by PCR-based amplification of particular microsatellite sequences, which is the most widely used approach, or indirectly by immunohistochemistry (IHC) staining to examine the expression of mismatch repair proteins. The process of IHC analysis entails determining whether cells have mismatch repair

proteins or not. The DNA mismatch repair system's functioning is assessed using antibodies against proteins such as MLH1, MSH2, PMS2, and MSH6. Most anomalies in the relevant genes and mutations in MLH1 and MSH2 can be found by employing IHC analysis with PMS2 and MSH6 antibodies. Screening for Lynch Syndrome is the primary goal of IHC and MSI. Globally, the practice of performing universal MSI/IHC testing on cancers is growing. Using fluorescent multiplex PCR-based techniques, the presence of distinct microsatellite markers with varying lengths in tumor cells is quantified in normal cells. Three dinucleotide repeats (D5S346, D2S123, and D17S250) and two mononucleotide repeats (BAT25 and BAT26) were initially suggested for the diagnosis of microsatellite instability in colorectal cancer. Three MSI phenotypes exist: Microsatellite Stable (MSS) if no instability is seen, MSI-high (MSI-H) if two or more markers are mutated, and MSI-low (MSI-L) if only one marker is mutated. The Bethesda panel was the name given to this panel. Nonetheless, subsequent research revealed that mononucleotide markers offer superior specificity and sensitivity, prompting the National Cancer Institute (NCI) to later modify the Bethesda criteria. Because these panels are more accurate at diagnosing MSI in CRCs, their use has expanded.

Conclusion: It is commonly known that there is a rising trend in the incidence and early death of CRC in individuals under 50. Due to the prognostic and predictive value of this tumor biomarker, patients with MSI are of particular interest among these molecular subgroups. This increasing trend has intensified the need for serious research focusing on identifying strategies for the prevention and early detection of this disease. When it comes to CRC, MSI is a noteworthy genetic marker that can help with diagnosis, prognosis, and chemotherapeutic therapy efficacy prediction. These days, certain tumor molecular features are the focus of drug development methods, and molecular approaches have been created for MSI detection.

Keywords: CRC, MSI, Genomic Instability, DNA MMR system

Modulating Glycolysis to Improve Cancer Therapy (Review)

Issa Layali,[1,*] Negar Jafari,[2] Fatemeh Shahbazi,[3]

1. Department of Biochemistery and Biophysics,Faculty of Advanced Sciences and Technology,Tehran Medical Sciences Branch, Islamic Azad University
2. Faculty of Advanced Sciences and Technology,Tehran Medical Sciences Branch, Islamic Azad University
3. Faculty of Advanced Sciences and Technology,Tehran Medical Sciences Branch, Islamic Azad University

Introduction: Altered metabolism in cancer cells provides a way to develop therapeutic targets for cancer cells and anti-cancer agents. cancer cells reprogram their metabolism to increase growth, metastasis and survival. Increasing glycolysis is not only important for meeting the energy needs of cells, but also for the production of metabolic mediators necessary for the synthesis of macromolecules in cancer cells. This phenomenon is often known as the Warburg effect. Glycolytic inhibition alone is not effective in a clinical setting. Targeted metabolism, especially in combination with chemotherapy, is expected to improve therapeutic responses and may help to overcome drug resistance. Increased glycolysis in cancer cells and latic acidosis caused by that stroma. modifies the tumor into a tumorigenic microenvironment. In this review, we examine glycolytic modification in cancer cells and how it can help as a therapeutic strategy in combination therapies with hormonal therapy.

Methods: Targeting Glycolysis to Enhance Hormonal Therapy: Hormone therapy has shown significant progress as a therapeutic strategy for hormone-dependent cancers, especially in breast, prostate and other gynecologic diseases. Cancers are aromatase inhibitors (Al), estrogen receptor antagonists (ER), ER-modulators, anti-estrogens and GnRH antagonists are effective therapeutic drugs and have shown high success rates in patients with recurrent or metastatic gynecologic malignancies sensitive to hormone. Hormone therapy interferes with the restricting of hormone production in the body by reliance on cancer cells, while hormone therapy improves survival and reduces recurrence in various types of cancer. New or acquired resistance to hormone therapy is a major clinical problem that requires the development of innovative strategies. Resistance to hormone therapy always occurs in most patients with ER+ metastatic BC and castration-resistant PC (CRPC). Metabolic reprogramming is an intrinsic feature of endocrine resistant cancer cells, suggesting that combined therapy with metabolic regulators and conventional hormone therapy may be helpful in overcoming resistance, but it is unclear whether metabolic rewiring is the cause or consequence of endocrine resistance, and several studies are investigating the interplay between hormonal signaling and cancer cell metabolism.

Results: Somatic mutations in estrogen receptors have been linked to the clinical development of resistance to hormone therapy. The Y537S mutation in ER-a increased mitochondrial and glycolysis metabolism in BC cells, suggesting that increased glucose metabolism is a highly protected mechanism of endocrine resistance. Pharmacological inhibition of glycolysis has been investigated with PFK-158, a PFKFB3 inhibitor, with tamoxifen or folusterant as a potential therapeutic intervention to overcome endocrine resistance. Involved PFKFB3, with high expression of the mRNA base of the PFKFB3 gene, is found in endocrine treatment-resistant BC cells and is associated with undesirable non-recurrence survival in BC patients. The anti-tumor effect of PFK-158 is exacerbated when combined with tamoxifen and folusterant therapy. PFKFB3 inhibited necroptosis markers that are activated by the synthetic lineage kinase pseudodomain kinase receptor (MLKL) and the pseudodomain kinase receptor (MLKL), implicating the possible mechanism of cell death caused by PFK-158. In a long-term estrogen deprivation (LTED) model of artificial intelligence resistance, cancer cells increased glycolysis dependence. Inhibition of glycolysis by HK2 inhibitors, along with Al and Letrozole, reduced cell viability. Targeting glucose metabolism with established glycolytic inhibitors has been shown to increase sensitivity to endocrine treatment in breast and PC models. The interaction between glucose metabolism and androgen receptor/ER signaling suggests that combined endocrine therapy approaches with metabolic modulators can be a standard care for overcoming resistance. Also, dietary interventions targeting metabolic rewiring and modulating glucose metabolism have also shown to improve the effectiveness of endocrine treatment in metastatic patients of BC liver.

Conclusion: The metabolic signatures of tumor cells are different from normal cells, which allows the tumor cells to adapt to the increased energy and metabolite demands.Though the inhibition of glycolysis might inhibit cancer cell proliferation, cancer cells may adapt by upregulating or glutaminolysis, which could result in the development of resistance to therapy, in addition to co-morbidities such as cachexia in patients. This rewiring of metabolic pathways poses challenges to precision therapies. In-depth analytical and extensive pre-clinical studies should identify targetable metabolic enzymes/enzyme isoforms that are efficacious in different tumor types with minimal toxicity to normal cells. Another major challenge in the clinical development of cancer therapeutics is the need to identify patient groups that would benefit from the therapy.

Keywords: Glycolysis, Combination theraphy, Hormonal Therapy

Molecular analysis of GJB2 (connexin 26) and GJB6 (connexin 30) gene mutations in non-syndromic hereditary deafness in Torbat-Jam from South Khorasan Razavi (Research Paper)

Tayebeh Hamzehloei,[1,*] Faeze Khaghani,[2]

1. Mashhad university of medical sciences, medical genetics department, Mashhad-Iran
2. Mashhad university of medical sciences, medical genetics department, Mashhad-Iran

Introduction: Introduction: The most common inherited sensory disorder that affects I in 1 000 children is severe hearing loss. There are two genes linked to DFNB 1, GJB2 and GJB6, which are the major genetic cause of non-syndromic autosomal recessive deafness. The specific aim of this study was to determine the role of GJB2 and GJB6 in deafness within the Torbat-Jam patients in South Khorasan-Razavi.

Methods: Methods: A total of 44 families were recruited and divided into either the familial or sporadic study group, which consisted of 16 and 28 families, respectively. To achieve the aims of this study, polymerase chain reaction (PCR) amplification followed by automated DNA sequencing of the coding regions of GJB2 and GJB6 was performed.

Results: Results : In total, six previously reported mutations (35delG, 312de1l4, W24X, M34T, V37I and W44X), and polymorphisms (V27I, A40A, R127H and V153I) were detected in GJB2. In the GJB6 gene only the S199T polymorphism was observed.

Conclusion: conclusion: It was determined that the most common mutations found within the Torbat-Jam patients were 35delG and 312de1l4 of GJB2. An overall detection rate of 35% was achieved in non-syndromic autosomal recessive deafness amongst this patient cohort. This study therefore, provides information that can be used in the formulation of a screening program for non-syndromic autosomal recessive deafness specific

Keywords: mutation detection, GJB2, GJB6

Molecular Progression and Multiple-Target Biomarkers in Multiple Myeloma: A Brief Review (Review)

Amin Hasanpour,[1] Tahereh Kalantari,[2,*]

1. Division of hematology and blood banking, Department of Medical Laboratory Sciences, School of Paramedical Sciences, Shiraz University of Medical Sciences, Shiraz, Iran
2. 1. Division of hematology and blood banking, Department of Medical Laboratory Sciences, School of Paramedical Sciences, Shiraz University of Medical Sciences, Shiraz, Iran 2. Diagnostic Laboratory Sciences and Technology Research Center, School of Paramedical Sciences, Shiraz University of Medical

Introduction: Multiple myeloma (MM) is a cancer affecting plasma cells with different variations. It starts with monoclonal gammopathy of uncertain significance (MGUS), a pre-malignant stage that often goes unnoticed. MGUS progresses to MM at a rate of 1% per year. Asymptomatic or smoldering myeloma (SMM) is a condition where the level of plasma cells is above 10% or the monoclonal protein level is above 30 g/l. Standard-risk SMM patients have a 10% risk of progression to active myeloma for the first five years. The International Myeloma Working Group (IMWG) updated the definition of MM with three new criteria in addition to hypercalcemia, renal impairment, anemia, bone disease (CRAB criteria) for therapy initiation, including plasma cell infiltration >60%, serum free light chain level/ratio >100mg/l, and the presence of focal lesions on advanced imaging. The treatment of multiple myeloma typically includes the use of chemotherapeutic medications, although relapse is common in the majority of cases. Research has led to newer markers for diagnosis, prognosis, and therapeutics. This review discusses molecular progression from MGUS to MM and summarizes conventional and new approaches for better management, considering patient convenience.

Methods: In this review, we demonstrated searches with PubMed, Google Scholar, and medical journals identifying articles relevant to our topic.

Results: 1. Molecular progression MM is caused by molecular events like chromosomal translocations and hyperdiploidy. About 55% of MM patients show recurrent chromosomal translocations at the immunoglobin heavy chain (IgH) locus at 14q32. The most common translocations are t(11;14) and t(4;14). In multiple myeloma (MM), chromosomal hyperdiploidy is seen in up to 50% of patients, leading to abnormal gene expression of the cyclin D family and cell growth. In MGUS, genetic abnormalities increase malignant plasma cells to >10% of bone marrow mononuclear cells. MM cells acquire Ras family oncogene mutations involving APOBEC3B, and c-Myc overexpression occurs in MGUS to MM progression. DNA hypomethylation may accelerate disease progression. In the terminal stage of myeloma, MM cells exhibit stroma-

independent growth, sustained by the activation of NF-kB. In terminal-stage myeloma, genes encoding NF-kB pathway inhibitors are lost, and there are extensive structural abnormalities of chromosomes, such as complex translocations involving the c-Myc gene, duplication of chromosome 1q, and deletions of 1p32 or 17p13. TP53 mutations usually occur with 17p deletion, especially in refractory cases, and they have oncogenic functions, including up-regulation of c-Myc and genes encoding proteasome subunits, which induce anti-cancer drug resistance. 2. Biomarkers MM is diagnosed using nongenomic and genomic biomarkers. Nongenomic biomarkers include staging systems such as DSS, ISS, and IRSS, plasma cell percentage, chromosomal abnormalities, serum protein electrophoresis, urinary Bence-Jones protein, FLC, and imaging techniques. Genomic biomarkers include IFISH and GEP. Commonly used markers for diagnosing and staging MM include plasma cell percentage, Î²2 microglobulin, albumin, and Bence Jones proteins. Newer markers like ECM proteins, circulatory tumor cells (CT cells), micro RNAs, and cell-free (cf) DNA offer a non-invasive approach to detecting MM and can improve prognostic accuracy. Immunotherapy using immune-modulating drugs like lenalidomide is followed by monoclonal antibodies such as daratumumab for treating relapsed cases of MM. Certain proteins like amyloid A protein, vitamin D-binding protein isoform-1, and HSP 90 are dysregulated in MM patients and could serve as markers for diagnosis or prognosis prediction. Liquid biopsy is a non-invasive method to evaluate plasma cells and nucleic acids for efficiently detecting MM. This technique offers a comprehensive understanding of the disease's molecular profile in the peripheral circulation, making it a promising tool for diagnosis and treatment response assessments.

Conclusion: It's important to have a good understanding of the molecular mechanisms of MM in order to fully comprehend its progression. It also suggests that both nongenomic and genomic biomarkers should be used to diagnose MM, and newer markers like CT cells and cfDNA could be used to detect MM non-invasively with improved prognostic accuracy. The article also discusses the use of immunotherapy and monoclonal antibodies in treating relapsed MM cases. However, there is still a lack of validated biomarkers that can predict the risk of progression to symptomatic disease for both MGUS and SMM, indicating the need for more research in this field. Overall, this review provides valuable insights into the diagnosis, management, and treatment of MM, emphasizing the necessity for continued research to improve patient outcomes.

Keywords: MM, MGUS, SMM, molecular progression, Biomarkers

Nanopore Sequencing for the Identification of Genetic Mutations in Cancer Patients (Review)

Yasaman Alirezaei,[1,*]

1. Student of cellular and molecular biology at Gorgan Azad University

Introduction: Cancer is a complex disease characterized by the accumulation of genetic mutations that lead to uncontrolled cell growth and proliferation. The identification of these mutations is critical for the diagnosis, prognosis, and treatment of cancer patients. Traditional sequencing methods, such as Sanger sequencing and next-generation sequencing (NGS), have been widely used to identify cancer-associated mutations. However, these methods have limitations in terms of cost, scalability, and sensitivity. Nanopore sequencing is a promising new approach that offers several advantages over traditional methods, including real-time sequencing, high accuracy, and low cost. In this review, we will discuss recent advances in the use of nanopore sequencing for the identification of genetic mutations in cancer patients. The objectives of this review are to describe the principles of nanopore sequencing, to discuss recent studies that have used this technology to identify cancer-associated mutations, and to evaluate the potential advantages and limitations of nanopore sequencing for cancer research and clinical practice.

Methods: I conducted a comprehensive review of the literature on the use of nanopore sequencing for the identification of genetic mutations in cancer patients. We searched PubMed for relevant articles published in the last five years using the following search terms: "nanopore sequencing," "cancer," "genetic mutations," and "diagnosis." We also reviewed the reference lists of identified articles for additional relevant studies. Principles of nanopore sequencing: Nanopore sequencing is a single-molecule sequencing technology that uses a nanopore to detect changes in electrical current as DNA or RNA molecules pass through the pore. The nanopore is typically embedded in a membrane that separates two fluid compartments. A voltage is applied across the membrane, which creates an electrical field that drives the DNA or RNA molecules through the pore. As the molecules pass through the pore, changes in the electrical current are detected and recorded. These changes are then used to reconstruct the sequence of the DNA or RNA molecule. Recent studies using nanopore sequencing for cancer research: Several recent studies have demonstrated the potential of nanopore sequencing for the identification of cancer-associated mutations. For example, a study by Maura et al. (2019) used nanopore sequencing to identify mutations in chronic lymphocytic leukemia (CLL) patients. The authors found that nanopore sequencing had a high concordance with NGS and was able to detect additional mutations that were missed by NGS. Another study by Plesa et al. (2020) used nanopore sequencing to identify mutations in circulating tumor DNA (ctDNA) from patients with metastatic breast cancer. The authors

found that nanopore sequencing had a high sensitivity and was able to detect mutations that were missed by other sequencing methods. Advantages and limitations of nanopore sequencing for cancer research: Nanopore sequencing offers several advantages over traditional sequencing methods for cancer research. First, nanopore sequencing is a real-time sequencing technology that allows for the rapid detection of mutations. This can be particularly useful in clinical settings where timely diagnosis and treatment are critical. Second, nanopore sequencing is a portable and scalable technology that can be used in a variety of settings. This makes it particularly useful for field studies and resource-limited settings. Third, nanopore sequencing has a high accuracy and can detect a wide range of mutation types, including single nucleotide variants, insertions, deletions, and structural variants.

Results: However, nanopore sequencing also has some limitations that need to be addressed. One limitation is the relatively high error rate of the technology, particularly for long reads. This can result in false positive and false negative results. Another limitation is the relatively low throughput of the technology, which can limit its application in large-scale studies. Finally, nanopore sequencing requires specialized equipment and expertise, which can limit its accessibility in some settings.

Conclusion: Nanopore sequencing is a promising new approach for the identification of genetic mutations in cancer patients. The technology offers several advantages over traditional sequencing methods, including real-time sequencing, high accuracy, and low cost. However, further studies are needed to optimize the technology and address its limitations. With continued progress, nanopore sequencing has the potential to become a valuable tool for cancer research and clinical practice.

Keywords: cancer, genetic mutations, nanopore sequencing, diagnosis, NGS

Nanotechnology-Based Point-of-Care Diagnostics for Resource-Limited Settings (Review)

Hossein Rezvan,[1,*] Fatemeh Behdarvand,[2]

1. Department of Pathobiology, Faculty of veterinary Sceince, Bu-Ali Sina University, Hamedan, Iran
2. Department of Pathobiology, Faculty of veterinary Sceince, Bu-Ali Sina University, Hamedan, Iran

Introduction: Nanotechnology has the potential to revolutionize healthcare by creating portable and inexpensive diagnostic tools, particularly in resource-limited settings. These nanotechnology-based point-of-care (POC) diagnostics can provide rapid and accurate results, enabling timely intervention and improving patient outcomes. Traditional diagnostic approaches in these settings face challenges due to a lack of access to sophisticated lab facilities and trained personnel, leading to delays in diagnosis and treatment. Nanoparticles, with their unique properties, offer a versatile platform for developing POC diagnostic tools, allowing efficient delivery of agents to target tissues or cells and selective detection of specific biomarkers associated with various diseases. The integration of nanotechnology and microfluidics has led to the development of a wide range of POC diagnostic tools for various diseases, offering rapid, accurate, and cost-effective diagnostic capabilities. As research in nanotechnology and microfluidics advances, the potential for developing even more sophisticated and versatile POC diagnostic tools for resource-limited settings is immense, improving healthcare access, reducing costs, and enhancing lives in underserved communities worldwide.

Methods: This study reviews the advancements in nanotechnology-based point-of-care (POC) diagnostics for resource-limited settings. A literature search was conducted using reputable scientific databases, including PubMed, Scopus, and Web of Science. The studies were published in peer-reviewed scientific journals between 2015 and 2023. The analysis aimed to identify emerging trends and patterns in the development and application of nanotechnology-based POC diagnostics for resource-limited settings. The study focused on emerging nanotechnology platforms, advancements in diagnostic methods, enhanced performance characteristics, cost-effectiveness, and key challenges and opportunities associated with the implementation of nanotechnology-based POC diagnostics in resource-limited settings. The review highlights the use of nanotechnology platforms for POC diagnostics in resource-limited settings, such as gold nanoparticles, carbon nanotubes (CNTs), and quantum dots. These platforms offer advantages in size, scalability, and integration with microfluidics. Nanotechnology has led to significant advancements in diagnostic methods, particularly in terms of sensitivity and specificity. Nanoparticles have been used to enhance the sensitivity and specificity of biosensors, while nanostructures integrated into

microfluidic devices have facilitated miniaturization and improved sample handling. Nanotechnology-based POC diagnostics have demonstrated significant improvements in performance characteristics compared to conventional diagnostic approaches. These include enhanced sensitivity, specificity, and accuracy. Nanotechnology-based POC diagnostics are also more cost-effective than conventional approaches due to miniaturization, single-use cartridges, and faster turnaround times. However, challenges and opportunities need to be addressed to fully realize the potential of nanotechnology-based POC diagnostics in resource-limited settings. Challenges include regulatory approval, sustainable supply chains, training and user education, and cultural acceptance. Opportunities include public-private partnerships, investment in research and development, and promoting global partnerships. Addressing these challenges and opportunities will help accelerate the development and commercialization of POC diagnostics in resource-limited settings.

Results: The overview of point-of-care (POC) diagnostics based on nanotechnology for settings with limited resources shows how nanotechnology has had a major influence on the creation of sophisticated POC testing systems. It has been demonstrated that nanomaterials and nanoparticles, such as carbon nanotubes (CNTs), quantum dots (QDs), and gold nanoparticles (AuNPs), provide unique benefits in terms of mobility, miniaturization, and smooth integration with microfluidic devices. The sensitivity, specificity, and cost-effectiveness of POC diagnostics have significantly improved as a result of these developments, making them extremely promising for efficient disease management in environments with limited resources.

Conclusion: The integration of nanomaterials and nanoparticles in point-of-care (POC) diagnostics holds great promise for revolutionizing healthcare delivery in resource-constrained settings. These diagnostics are more sensitive, specific, and economical than traditional methods; however, overcoming obstacles such as regulatory approval, sustainable supply chains, and user education is essential. Opportunities such as public-private partnerships and investment in research and development can accelerate the development and commercialization of POC diagnostics based on nanotechnology, improving patient outcomes and healthcare access in resource-constrained settings. Nanotechnology can be used to create small, lightweight, and reasonably priced diagnostic instruments that medical professionals can easily implement.

Keywords: Nanotechnology-diagnostic-healthcare

Navigating Helicobacter Pylori Outbreaks: A Comprehensive Guide to Antibiotic Strategies for Eradication (Review)

Sajjad Ghorbani Disfani,[1,*] Nazanin Sadat Seyyedein,[2] Tarannom Rezaof,[3]

1. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad
2. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad
3. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad

Introduction: Helicobacter pylori, often referred to as H. pylori, is a type of bacteria that infects the stomach and the upper part of the small intestine. The bacteria are known to cause various stomach-related issues, including gastritis and peptic ulcers, and have also been linked to an increased risk of stomach cancer. Understanding the mechanism of H. pylori infection is crucial in devising effective treatment strategies. Given the serious health implications associated with H. pylori infections, it is essential to comprehend the role of antibiotic treatment in eradicating this persistent pathogen. Antibiotic therapy plays a pivotal role in the eradication of H. pylori infections. Eradication of H. pylori is crucial in reducing the risk of recurrent peptic ulcers and lowering the chances of developing gastric cancer. Moreover, successful eradication of H. pylori can lead to long-term symptom relief for individuals suffering from gastritis and peptic ulcers. It is important to note that antibiotic treatment for H. pylori eradication should be administered under the guidance of a healthcare professional.

Methods: None (Review article)

Results: While antibiotic therapy is instrumental in eradicating H. pylori infections, it is important to be mindful of the potential side effects and considerations associated with these medications. Common side effects of antibiotics used in H. pylori eradication therapy include gastrointestinal symptoms such as nausea, vomiting, diarrhea, and abdominal discomfort.

Conclusion: The selection of antibiotics, consideration of antibiotic resistance, and implementation of combination therapy and alternative antibiotic strategies are pivotal in achieving successful H. pylori eradication. Looking ahead, ongoing research and clinical efforts are focused on advancing our understanding of H. pylori infections and optimizing antibiotic strategies for eradication.

Keywords: H.pylori, antibiotic resistance, infection, eradication, treatment

Navigating the Duality of Autophagy in Leukemia Therapy (Research Paper)

Baran Safdari,[1,*] Zahra Norizadeh,[2] Ghazal Mohammadi,[3] Issa Layali,[4]

1. Islamic Azad University, Tehran Medical Branch
2. Islamic Azad University, Tehran Medical Branch
3. Islamic Azad University, Tehran Medical Branch
4. Islamic Azad University, Tehran Medical Branch

Introduction: Autophagy, a ubiquitous cellular process, has evolved to degrade and recycle damaged or malfunctioning cellular components. This remarkable pathway plays a pivotal role in various cellular processes, encompassing cell survival, stress resistance, and metabolic regulation. In the context of leukemia, autophagy exhibits a dualistic nature, exhibiting both tumor-suppressing and tumor-promoting effects, contributing to the complex and intricate dynamics of this malignancy. Regulation of Autophagy in Leukemia: The intricate regulation of autophagy in leukemia is a multifaceted phenomenon, influenced by a diverse array of factors, including oncogenes, tumor suppressor genes, and environmental conditions. For instance, the oncogene MYC has been shown to enhance autophagy activity, whereas the tumor suppressor gene PTEN exerts an inhibitory influence on autophagy. Additionally, environmental factors such as hypoxia and nutrient deprivation can modulate autophagy activity.

Methods: To fully comprehend the tumor-suppressive role of autophagy in leukemia, a comprehensive literature search was conducted across reputable databases, including PubMed, Google Scholar, and NCBI. The search yielded 31 pertinent articles that were painstakingly reviewed and analyzed to gain a thorough understanding of this subject.

Results: A. Tumor-Suppressive Role of Autophagy in Leukemia: Autophagy, the process of degrading damaged cell components, can inhibit the growth and spread of leukemia by eliminating faulty mitochondria and cells carrying mutated oncogenes. Mitochondria, the cell's energy generators, can become dysfunctional, leading to the release of harmful reactive oxygen species (ROS) that damage DNA and other cellular structures. Autophagy acts as a scavenger, removing these damaged mitochondria, thereby reducing ROS production and safeguarding the cell's integrity. Additionally, autophagy efficiently eliminates oncogene- expressing cells, which are the driving force behind uncontrolled cell growth and leukemia. By engulfing these oncogene-expressing cells in Autophagosomes and delivering them to lysosomes for breakdown, autophagy effectively curbs leukemia progression. B. Tumor-Promoting Role of Autophagy in Leukemia: Despite its tumor-suppressing properties, autophagy can also exert tumor-promoting effects in the context of leukemia. Autophagy can provide cancer cells with a survival advantage by

replenishing their nutrient and energy reserves, a particularly crucial factor in the nutrient-deficient environment of the bone marrow, where leukemia cells predominantly reside. Furthermore, autophagy contributes to leukemia progression by facilitating cancer cell evasion from immune surveillance. Autophagy degrades damaged proteins and organelles that would otherwise serve as potential markers for immune recognition, rendering cancer cells less apparent to the immune system, thereby granting them a clandestine advantage in the face of therapeutic interventions. C. Targeting Autophagy in Leukemia Therapy: Leukemia therapy has gained interest in targeting autophagy due to its ability to both promote and suppress leukemia growth. Two primary approaches to targeting autophagy are employed: inhibition and induction. Inhibition of autophagy involves targeting autophagy-related proteins (ATGs). Rapamycin, for instance, inhibits mTOR, a critical regulator of autophagy. Conversely, induction of autophagy targets autophagy-stimulating factors (ASFs). Chloroquine, for example, induces autophagy by increasing the activity of Beclin-1, an ATG protein.

Conclusion: Autophagy's influence in leukemia is intricate and multifaceted. It can both impede and accelerate leukemia's development and advancement. The mechanisms regulating autophagy in leukemia are complex and involve various factors. Exploring autophagy as a therapeutic target in leukemia is a burgeoning area of research.

Keywords: Autophagy, Leukemia, tumorigenesis

Navigating the Microfluidic Immunoassay Landscape: A Comparative Analysis of Luminexâ„¢ xMAPâ„¢, LabChipÂ® on a Chipâ„¢, and Aptasensors (Review)

Hossein Rezvan,[1,*] Fatemeh Behdarvand,[2]

1. Department of Pathobiology, Faculty of veterinary Sceince, Bu-Ali Sina University, Hamedan, Iran
2. Department of Pathobiology, Faculty of veterinary Sceince, Bu-Ali Sina University, Hamedan, Iran

Introduction: Medical diagnostics has revolutionized healthcare by enabling early and accurate disease identification. Immunoassays, a key component of clinical diagnostics, use antibodies to identify and measure target molecules in biological samples, providing crucial insights into disease progression and patient treatment. These assays are widely used in medicine, environmental monitoring, disease diagnosis, and drug screening due to their accuracy, affordability, and low-concentration detection. They also play a significant role in pharmacological studies, including therapeutic medication monitoring. Microfluidic immunoassays are an effective method for drug screening, environmental monitoring, and illness diagnosis. They are useful for many applications because they allow the simultaneous detection of many biomarkers in a small sample volume.

Methods: The labor-intensive and complex methods associated with conventional immunoassays restrict their scalability and adaptability. The field of microfluidics, which deals with the manipulation of fluids at minuscule sizes, has led to the development of automated and compact diagnostic systems. LuminexTM xMAPTM technology is a significant advancement in immunoassays, enabling simultaneous detection of up to 100 analytes in a single sample. This technology uses microspheres coated with luminous barcodes, allowing for high-volume biomarker testing. The technique allows for the simultaneous collection of multiple analytes from a single reaction. The unique fluorescent barcodes on microspheres enable the identification of multiple analytes in a single sample. xMAP technology is used in immunogenicity, drug screening, environmental monitoring, and disease diagnostics, offering benefits like biomarker identification and unique assays. A noteworthy development in microfluidic immunoassays is LabChipÂ® on a ChipTM technology, which provides accurate sample preparation, incubation, and detection processes together with automated liquid handling. The chip's microfluidic channels facilitate the sample's passage through a sequence of processes, guaranteeing effective and precise reagent mixing. This downsized apparatus reduces the possibility of cross-contamination and improves the assay's overall repeatability. This technology streamlines laboratory processes like slab gel electrophoresis, using microfluidic channels for efficient reagent mixing. It minimizes cross-contamination, reduces sample volumes, and allows for the integration of various techniques on a

miniaturized chip, offering a wide range of applications. Short, single-stranded nucleic acid molecules called Aptamers are used by Aptasensors, a unique kind of biosensors, to selectively bind target analytes. These Aptamers are coupled to a reporter molecule, whether it is an electrochemical indicator or a fluorescent dye. The reporter molecule changes in fluorescence or electrochemical signal upon binding to the target, signifying the presence of the analyte. With their great sensitivity and specificity, Aptasensors have been employed extensively for the detection of a wide range of targets, including infectious pathogens. High selectivity, adjustable qualities, and the possibility of point-of-care testing are only a few of its benefits. Furthermore, Aptasensors have been used to identify infectious diseases, and current research has concentrated on their cutting-edge technologies and design principles.

Results: Luminexâ„¢ xMAPâ„¢ is a multiplexed immunoassay system that allows simultaneous detection of multiple targets in a single sample. It has applications in immunogenicity, drug screening, environmental monitoring, and disease diagnostics. LabChipÂ® on a Chipâ„¢ technology streamlines laboratory processes by providing accurate sample preparation, incubation, and detection processes, with microfluidic channels for efficient reagent mixing. Aptasensors, which use short, single-stranded nucleic acid molecules called Aptamers, have high sensitivity and specificity, making them useful for detecting infectious pathogens and providing point-of-care testing. These technologies offer various benefits and streamline laboratory processes.

Conclusion: Microfluidic immunoassay platforms have revolutionized diagnostics by offering miniaturization, high throughput, and enhanced sensitivity. Luminexâ„¢ xMAPâ„¢ technology, LabChipÂ® on a Chipâ„¢ technology, and Aptasensors are three advanced platforms with unique capabilities. Luminexâ„¢ xMAPâ„¢ allows simultaneous detection of up to 100 analytes in a single sample, LabChipÂ® on a Chipâ„¢ provides accurate sample preparation and automated liquid handling, and Aptasensors excel in specific nucleic acid analyte detection.

Keywords: Immunoassay-Microfluid-Comparative Analysis

New techniques and methods for laboratory diagnosis of malaria disease (Review)

Mina Monavvary,[1,*] Mina Khodayari,[2] Mohammad Taghi Ahady,[3]

1. Undergraduate Student of Microbiology, Department of Biology, Ardabil Branch, Islamic Azad University
2. Postgraduate Student of Biotechnology, Department of Biotechnology, University of Verona
3. PhD of Parasitology, Department of Biology, Ardabil Branch, Islamic Azad University

Introduction: Introduction: Malaria is a very common and important parasitic disease that has affected the lives of more than three billion and four hundred million people in the world. According to the World Health Organization (WHO), there are more than 300-500 million malaria cases and almost 1 million deaths per year. This disease became a big issue especially in areas of Africa, Asia, and South America. The causative agent of fatal and malignant malaria is a protozoan called Plasmodium falciparum. One of the most important reasons for the high mortality in this disease is that it is difficult to detect the infection in the early stages and there is still no method or technique for early detection of malaria. On the other hand, common diagnostic methods are usually expensive and not easily accessible to everyone, especially in underdeveloped and developing countries. The purpose of this systematic review was to review and introduce all malaria diagnostic techniques and methods, especially the newest and most effective methods of laboratory diagnosis of this parasitic disease.

Methods: Methods: The present study was conducted using a systematic review method. In order to collect scientific resources and specialized information, it was referred to reliable sites and databases including Google Scholar, Web of Sciences, PubMed, Scopus, SID, and Irandoc. The key words and phrases used in this study were: malaria disease, diagnostic techniques, Plasmodium falciparum, new methods of malaria diagnosis. Persian and English research articles published in the last 10 years (2012-2023) were collected and studied.

Results: Results: A total of 118 articles were collected, among them 83 articles were excluded from the study due to the similarity and repetition of topics, as well as their content not being related to the main variable of the research. Therefore, 35 articles were selected for this study. Based on the results of selected research articles there are many types of laboratory methods and techniques to diagnose malaria. The most important diagnostic methods and techniques for malaria, from traditional and common methods to the latest and most advanced methods, are as follows: Microscopy technique (preparation of thin and thick blood smears and microscopic observation),

Computer imaging of the parasite with two techniques; MKM (Moving k-Means), and FCM (Fuzzy c-Means), Serological test, Antibody Testing (IFA), Rapid Diagnostic Tests (RDTs), Quantitative Buffy Coat (QBC), Biosensor (electrochemical immunosensor), Molecular technique qPCR, Nested PCR, Immunochromatography, LAMP assay, Flow Cytometry, Biomarkers, and Quantitative Buffy Coat (QBC) test. A novel testing platform under development by researchers at the Yale School of Public Health (YSPH) and CytoAstra, LLC could provide a new noninvasive test for malaria that doesn't require a blood sample. A portable cytophone prototype that could detect malaria infection in people living in endemic settings. For malaria, the cytophone technology uses lasers at specific wavelengths focused on superficial blood vessels. When the parasites that cause malaria infection enter red blood cells, they use the hemoglobin inside those cells to liberate amino acids. New techniques based on digital imaging analysis by deep learning and artificial intelligence methods are a challenging alternative tool for the diagnosis of infectious diseases. In particular, systems based on Convolutional Neural Networks for image detection of the malaria parasites emulate the microscopy visualization of an expert. Microscope automation provides a fast and low-cost diagnosis, requiring less supervision.

Conclusion: Conclusion: Based on the results of this study, it is concluded that new techniques including noninvasive test (a portable cytophone prototype), and digital imaging analysis and artificial intelligence methods can provide fast, accurate, and low-cost diagnosis for malaria.

Keywords: Keywords: Malaria, Plasmodium falciparum, Laboratory diagnosis of malaria, Diagnostic techniques

Non-Invasive Monitoring of Multiple Myeloma Using Plasma Cell-Free DNA (Review)

Mohadeseh Ramezani,[1] Sina Eshaghi,[2] Mohammad Hossein Ahmadi,[3,*]

1. Department of Laboratory Sciences, School of Paramedical and Rehabilitation Sciences, Mashhad University of Medical Science, Mashhad, Iran.
2. Department of Laboratory Sciences, School of Paramedical and Rehabilitation Sciences, Mashhad University of Medical Science, Mashhad, Iran.
3. Department of Laboratory Sciences, School of Paramedical and Rehabilitation Sciences, Mashhad University of Medical Science, Mashhad, Iran.

Introduction: Multiple myeloma (MM) is a malignant clonal plasma cell tumor with a median survival of 5 years, characterized by malignant proliferation of clonal plasma cells in the bone marrow and secretion of monoclonal immunoglobulin (M protein). Multiple myeloma is the second most common malignant hematologic tumor after lymphoma. The term â€œCell-free DNA (cfDNA)â€• refers to fragmented DNA found in the non-cellular component of the blood. In healthy people, small amounts of cfDNA from normal cells are present in plasma. The aim of this study was to evaluate the potential of cell-free DNA released from cancer cells into patient biofluids, as an accurate biomarker for the diagnosis, prognostic assessment and monitoring of multiple myeloma disease.

Methods: The search was conducted in PubMed and Google Scholar databases using keywords such as multiple myeloma and cell free DNA, and articles published between 2020 and 2023 were evaluated.

Results: Studies have shown that there is an increase in cfDNA in the body fluids of people with multiple myeloma, and by examining the mutations that have occurred in the genome sequence, the presence of this disease, prognosis and minimal residual disease (MRD) can be assessed. Next-generation sequencing (NGS) using cfDNA has been proposed to investigate the profile of the GEP70 gene (70 gene expression profile, as a tool to predict disease recurrence and survival outcome) as well as ALU115 and ALU247 gene fragments. ALU tandem repeats, the most common sequence in the human genome, make up 10% of the human genome and are typically 300 nucleotides long. Because their methylation level is lower than that of coding genes, they are not easily affected by other factors, making them easier to identify. The concentration of ALU247 (long fragments) and ALU115 (short fragments) in the MM patients is significantly higher than that of healthy individuals, which is due to the large amount of cell death and the inability of the liver to destroy these DNA fragments. Also, the ratio of the number of

ALU115 genome (representing total cfDNA) to ALU247 genome (representing free DNA release from non-apoptotic cells) in the cfDNA integrity assay, representing the number bone marrow plasma cells, is increased in MM. It was also found that the levels of ALU247, ALU115, and cfDNA integrity after chemotherapy were lower than before chemotherapy. In addition, recent studies show that minimal residual disease (MRD) Monitoring by next-generation sequencing (NGS) of cfDNA has achieved sensitivity levels of 10^-6 and can be applied to the vast majority of MM patients.

Conclusion: According to the impossibility of repeating bone marrow sampling as an invasive method and the patchy distribution of cells in the bone marrow, at the same time due to acceptable sensitivity, the possibility of transfer at room temperature, the ease of examination of cfDNA that is present even in peripheral blood and also, due to significant progress in the diagnostic ways of mutations in the genome sequence, screening of cfDNA samples as a non-invasive method for disease diagnosis, prognostic assessment and monitoring of MRD is recommended.

Keywords: Cell-free DNA; multiple myeloma; minimal residual disease (MRD)

Oncolytic Viruses: Harnessing the Power of Viruses to Fight Cancer (Review)

Atefeh Bozorg Panah,[1] Shaghayegh Yazdani,[2,*]

1. Bachelorâ€™s student, Microbiology group, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran.
2. Department of Microbiology, Faculty of Medicine, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran.

Introduction: Cancer remains a formidable adversary, with a complex biology that often defies conventional treatments. In recent years, scientists have turned their attention to an unlikely weapon: viruses. Oncolytic viruses (OVs) are genetically engineered viruses that have been specifically designed to selectively infect and kill cancer cells. The concept of using viruses to combat cancer is not new. In the 1950s, a scientist named Dr. Chester Southam injected live herpes simplex virus into patients with melanoma, with some patients experiencing tumor shrinkage. However, these early experiments were limited by the lack of advanced genetic engineering techniques and a deeper understanding of cancer biology. Today, advances in molecular biology and virology have paved the way for the development of more sophisticated OVs. These engineered viruses are often derived from viruses that are naturally found in humans or animals, such as adenoviruses, herpesviruses, or measles viruses. Through genetic modifications, OVs can be equipped with tumor-specific targeting mechanisms, enhanced replication properties, and the ability to induce an anti-cancer immune response.

Methods: A thorough examination was conducted to comprehensively scrutinize the concept of "Oncolytic Viruses: Harnessing the Power of Viruses to Fight Cancer". This examination involved an in-depth literature search across PubMed, Google Scholar, and NCBI databases. The outcome of this search resulted in the discovery of 33 pertinent articles that were meticulously assessed and analyzed in order to acquire a more profound comprehension of this subject matter.

Results: The mechanism of action of OVs is multifaceted. Upon infection, OVs replicate within cancer cells, releasing viral particles that can further infect neighboring tumor cells. This process of intratumoral spread can lead to the destruction of large tumor masses. Additionally, OVs can induce cell death by activating apoptosis, a programmed cell death pathway. In addition to direct tumor killing, OVs can also exert their anti-cancer effects by activating the immune system. The release of viral antigens can trigger an immune response that targets both the infected cancer cells and other cancer cells nearby. This phenomenon is known as immunomodulation, and it is considered a key component of the overall therapeutic effect of OVs. OVs

have demonstrated promising results in preclinical and clinical studies across a wide range of cancer types. In a clinical trial involving patients with glioblastoma, an aggressive type of brain cancer, an OV called ONYX-015 showed significant tumor shrinkage and prolonged survival rates. Despite the encouraging progress, challenges remain in the development and clinical application of OVs. One challenge is ensuring the specificity of OVs, as they should not target healthy cells. Additionally, the immune system can sometimes recognize OVs as foreign invaders and mount an immune response against them, limiting their effectiveness. Researchers are actively addressing these challenges by developing more targeted and immunomodulatory OVs. Additionally, combination therapies that combine OVs with other cancer treatments, such as chemotherapy and immunotherapy, are being explored to enhance the overall efficacy of OV therapy.

Conclusion: The field of OV therapy is rapidly evolving, and there is growing optimism that these engineered viruses will play a significant role in the future of cancer treatment. As research continues to refine OVs and develop more effective combination therapies, OVs have the potential to revolutionize cancer treatment and improve the lives of cancer patients worldwid.

Keywords: Cancer, OV, Oncolytic Virus

Platelet large cell ratio (P-LCR) as a Diagnostic Biomarker: From Inflammation to Hematological Disorders (Review)

Alireza Khanahmad,[1,*]

1. Department of Hematology and Medical Laboratory Sciences, Faculty of Allied Medicine, Kerman University of Medical Sciences, Kerman, Iran

Introduction: Platelets (PLTs), also known as thrombocytes, are small discoid-shaped anucleated cells. The primary role of PLTs is to prevent and stop bleeding. Furthermore, tissue remodeling, wound healing, inflammation, and proliferative processes are conducted in the presence of PLTs. Platelet indices may dysregulate in several disorders. Platelet large cell ratio (P-LCR) demonstrates the percentage of large PLTs with a higher volume than 12 fl. The normal range of P-LCR is up to 50%. Younger and more active platelets tend to be larger. The increased levels of P-LCR may indicate higher production of platelets in response to various situations. Therefore, P-LCR can be an important parameter to help the diagnosis of various pathological conditions. This study aims to overview the situations in which P-LCR either elevates or decreases. This paper provides new insights into the importance and diagnostic roles of P-LCR.

Methods: A search was conducted in PubMed utilizing the following keywords: â€œplatelet indicesâ€□ OR â€œplatelet large cell ratioâ€□ OR â€œP-LCRâ€• OR PLCR. All the literature was included without the consideration of time and article type. Non-English publications were excluded. An additional manual search was also conducted in the reference list of the related publications.

Results: P-LCR is now used in clinical settings to provide additional information about a patient's health, especially in cases where platelet characteristics may be of interest. It is considered alongside other blood parameters to help diagnosis and risk assessment, particularly in the context of inflammatory and cardiovascular diseases. According to the previous literature, elevated P-LCR may accompany Inflammatory disorders, infectious diseases, bone marrow disorders, recovery from bleeding, and certain drug administration (e.g., corticosteroids). In contrast, aplastic anemia, hematological disorders, and administration of chemotherapeutic agents can decrease the P-LCR level. During an acute phase as well as a major trauma, the patient's need for producing platelets increases. These conditions may result in the release of younger and larger platelets. Thus, P-LCR level elevates. Besides, hematologic disorders such as myeloproliferative disorders may result in the presence of large circulating platelets. Generally, most of the conditions with cytopenia especially thrombocytopenia such as aplastic anemia or myelodysplastic syndromes lead to a lower generation of platelets and subsequent P-LCR drop. Some other therapeutic agents including

chemotherapeutic drugs (e.g., methotrexate, 5-fluorouracil, and others), radiotherapy, anti-platelet agents (e.g., aspirin and clopidogrel), thrombopoietin receptor agonists (e.g., romiplostim), and bone marrow suppressive drugs (e.g., azathioprine) affect the P-LCR level.

Conclusion: Although the development of new parameters such as P-LCR has provided new insights into the interpretation of the laboratory results, further research is needed to determine the regulators and interfering factors of these indices. It is also suggested that P-LCR should be considered in conjunction with the overall health and the clinical symptoms of the patient along with some other platelet indices, such as platelet count and mean platelet volume (MPV), to provide a more accurate assessment of a patient's platelet function. Overall, an increased P-LCR may indicate a higher demand for PLT production. On the other hand, both elevated destruction and diminished production of PLTs may lower the P-LCR.

Keywords: Platelet large cell ratio, Platelet, Hematologic disease, Inflammation, Diagnosis

Preparation and evaluation of ointment based on spirulina algae and plant extracts including tea tree oil and marshmallow extract and investigating the effects of herbal compounds in improving the treatment of acne scars (Research Paper)

Farnaz Karbasi,[1,*] Golafrooz Amini,[2]

1. Department of Chemistry, East Tehran Branch, Islamic Azad University, Tehran, Iran
2. Polymer Technology, School of Chemical Engineering, Islamic Azad University, Science and research Branch, Tehran, Iran

Introduction: Acne is one of the most common skin problems, especially among teenagers and adults.Today, various treatments for this problem have been found . Retinoids are derivatives of vitamin A, among which are medicines that are used to improve the treatment of acne scars. It is prescribed to patients and is often used as a first-line treatment for patients with mild to moderate acne, especially when the acne is predominantly comedogenic. While retinol is used as the main active ingredient in many skin care formulations, its effectiveness is often limited by its extreme sensitivity to degradation and toxicity at high concentrations. In addition, a significant number of people who are under treatment with Retinoids are faced with several side effects including, dry skin, dry eyes and blurred vision, eczema, liver damage and etc. In this research, an attempt was made to provide an ointment consisting of common ointments in the market, including retinoids and base ointment (Ocerin) and plant extracts which can reduce the duration of treatment and use of medicine for patients by focusing on improving the antibacterial properties of the new ointment .

Methods: Due to the antibacterial properties of spirulina algae, tea tree oil and marshmallow plant, as well as the softening property of glycerin, it is expected that an ointment with better properties can be produced in order to heal acne faster and also reduce side effects such as dry skin. Considering this, with the aim of reducing these side effects and speeding up the recovery process, spirulina algae, plant extracts including tea tree oil and marshmallow extract, and glycerin were added to commercial ointments including isotretinoin ointment 0.01% of Raha Daro Company and base ointment (Oserin) and the antibacterial effects of these herbal compounds on commercial ointments were investigated. First, spirulina algae with 0.5, 1, 2, and 2.5 wt% were added to the base ointment (Oserin) and commercial isotretinoin ointment and FTIR and DSC test materials were carried out. Then, 2, 3, and 4 wt%of marshmallow extract were added to the base ointment specimens (Oserin) and 0.5 and 2 wt% of algae, as well as isotretinoin ointment and algae 0.5% by weight. The specimens containing the Oserin and algae 0.5% and 2% by weight had physical stability after the addition of marshmallow extract, for this reason, FTIR test was carried out for these specimens. After this stage and considering that marshmallow extract and

algae cannot be used together, we added glycerin polymer to the ointments containing algae. As we mentioned, one of the side effects of common acne treatment drugs is skin dryness, which sometimes even leads to skin redness and eczema. Our purpose of using glycerin is to increase the softening level of ointments to reduce the dryness of the treated skin. Research has shown that the best effective percentage of glycerin in different combinations is 5 wt %. For this reason, at this stage, the effect of the presence of glycerin at 2, 5, 10 and 15wt% on the structure of the Oserin and Isotretinoin ointments accompanied with algae was investigated. Since the optimal percentages of algae in Oserin and Isotretinoin ointment were 2 and 0.5%, respectively, glycerin was added to these compounds. From all the new samples, FTIR test was performed to explore the effectiveness of the new compounds and DSC test was performed to analyze the thermal performance graph of the compounds. Another combination that we considered for comparison is the combination of Oserin and Isotretinoin ointments with tea tree oil. According to previous studies, the best percentage of tea tree oil effect is 5wt %. 4, 5 and 6 wt %of tea tree oil were added to isotretinoin ointment and Oserin ointment and the stability of the specimens was evaluated. For all specimens containing tea tree oil, favorable results were not obtained and they were excluded from the testing process. According to the optimal specimens that were obtained in this research, Antibacterial tests were applied on the samples containing Oserin and algae 2wt % and glycerin 15 wt %, as well as the combination of isotretinoin and algae 0.5wt % and glycerin 10 wt %, as well pure isotretinoin and oserin . This test shows us whether the bacteria will continue to grow in the presence of these compounds. The larger the diameter of the areas of non-growth of bacteria around the material, the more antibacterial the material.

Results: The results of the tests showed that the combination of base ointment and algae 0.5wt% and 2wt % and isotretinoin ointment and algae 0.5 wt% had the best results. The reason why these samples were chosen is that the peaks of the FTIR graph of algae appeared better in the graph of these three compounds and the peaks had less displacement compared to the peaks of the graphs of raw materials. Also, in the DSC charts, the peaks of the chart are better seen in the lower percentages of algae, and the ointments do not cause many changes on the charts compared to the time when the algae were not added. Specimens of Oserin and algae 0.5% and 2% by weight with 2, 3 and 4% by weight of Marshmallow extract, as well as isotretinoin and algae ointment 0.5% by weight with 2, 3 and 4% by weight of Marshmallow extract have unfavorable test results. In the case of compounds containing isotretinoin and algae and marshmallow extract, after adding marshmallow extract, the ointment became completely unstable after a short period of time and became two phases, where the thicker phase had a clot-like state and contained algae. The liquid on this clot was a very runny liquid with a very pale green color. The FTIR test of compounds containing base ointment (oserin) and algae at 0.5 and 2% by weight with 2, 3 and 4% by weight of marshmallow extract indicated that after adding marshmallow

extract to the Oserin and algae, the property of algae was lost in the ointment, and in a way, the marshmallow extract had an overlapping effect on the algae, and the FTIR diagram of the specimen was very similar to the graph of the pure Oserin, and neither the peaks of the algae nor the extract of the marshmallow extract were seen in these results. These results mean that in medicinal compounds These two substances neutralize each other's effect and cannot be used. Due to the inappropriate results of this test, DSC test were not performed. The results of the DSC tests showed that after adding glycerin to the ointments and Algae, glycerin reduces the effect of algae, or the peaks are seen with a little shift in the results, or in most cases the peaks have disappeared, and even in some results, peaks are seen that are not related to our raw materials. This shows the decrease in the quality of the new ointment in terms of chemical structure. For the compounds containing Oserin, algae and glycerin, the results indicate that oserin and algae 2wt% and glycerin 2 and 10 wt % had better results .Regarding the combinations of isotretinoin ointment, algae and glycerin, the FTIR diagram of isotretinoin ointment and algae 0.5wt % and glycerin 5 wt% had better results. In 2 wt % glycerin, the effect of algae is not seen and also a new peak is seen. For 10 wt % glycerin, the effect of isotretinoin ointment has disappeared, most of the peaks are related to glycerin and two peaks are near the peaks of algae, and in the case of 15 wt % glycerin, there are three peaks near the peaks of isotretinoin, one peak near algae and most of the peaks of glycerin. Also, the best result is related to the composition containing 5wt % glycerin, but an unknown broad peak that is not related to any of our raw materials is seen in the graph, which is not acceptable based on our results. In general, the results are not very suitable, however, the DSC results were evaluated of the compound containing 5 wt % glycerin, which has a relatively peak at an acceptable temperature. The antibacterial test results of optimal specimens containing Oserin and algae 2 wt % and glycerin 15 wt%, as well as the combination of isotretinoin and algae 0.5 wt% and glycerin 10wt % and isotretinoin ointments and pure base ointment showed that the sample of base ointment and algae 2 wt% and glycerin 15wt % showed better antibacterial properties compared to the sample of isotretinoin and 0.5 wt% algae and 10 wt% glycerin, and this better performance was observed even in pure base ointment compared to pure isotretinoin.

Conclusion: Among the samples of base ointment and isotretinoin and spirulina algae with weight percentages of 0.5, 1, 2 and 2.5, the best results of FTIR and DSC tests were obtained by the sample of base ointment and algae at 0.5wt % by weight, the sample of base ointment and algae at 2% by weight and the sample Isotretinoin and algae were 0.5% by weight. Even though the algae and marshmallow extract are well dissolved in oserin and the combinations of oserin and spirulina algae with weight percentages of 0.5 and 2 are stable with the addition of marshmallow extract with 2, 3 and 4 weight percentages, the FTIR diagrams show that the marshmallow extract neutralizes the effect of algae and the composition diagram is very similar to the diagram of pure Oserin. Compounds containing isotretinoin ointment and

algae 5 percent by weight and marshmallow extract with 2, 3, and 4 percent by weight do not have physical stability, and the hypothesis that is probable is that in an ointment like Oserin, due to the high concentration of fat and the low amount of marshmallow extract, it is probably extract-like The emulsion is spread in the ointment environment, but in isotretinoin, because the ointment is much smoother and with very little fat, the extract reacted more with the algae and dissolved the algae in itself and became a clot. After adding glycerin to the combination of oserin and spirulina algae with 2% by weight and containing isotretinoin ointment and 0.5% by weight algae, we found that the effect of algae is reduced, but still according to the FTIR results, the effect of this substance can be seen in our composition. Considering that for anti-acne ointments, the emphasis is on both the properties of antibacterial substances such as algae and the properties of skin softening substances such as glycerin, we ignore the amount of reducing the effect of algae. Among the samples of oserin ointment and spirulina algae with 2% by weight and glycerin with 2, 5, 10 and 15% by weight and isotretinoin ointment and 0.5% by weight of algae and glycerin with 2, 5, 10 and 15% by weight have the best FTIR and DSC results. The samples of oserin and spirulina algae with 2% by weight and glycerin with 15% by weight, and isotretinoin and algae with 0.5% by weight and glycerin with 10% by weight, which due to the optimality of these two compounds, we carried out an antibacterial test from them. According to the results of the antibacterial test, we found that the mixture prepared based on Oserin ointment, the sample of Oserin and spirulina algae with 2% by weight and glycerin with 15% by weight, compared to the mixture based on isotretinoin, has better functionality against the growth of Staphylococcus epidermidis. The effect of tea tree oil in combination with Oserin and Isotretinoin ointments is very small and they do not have favorable results, they were from the experimental tests.

Keywords: Acne, Spirulina algae, Marshmallow extract, tea tree oil, Staphylococcus epidermidis

Prevalence of enterotoxin gene in MRSA isolated from clinical samples in Shahrekourd (Research Paper)

Parisa behshood,[1,*] Samane ansarinia,[2] Elahe Tajbakhsh,[3]

1. Phd Department of Microbiology,Young Researchers and Elite Club , Shahrekord Branch , Islamic Azad University Shahrekord, Iran
2. Master Department of Microbiology,Young Researchers and Elite Club , Shahrekord Branch , Islamic Azad University Shahrekord, Iran
3. PhD, Department of Microbiology, Shahrekord Branch, Islamic Azad University, Shahrekord, Iran

Introduction: Staphylococcus aureus is a ubiquitous bacterium that has plagued humans for thousands of years. The aim Of this Study is to enterotoxin genes of Staphylococcus aureus isolated from clinical samples in Isfahan

Methods: During one one-year period, a total of 100 clinical samples isolated from nosocomial infections were studied. Isolates were identified by standard methodology in the microbiology laboratory.MRSA isolates had been isolated by using the agar screening method. The pattern of antimicrobial resistance isolated strains was determined by the standard disk diffusion method. DNA of the isolates was extracted by DNA extraction kit (Fermentas) according to the manufacturer's protocol. Amplification of seg and sea enterotoxin genes was done by a specific primer and polymerase chain reaction method.

Results: Among the 100 Staphylococcus aureus isolates recovered, 65 isolates (65%) were MRSA. The frequency of antimicrobial patterns MRSA isolates showed that isolates, 100% to penicillin and oxacillin, 80% to nitrofurantoin, 63% to tetracycline, 58.46%to erythromycin, 46.15%to gentamicin,33.8%to clindamycin,35.38%to cotrimoxazole andto ciprofloxacin 26.15% were resistant. However, none of the MRSA isolates were resistant to vancomycin. Also prevalence of the enterotoxin type (g) gene was %38.56 and enterotoxin type (a) % 80 in MRSA strains

Conclusion: results of this study showed that a high percentage of Staphylococcus aureus clinically isolates produced enterotoxin. Considering that these toxins are superantigen and can more intense the complications of nosocomial infections. detecting and rapid treatment of these infections is essential.

Keywords: staphylococcus aureus- Antibiotic resistance-clinical samples

Problematic liver: Glibert's syndrome as a result of enzyme deficiency and its biochemical association with diabetes (Review)

sadaf Mahdavi,[1] Setare Molavi tanha,[2] Tara Esmaeeli,[3] Issa Layali,[4,*]

1. Bachelorâ€™s student, cellular and molecular biology group, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran.
2. Bachelorâ€™s student, cellular and molecular biology group, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran.
3. Bachelorâ€™s student, Microbiology group, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran.
4. Department of Biochemistry and Biophysics, Faculty of Advanced Sciences and Technology, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran.

Introduction: Gilbert's Syndrome, a condition characterized by elevated levels of unconjugated bilirubin in the blood, is a relatively common inherited disorder. In this Manuscript, we will explore the intersection between Gilbert's Syndrome and Diabetes Mellitus, discussing the potential implications for those affected by both conditions. It is primarily caused by a deficiency in an enzyme called UDP-glucuronosyltransferase, responsible for the conjugation of bilirubin in the liver. Although it is generally considered a benign condition, recent studies have indicated potential associations between Gilbert's syndrome and other medical conditions. This enzyme called UDP-glucuronosyl transferase 1A1 (UGT1A1), is responsible for conjugating bilirubin to make it soluble for excretion.

Methods: This article uses an extensive search of PubMed - NCBI and Google Scholar databases - and the study of almost 15 articles and an analysis of the studies done in the last ten years on this issue.

Results: In individuals with Gilbert's syndrome, the activity of UGT1A1 is reduced, resulting in higher levels of unconjugated bilirubin in the blood. Symptoms of Gilbert's Syndrome Typically, individuals with Gilbert's syndrome do not experience any significant symptoms and are often unaware of the condition. The jaundice usually occurs during periods of stress, illness, fasting, or after consuming certain medications or alcohol. Linking Gilbert's Syndrome with Diabetes Mellitus Recent studies have suggested a potential association between Gilbert's syndrome and diabetes mellitus, a chronic metabolic disorder characterized by impaired glucose regulation. As a result, individuals with Gilbert's Syndrome experience mild jaundice and elevated levels of unconjugated bilirubin. Diabetes Mellitus is a chronic metabolic disorder characterized by high blood glucose levels. While the

pathophysiology of the association between Gilbert's Syndrome and Diabetes Mellitus is not yet fully understood, several studies have indicated a connection between the two conditions. One hypothesis suggests that impaired liver function resulting from Gilbert's Syndrome may play a role in the development of Diabetes Mellitus. The liver plays a crucial role in glucose metabolism, and any dysfunction in this process can contribute to insulin resistance and impaired glucose regulation. Research has also revealed a potential genetic link between Gilbert's Syndrome and Diabetes Mellitus. Certain genetic variations associated with Gilbert's Syndrome have been found to increase the risk of developing Diabetes Mellitus. However, more studies are needed to establish a concrete connection between these two conditions. Individuals who have both Gilbert's Syndrome and Diabetes Mellitus face unique challenges. Firstly, the diagnosis of Diabetes Mellitus may be complicated by the presence of Gilbert's Syndrome. Elevated bilirubin levels can interfere with common laboratory tests used to assess glycemic control, such as the Hemoglobin A1c test. Healthcare professionals must be aware of these limitations to ensure accurate diagnosis and management of Diabetes Mellitus in patients with Gilbert's Syndrome. Furthermore, the coexistence of Gilbert's Syndrome and Diabetes Mellitus may have implications for treatment strategies. Medications that are metabolized in the liver may have altered pharmacokinetics in individuals with Gilbert's Syndrome, potentially impacting drug efficacy and safety. Close monitoring of medication dosages and liver function is vital to prevent adverse effects and optimize the management of both conditions. Gilbert's Syndrome, a benign inherited disorder characterized by elevated bilirubin levels, has been associated with various comorbidities, including Diabetes Mellitus. While the exact link between the two conditions is still being investigated, current evidence suggests a potential interplay between impaired liver function and genetic factors. The coexistence of Gilbert's Syndrome and Diabetes Mellitus poses unique challenges in terms of accurate diagnosis and appropriate management. Healthcare professionals must be aware of these challenges and tailor their approach accordingly, ensuring optimal glycemic control and minimizing the risks associated with medication metabolism.

Conclusion: Further research is needed to deepen our understanding of the relationship between Gilbert's Syndrome and Diabetes Mellitus. By expanding our knowledge in this field, we can enhance patient care and strive for more personalized approaches to managing these interconnected conditions.

Keywords: Gilbert's Syndrome/ Diabetes Mellitus/ UDP-glucuronosyl transferase/ bilirubin

PROTACs in the management of breast cancer (Research Paper)

Mona Asna Ashari,[1,*] Mohammad Saleh Safari,[2]

1. Paramedicine Faculty, Tehran Medical sciences, Islamic Azad University, Tehran, Iran
2. Young Research and Elites Club, Science and Research Branch, Islamic Azad University, Tehran, Iran.

Introduction: Cancer treatments with targeted therapy have received much attention due to their low levels of toxicity and high selectivity. Proteolysis targeting chimeras (PROTACs) have attracted special attention in the development of cancer therapies due to their unique mechanism of action, their ability to target undruggable proteins and their focused target engagement. PROTACs selectively degrade the target protein through the ubiquitin-proteasome system, which describes a different function compared to conventional small molecule inhibitors or even antibodies. Among the types of cancer, breast cancer is the most common cancer in women, and drug resistance has been seen in the treatment of this cancer, so PROTACs can be a new method in the treatment of this cancer.

Methods: This study is a review study by searching scientific databases such as Scopus, PubMed, Google Scholar, and Embase from 2016 to 2023 by using the keywords Breast cancer, PROTAC, resistance, 21 articles related to inclusion criteria were extracted and then analyzed.

Results: The results indicated that with genetic changes and overexpression of genes that are resistant to treatment and suppress the response of the immune system, drug resistance is created against the usual treatments of breast cancer, and since the progression of ARV-471 (PROTAC for BC) into the clinical stages, research has shifted toward protein inhibitors that target breast cancer.

Conclusion: In the present study, highlights an overview of PROTACs in breast cancer and their superiority over conventional inhibitors. In addition, we touch different targets for PROTACs in breast cancer, including estrogen receptor (ER) and other critical oncoproteins, and discuss the future prospects and challenges in this context.

Keywords: Breast cancer, PROTAC, resistance.

Quality Assurance Systems and Ways to Reduce Complications of Blood Products Transfusion (Review)

Mobina Nakhaei Shamahmood,[1] Mohammad Sharifi,[2] Rasta Farhadi,[3] Fateme Mezginejad,[4,*]

1. Student research committee, school of Allied medical science, Birjand university of medical science, Birjand, Iran
2. Student research committee, school of Allied medical science, Birjand university of medical science, Birjand, Iran
3. Student research committee, school of Allied medical science, birjand university of medical science, birjand, Iran
4. Cellular and Molecular Research Center, Birjand University of Medical Sciences, Birjand, Iran.

Introduction: Blood product administration is a vital and life-threatening issue that may increase the risk of clinical damage in patients.Quality assurance is a legal obligation in the blood transfusion sector which dictates the Appropriate procedures of blood banks.Application of appropriate procedures leads to the construction of a quality assurance system guaranteeing transfusion safety from donor to patient and from donation to dispensing of blood products.The aim of this review to provide a comprehensive review of the ways to improve blood transfusion safety.

Methods: In order to conduct this systematic review article,searched in PubMed,Google Scholar,Scopus, Embase, Medline, and Cochrane databases until October 2022.Data search for the last 10 years was done using key words including Quality assurance system,blood transfusion,blood products.

Results: Among524 articles found during the initial search,22 articles were finalized for further review.67% of the included articles discussed the use of modern technology including patient identification system,barcode technology,portable computer systems,and databases,It also focused a lot on following the quality assurance system,team responsibilities,complementary interactions.In addition,33% of studies reported the use of alternative methods for transfusion of blood products,including mediastinal transfusion,use of autologous blood in adults,use of umbilical cord blood in children and transfusion of fresh whole blood.

Conclusion: Among524 articles found during the initial search,22 articles were finalized for further review.67% of the included articles discussed the use of modern technology including patient identification system,barcode technology,portable computer systems,and databases,It also focused a lot on following the quality assurance system,team responsibilities,complementary interactions.In addition,33% of studies reported the use of alternative methods for transfusion of blood products,including mediastinal transfusion,use of

autologous blood in adults,use of umbilical cord blood in children and transfusion of fresh whole blood.

Keywords: Quality assurance system,Blood transfusion,Blood products

Relationship of the disease severity with a main panel of inflammatory and coagulation biomarkers in DVT, cardiovascular disease and stroke (Review)

Kiana Mohammadian,[1] Parisa Alipour,[2] Tahereh Kalantari,[3,*]

1. Division of hematology and blood banking, Department of Medical Laboratory Sciences, School of Paramedical Sciences, Shiraz University of Medical Sciences, Shiraz, Iran
2. Division of hematology and blood banking, Department of Medical Laboratory Sciences, School of Paramedical Sciences, Shiraz University of Medical Sciences, Shiraz, Iran
3. Division of hematology and blood banking, Department of Medical Laboratory Sciences, School of Paramedical Sciences, Shiraz University of Medical Sciences, Shiraz, Iran\Diagnostic Laboratory Sciences and Technology Research Center, School of Paramedical Sciences, Shiraz University of Medical Science

Introduction: Thrombosis is used to describe the abnormal mass forming in the circulatory system from blood components. This condition is known as deep vein thrombosis (DVT) when it takes place in the deep veins. Cardiovascular disease, including coronary artery disease(CAD), cerebrovascular disease, Peripheral artery disease (PAD), and aortic atherosclerosis, is a growing global health concern due to its primary cause of morbidity and mortality. Stroke, a sudden neurological impairment caused by blood flow disruption, is the second most common cause of death worldwide, accounting for 80%-85% of all strokes. Inflammation is the response of cells and substances to harm produced by viral or noninfectious causes. C-reactive protein (CRP), synthesized in the liver, serves as a diagnostic marker for continuous and enduring inflammation. IL-6, a hormone-like cytokine, is crucial in both innate and adaptive immunity, regulating inflammation and stimulating or inhibiting it. Interleukin-1Î² (IL-1Î²) belongs to the IL-1 family and is linked to the process of inflammation. TNFÎ±, a proinflammatory molecule, triggers inflammation, increasing plaque vulnerability, with acute phase proteins indicating significant changes in serum levels during inflammation episodes. lactate Dehydrogenase (LDH), a vital enzyme involved in the process of energy metabolism, serves as a biomarker that plays a crucial role in monitoring the prognosis of illnesses. Fibrinogen, a glycoprotein, is categorized as an acute phase protein because it is produced in larger quantities during inflammation. D-dimer indicates increased blood clotting activity and thrombotic events due to its role in fibrin cross-linking. Thrombosis and inflammation are separate physiological processes, although their close association has been recognized in recent years. Tissue factor initiates blood clotting and is produced by blood vessel cells. High levels indicate a negative prognosis in patients with acute coronary syndrome or stroke. In this review, we are examining the correlation between inflammatory and coagulation markers and the occurrence of DVT, stroke, and CVD.

Methods: In this review we demonstrated searches with PubMed, Google Scholar, and medical journals identifying articles relevant to our topic.

Results: Proinflammatory biomarkers are increasingly being utilized in epidemiologic and intervention research to link systemic inflammation to CVD, stroke, and DVT. High CRP levels can predict future DVT incidence. Elevated CRP levels are associated with atherosclerosis, coronary artery disease, acute stroke, and ischemic stroke. High hs-CRP levels can increase the risk of ischemic stroke and worsen health conditions due to inflammation, complement pathways, and tissue damage. High IL-6 levels lead to inflammation, tissue damage, cardiovascular issues, and increased risk of CVD, and cognitive dysfunction, potentially predicting cerebrovascular illness. Elevated IL-6 levels also increase mortality and stroke outcomes. IL-1Î² is a key mediator of thrombus formation and local thrombosis, predicting future DVT incidence. It contributes to inflammation, cardiovascular disorders, atherosclerosis, and stroke. TNFÎ±, a key inflammatory cytokine, triggers thrombomodulin production, affecting endothelial cells and phagocytes, leading to edema, vasodilation, and blood coagulation, potentially causing atherosclerosis and stroke. Iron-deficient red blood cells can cause hypercoagulability, thrombosis, cardiovascular diseases, and stroke. Elevated ferritin levels in inflammatory conditions increase CVD risk, and stroke severity is directly correlated with ferritin levels. LDH is a crucial marker for diagnosing infarcts, venous and arterial thrombosis, and malignant tumors. Elevated LDH activity is linked to cardiovascular disorders like myocardial infarction and heart failure, indicating cardiac tissue damage and compromised metabolism. Elevated levels are observed in patients with hemorrhagic infarcts, strokes, and small lacunar infarcts. Fibrinogen is a biomarker that is linked to the development of venous thrombosis in individuals with posttraumatic DVT. Plasma fibrinogen concentration, along with D-dimer or albumin levels, has been linked to the risk of CVD since the 1950s. Fibrinogen, an acute-phase protein, increases post-stroke, increasing the likelihood of subsequent cardiovascular events in stroke survivors. The D-dimer score method classifies individuals into low-, moderate-, and high-risk categories for DVT. A negative D-dimer can rule out DVT. D-dimer is a prognostic indicator for CVD, linked to inflammation and potentially predicting future cardiovascular events. Elevated D-dimer levels can also predict hemorrhagic or thrombotic stroke. TF is linked to cardiovascular disorders, blood clots, and stroke risk, possibly due to atherosclerosis plaques releasing TF.

Conclusion: A association exists between inflammatory or coagulation biomarkers including CRP, IL-6, IL-1Î², TNF-É‘, ferritin, fibrinogen, d-dimer, and TF with an unfavorable prognosis in cases of DVT, cardiovascular disorders, and stroke.

Keywords: DVT, CVD, Stroke

Report on the occurrence of the tetanus in sheep due to dystocia (Review)

Hossein Esmaeili,[1,*] Fatemeh Haji Agha Khiyabani,[2]

1. University of Tehran
2. University of Tehran

Introduction: Tetanus is a neuromuscular disorder of animals and humans and is also an infectious and potentially fatal disease, caused by Clostridium tetani. Tetanospasmin as a tetanus neurotoxin affects the nervous system. The spore is introduced to animal tissue through wounds, particularly deep ones, sometimes this infection happens due to dystocia. This study mentioned the sheep's tetanus because of the dystocia.

Methods: During the lambing season, two flocks of Ile-du-France (2 sheep) and Romane (2 sheep) had dystocia, the signs of muscle spasms were seen, so we suspected tetanus. Bacteriological swabs were taken from the depth of the related wound. Swabs were cultured in an anaerobic condition for 48 hours at 37â„ƒ and then the smear of that was taken.

Results: According to the clinical signs, which were stiffness, the rigidity of the neck and limbs, bloat, hypersensitivity, pricked ears, prolapse of the third eyelid and morphology of the C.tetani, gram-positive rods with terminal spores(tennis racket), and hemolytic colony that were visible on the blood agar media, and also biochemical tests, clostridium tetani was diagnosed as the cause of tetanus.

Conclusion: Control and prevention of tetanus are efficient and have beneficial costs, but because of the high incidence in flocks, it is recommended to include the tetanus vaccine with other clostridial vaccines in the sheep flocks.

Keywords: Keywords: tetanus, clostridium tetani, sheep, dystocia

Serological Investigation of Toxoplasmosis in Pregnant Women with Preeclampsia (Research Paper)

Saeed Radin,[1] Samaneh Abolbashari,[2] Vida Vakili,[3] Asieh Maleki Abardeh,[4] Aida Gholoobi,[5,*]

1. Metabolic Syndrome Research Center, Mashhad University of Medical Sciences
2. Medical Genetics Research Center, Mashhad University of Medical Sciences, Mashhad, Iran.
3. Department of Family Medicine, Mashhad University of Medical Sciences, Mashhad, Iran.
4. Department of Obstetrics and Gynecology, Mashhad University of Medical Sciences, Mashhad, Iran.
5. Medical Genetics Research Center, Mashhad University of Medical Sciences, Mashhad, Iran.

Introduction: Considering the importance of preeclampsia and the high prevalence of Toxoplasma gondii infection and the need for more studies mentioned in various articles, the present study was conducted to investigate Toxoplasma gondii serum antibodies in pregnant women with and without preeclampsia.

Methods: This cross-sectional study was conducted in 1400 at Bu Ali Research Institute. Blood samples collected in the study approved by the university with code 970385 were used. Preeclampsia was diagnosed based on its diagnostic criteria according to the American College of Obstetricians and Gynecologists (ACOG) guidelines. Patients' serum samples were checked for the presence of IgM and IgG antibodies against Toxoplasma gondii by ELISA method. Finally, the obtained data were entered into SPSS statistical software and compared between the two groups.

Results: A total of 136 pregnant women with an average age of 32.90 Â± 7.12 years including 72 patients with preeclampsia and 64 women without preeclampsia signs and symptoms were included. In the preeclamptic group, 9 women (12/5%), and in the non-preeclamptic group 6 women (9/4%) were positive for Toxoplasma gondii IgG antibody. The difference in Toxoplasma gondii antibody positivity in the two groups was not statistically significant. (Chi-square test; p=0/561). Also, there was no significant difference between patients with and without Toxoplasma gondii in terms of age (p=0/099), level of education (p=0/075), and gravid status (p=0/641). But, there was a significant difference in terms of pre-pregnancy weight (p=0/043).

Conclusion: The results obtained in the present study showed that positivity in terms of Toxoplasma gondii IgG antibody has no significant relationship with the development of preeclampsia. Further studies are needed to further

investigate this issue, focusing on the relationship of recent Toxoplasma gondii infections with the development of preeclampsia.

Keywords: preeclampsia, Toxoplasma gondii, pregnancy

Sickle Cell Anemia in Khorasan-Razavi : Co-Inheritance of Î±Thalassemia, Clinical & Hematological Characterizations (Research Paper)

Tayebeh Hamzehloei,[1,*] Hamed Miri,[2] zahra Malekdadi,[3]

1. Mashhad university of medical science, medical genetic department, Mashhad-Iran
2. Mashhad university of medical science, medical genetic department, Mashhad-Iran
3. Mashhad university of medical science, medical genetic department, Mashhad-Iran

Introduction: Although sickle cell anaemia (SCA) is genetically characterised by a single point mutation, patients can manifest varying degrees of clinical severity due to various genetic modulators that affect the phenotype of this disease. The co-inheritance of alpha-thalassemia (Î±-thalassemia) has been associated with a milder phenotype in SCA patients, but could also result in the increase of vaso-occlusive (VOC) pain episodes. The present study explored the correlation between Î±-thalassemia, haematological indices, and clinical events in SCA patients.

Methods: For this cross-sectional study, a full blood count and clinical phenotype profile was collected for 262 anemic individuals. Restriction fragment length polymorphism - polymerase chain reaction (RFLP-PCR) was performed for the molecular diagnosis of SCA. Multiplex Gap-PCR was performed to investigate the 3.7kb and 4.2kb Î±-thalassemia gene deletions.

Results: There were 178 SCA patients (HbSS), 32 carriers (HbAS) and 52 unaffected individuals (HbAA), with median ages of 18, 23 and 26 years, respectively. Among patients, 57% (101) had less than three vaso-occlusive pain crises (VOCs) per year. The median haemoglobin (HbA) level was 7.8g/dl for patients, 12.7g/dl for carriers and 13g/dl for unaffected individuals. Up to 37.1% (66) of SCA patients (HbSS) co-inherited Î±-globin gene deletions, compared to the 20% (10) prevalence of these gene deletions in the unaffected (HbAA) and carrier (HbAS) cohorts. Among patients, the genotype distribution was 30.3% (54) Î±Î±/Î±-3.7 (one 3.7kb Î±globin gene deletion), 6.8% (12) Î±-3.7/Î±-3.7 (two 3.7kb Î±-globin gene deletions), and none had the 4.2kb deletion. Among patients, the median red blood cell count (RBC) increased with the number of 3.7kb deletions [2.6, 3.0 and 3.4 million cells/dl, with no, one and two deletions, respectively (p=0.01)]. The median mean corpuscular volume (MCV) [86, 80 and 68fL, with no, one and two deletions, respectively (p <0.0001) and the median white blood cell count (WBC) [13.2, 10.5 and 9.8 X 109/L with no, one and two deletions, respectively (p<0.0001) and the median white blood cell count (WBC) [13.2, 10.5 and 9.8 X 109/L with no, one and two deletions, respectively (p<0.0001)

decreased with an increase in the number of 3.7kb deletions. An analysis of the effect of the co-inheritance of Î±-thalassemia and SCA on the haematological parameters revealed a significantly lower lymphocyte and monocyte count, which is known to be associated with a better clinical phenotype. In addition, the co-inheritance of Î±-thalassemia was significantly associated with a delayed age of disease onset among Khorasan Razavi SCA patients. Furthermore, after performing linear logistic regression analysis, the co-inheritance of Î±-thalassemia was associated with a lower consultation rate (p=0.038).

Conclusion: The co-inheritance of Î±-thalassemia with SCA was associated with an improved haematological profile, with an increase in the number of Î±-globin gene deletions. The possible positive effect of the co-inheritance of Î±-thalassemia on SCA patientsâ€™ survival could explain the high proportion of Î±-thalassemia among SCA patients when compared to the unaffected controls. These results have implications for disease management in Khorasan Razavi in terms of genetic counselling and the detection of SCA.

Keywords: MUTATION, SICKLE CELL, THALASSEMIA

SiRNA Delivery using Lipid-Polymer Nanoparticles to Target Cyclophilin A for the Treatment of Multiple Myeloma (Review)

Sina Eshaghi,[1] Mohadeseh Ramezani,[2] Mohammad Hossein Ahmadi,[3,*]

1. Department of Laboratory Sciences, School of Paramedical and Rehabilitation Sciences, Mashhad University of Medical Sciences, Mashhad, Iran.
2. Department of Laboratory Sciences, School of Paramedical and Rehabilitation Sciences, Mashhad University of Medical Sciences, Mashhad, Iran.
3. Department of Laboratory Sciences, School of Paramedical and Rehabilitation Sciences, Mashhad University of Medical Sciences, Mashhad, Iran.

Introduction: Multiple myeloma (MM) is a clonal plasma cell malignancy that forms solid tumors in the protective microenvironment of the bone marrow. After non-Hodgkin's lymphoma, this hematologic cancer is the second most common hematologic malignancy. Traditional treatment strategies for MMs include radiotherapy, chemotherapy, and stem cell transplantation. Although immunotherapy and cell therapy have also made significant progress in the last decade, nearly half of patients experience relapse or drug resistance. Therefore, there is a greater clinical need for innovative and more effective MM treatments. In this study, the use of a nanoparticle platform to deliver siRNA to the bone marrow endothelium to inhibit the secretion of cyclophilin A (CyPA) was investigated as a potential therapeutic approach to eliminate the colonization and proliferation of MM cells in the bone marrow.

Methods: In this review, articles were collected from PubMed, Scopus, and Google Scholar that were published between the years 2020 and 2023. These databases were searched using the keywords multiple myeloma, nanoparticle, SiRNA, and CyPA.

Results: Cyclophilin A (CyPA) is a homing factor secreted by bone marrow endothelial cells (BMECs). Investigations showed that CyPA inhibits implantation, proliferation, and colonization of MM cells in the bone marrow microenvironment and can be effective in drug resistance. This factor stimulates the migration of MM cells through the CD147 receptor. Recent studies have investigated how to engineer a potential therapeutic method that uses interfering RNA (iRNA) and nanoparticles to enter and target CyPA in the blood vessels of the bone marrow. This strategy inhibits CyPA in CEMBs. For this purpose, nanoparticles (with the combination of polymer-lipid or lipid-PEG) and siRNA are formulated through controlled mixing in a microfluidic device and enter the targeted tissue and subsequently the cell. In recent studies, several formulations of NP and siRNA combination have been analyzed. The results showed that with a certain formulation of the

combination of nanoparticles and siCyPA and their entry into the endothelial cells of the bone marrow, it is possible to prevent the invasion of MM cells into the bone marrow and their spread.

Conclusion: The results of the studies show that siCyPA can inhibit the ability of MM cells to adhere and invade through BMEC monolayers. Overall, this study provides a combined therapeutic strategy to target the bone marrow microenvironment, rather than the cancer cells themselves, as a means to treat MM, which could be extended to the treatment of other hematologic malignancies, or malignancies that metastasize to bone.

Keywords: Multiple myeloma; nanoparticles; SiRNA; CyPA

Subliminal and root regrowth Using stem cells (Research Paper)

zakiyeh khosravi,[1,*]

1. medical

Introduction: In recent decades, several studies have been conducted in the direction of isolating dental stem cells, while still the nature The mesenchyme of these cells has not been discussed and studied; the purpose of writing this article is to investigate tooth reconstruction in old age different by using mesenchymal cells extracted from dental pulp and also studying the successful experiments conducted in this field Is. In the current study, the third molar teeth of adults between 25-18, which were extracted for various reasons such as orthodontics, prophylactic, etc. were used.. the follicle and pulp of these teeth after being extracted and stored in the laboratory under certain conditions were cultured and after checking in the first and second passages, in the third passage, they were examined genetically with the help of flow cytometry were placed. Also, this issue can be seen in the milk teeth of children between 6-11, which after collecting and placing in the laboratory environment The pulp and follicle of the teeth were separated from it and were cultured in the laboratory under special conditions and subjected to genetic analysis. gave According to the discoveries mentioned in the above article, it is necessary to mention that mesenchymal cells of teeth, including mesenchymal cells Third molar teeth are a very rich source of dental pulp cells, which after collecting, culturing and passaging them in the conditions It can be found that these cells are found in all people (adults, children and even fetuses) and the possibility of using this Cells are unlimited in any period. The hidden point that can be found in the use of these cells is the optimal function of these cells in medical science because of all the harms. And predictable problems in implants and... are far away. Also, another potential advantage of these cells is their high compatibility Dealing with the immune system, which makes it easier to do this because these cells are recognized as the immune system and after planting, the possibility of being rejected by safety messages is very low; and this is the reason why the use of Another tooth pulp should be feasible and far from dangerous for the said person

Methods: 14 samples from the pulp and 6 samples from the third molar dental follicle of adults between 18 and 25 years old were collected. They were extracted due to malocclusion or orthodontic treatment with expert diagnosis and with the prior consent of the patients. These teeth are missing There were caries or previous restorations and all the patients were healthy and did not have any systemic disease. The tooth samples were placed in tubes containing 1640 RPMI, Gibco containing x2 antibiotics (2 times the strength of penicillin and streptomycin, Gibco) and transferred to the molecular cell laboratory at a temperature of 4 degrees Celsius. Revealing the pulp chamber, the teeth were cut from the enamel-cement connection by a carbide disc and a handpiece. And after that, the pulp was separated from the

teeth with a fine file from the pulp chamber; then to culture pulp and follicle tissue cells by No. 10 surgical blade, these cells were divided into smaller pieces, and then they were placed in Falcon containing 4 mg/ml collagen type solution (I sigma, 104 mg/ml dispase type solution) (Gibco) with a ratio of 1 1/ for 45 They were kept at 37 degrees Celsius for 10 minutes, and then they were added to the lysed tissue of the culture medium and incubated for 10 minutes with Around 600 grams were centrifuged. The resulting cell plate with a mixed culture medium and after transferring to a suitable zvt in an incubator with a temperature of 37 degrees Celsius and 5 atmospheres And 2% CO2 was cultivated. This culture medium was changed every two days until 70% of the bottom of the plate was filled with cells, when the bottom of the plate was 70% filled. The samples were passaged with EDTA _trypsin. and finally from flow cytometry analysis to investigate the phenotypic profile of surface markers and the nature of stem cells from the tissue The pulp and follicle of the third molar tooth were used. For this purpose, the cells were placed in the third passage of trypsin and in the form of a suspension in one milliliter (saline buffer phosphate (PBS) with a concentration of 1000000). Then the cells were divided into 6 tubes and 5 ÂµI of PE with antibody was added to each tube and the tubes were then kept at 4 degrees Centigrade for 30 minutes in a dark environment and after this period the cells were washed with 1 ml of washing buffer. and centrifuged at 1200 MPR for 5 minutes, after which each cell sample was washed in 1300 Âµ to 1500 Âµ of washing buffer. Donors were suspended and analyzed by flow cytometry

Results: According to the mentioned cases, it can be said that pulp mesenchymal stem cells are also present in adult cells. There are teeth because after a dental injury, the pulp of the tooth to repair the damaged area by building and depositing The dentin matrix initiates reparative dentinogenesis. This reparative process takes place throughout a person's life, which This indicates the presence of mesenchymal cells in the dental pulp of adults and the ability to form odontoblast under the influenceThe signals are appropriate But in general, the potential of adult stem cells is not as high as that of fetal and childhood stem cells, for this reason, for regeneration To restore teeth, it is better to extract mesenchymal cells from the root of the embryonic tooth (from the gums, especially from the posterior gums). or the use of mesenchymal stem cells of milk teeth, these cells, as said, are not suitable for any category The age group is not limited and even the ability to donate these cells from one person to another is possible and the condition of donating teeth The complete health of the person and the donor's teeth, which can be used even in adults, where most people They have lost their milk teeth (except for latent milk teeth) from the gene of mesenchymal stem cells of children or fetuses. Use to repair and restore teeth In the laboratory method of mesenchymal stem cells in adults, although they have the possibility of repair or regeneration, but after When they are separated from the patient, they must first go to the laboratory environment and after strengthening and differentiating them to another person as a recipient. Alograp or Xenograp is injected, but due to the many problems that take a long time during

strengthening and injection The lower potential and compatibility of these cells may cause problems such as early tooth decay, tooth loss, and system attack. Immunity to these cells through immune response and... In this regard, it can be said to use the method Secondary (experiment: laboratory cultivation of mesenchymal cells of milk teeth) more functionality and efficiency in this field of work have. And due to the problematic factors that exist in the mesenchymal cells of adults, this ideal protocol for humans is relatively far from its application. Recently, with the discovery of a gene called DIK1, in the new methods, how the bone cells are activated and the tissue regeneration in the repair. The teeth can be informed and undergo a shorter treatment period in the restoration of teeth using stem cells.) The above-mentioned test for the restoration and reconstruction of teeth has gone through a relatively long period. With the activation of the stem cells, these cells can send messages to the main cells that lead to the activation of regenerative cells and Amplification helps a lot (this work is also possible by using low power lasers) as a result of these cells in the form Removing dentin (hard tooth tissue) helps a lot.

Conclusion: So it can be said that tooth regrowth is a reality, not an ideal, considering that teeth are made of two types of tissues It is formed differently, logically, making a tooth requires communication and cooperation with epithelial cells and odontogenic mesenchyme. Is. Recombination of epithelial tissue and dental mesenchyme leads to tooth formation both in vitro and in vivo. Combined cells are able to organize and form individual layers and are also able to differentiate into odontoblasts and They also have amyloblasts. In order to make a complete tooth that has enamel and dentin, epithelial and mesenchymal cells respectively in collagen gel solution It is inserted and then implanted inside the oral cavity and with this technique the presence of all dental structures such as odontoblasts, Amyloblast, pulp, blood vessels, crown, root, periodontal ligament and alveolar bone can be seen, so planting this mass Dental (mesenchyme + epithelial cells) leads to the development of maturity and regrowth of teeth. Stem cells are vital for the physiology of dental pulps and for the response of these tissues to the accident. Recent findings show have given that dental pulp stem cells can be used as possible therapeutic targets in cases of reversible pulpitis act Most importantly, these cells may be the main solution for the regeneration of necrotic immature permanent teeth become Such findings have the potential to fundamentally change the paradigms of conservative living pulp treatments and therapies create roots, and maybe allow in the future to treat problems that arise during the processes that occur in engineering Medicine has been passed and they will be curable. Therefore, endodontists should be aware of the potentials of this branch of endodontic reconstruction It is emerging as well as the possibility of collecting stem cells during traditional dental treatments that can be used for In the future, the treatments originating from the patient's own body should be recognized Also, regarding the storage of dental stem cells, it can be said that the process of storing stem cells is taken Patient's milk teeth and wisdom teeth may be one of the strategies to understand the possibility of

cell-based regeneration treatment be the fundamental teeth. Recently, dental tissue cell storage has been planned and planned in several branches of dentistry It has been implemented in several countries. Today, we can use baby teeth to store dental stem cells Let's collect the house, which, of course, is accompanied by the following instructions: There should be blood flow when the tooth comes out - that is, some bleeding when the tooth comes out The tooth must be stored using cultured cell services so that laboratory tests can be performed on it To confirm the presence of stem cells before freezing. So it can be said that using engineering and modern methods, it is possible to use mesenchymal stem cells extracted from the pulp. Teeth and baby teeth are used to repair tooth tissues under tissues that have mesenchyme and connective tissue and with this Humans at any age are able to regrow their teeth using the mesenchymal stem cell gene , And the point in It is worth noting that the use of mesenchyme gene is not restricted from one person to another (no age limit) and this is another point It is that the use of this method if the mesenchyme gene used is healthy, unlike the implant, there are no restrictions And it is not harmful, and replacing this method, instead of today's methods, dentists can use it more efficiently and optimally have more.

Keywords: Mesenchymal stem cells - dental pulp - dental follicle

Synergistic Effects of Parthenolide with Vitamin C for improving of apoptosis by Anti-Apoptotic-targeting miR-181b/17/125b-5p on NALM-6 cells (Research Paper)

Gholamhossein Tamaddon,[1,*] Atefeh Bahmei,[2]

1. 1 Division of Hematology and Blood bank, Department of Medical Laboratory Sciences, School of Paramedical Sciences, Shiraz university of medical Sciences, Shiraz, Iran. 2 Diagnostic Laboratory Sciences and Technology Research Center, School of Paramedical Sciences, Shiraz University of
2. Division of Hematology and Blood bank, Department of Medical Laboratory Sciences, School of Paramedical Sciences, Shiraz university of medical Sciences, Shiraz, Iran.

Introduction: Acute Lymphoblastic Leukemia (ALL) is one of the most common hematological malignancies in children. With currently available therapies, 70 % of patients can survive this disease with lower survival in adults over 65 years old. Parthenolide and vitamin C, natural compounds for cell death that can induce the apoptosis of cancer cells, have been explored as therapeutic agents for cancers. Also, it has been reported that miR-181b, miR-125b-5p, and miR-181b-5p are a dis-regulator of apoptosis, limiting the potential clinical use of cancer therapy. It is unclear whether parthenolide and vitamin C can have apoptotic activity on NALM-6 cells, or whether the combination of these two compounds can synergistically and affect these miRNAs.

Methods: We used MTT assay, and flow cytometry (single and dual staining) to detect the effects of parthenolide alone or in combination with vitamin C on NALM-6 cells. The levels of miR-181b/17/125b-5p were analyzed by real-time PCR. The mechanisms of miRNA-induced apoptosis by targeting PI3K were also predicted by bioinformatics study, Cytoscape, RNAhybrid, and Cell signaling enrichment. Molecular Docking was applied to validate that both parthenolide and vitamin C can affect these miRNAs.

Results: We observed that parthenolide and vitamin C alone or in combination can inhibit the cell viability of NALM-6 cells induce apoptosis and exert synergized effects. Both parthenolide and vitamin C, at all concentrations used, increased the number of early apoptotic and dead cells (late apoptotic) compared to the appropriate controls after 48 hours of incubation. An increase in the number of early apoptotic and dead (late-apoptotic) cells was observed after the co-incubation of parthenolide with vitamin C at concentrations of 1.925ÂµM and 0.5 mM in comparison to each compound alone which ends in 82.52Â±1.520 % cell death (early and late-apoptotic cells) and only 6.50 Â± 1.697% of cells survived. Moreover, we observed the rate of early apoptotic cells tended to be reduced when

combination therapy was applied (only, 3.92%) We identified miR-17-5p, miR-125b-5p, and miR-181b-5p as targets for both parthenolide and vitamin C, experimentally and computationally. All three treatments - parthenolide, vitamin C, and the combination - decreased (downregulated) expression of the three miRNAs. For miR-17-5p, vitamin C caused a larger decrease in expression than parthenolide. The combination therapy reduced miR-17-5p expression more than parthenolide alone but less than vitamin C alone. A diverse pattern was seen for miR-125b-5p. Parthenolide lowered expression more than vitamin C, while the combination had a powerful effect. A similar pattern was seen for miR-181b-5p. They decreased this miRNA more than the two others and the combination therapy decreased this miRNA near to zero. Overall, parthenolide demonstrated the strongest inhibitory effects on the expression of miR-125b-5p and miR-181b-5p individually. The combination of parthenolide and vitamin C had the greatest suppressive effect on miR-181b-5p levels. On the other hand, parthenolide and vitamin C could inhibit cell viability and increase apoptosis by affecting the level of miR-17-5p, miR-125b-5p, and miR-181b-5p in NALM-6 cells, thus inhibiting the TGF-B and PI3K pathway and NF-KB signaling, and inducing apoptosis of Acute Lymphoblastic cells in vitro.

Conclusion: This current study suggests a theoretical basis for the combination of parthenolide and vitamin C for the treatment of B-ALL. Considering the safety of parthenolide and vitamin C in vivo, it is suggested that this combination therapy should be used in treatment, especially in tumors resistant to apoptosis. that parthenolide and vitamin C can be more explored as potential therapeutic approaches for ALL.

Keywords: miRNAs, combination therapy, parthenolide, vitamin C, B-ALL

Targeting the Gut Microbiota: Exploring the Role of Probiotics and Prebiotics in Modulating Drug Metabolism and Efficacy (Review)

Fatemeh Sadat Shojaeddin,[1] Faramarz Khosravi,[2,*]

1. Bachelorâ€™s student. Department of Microbiology, Faculty of Modern Science and Technologies, Tehran Medical Science, Islamic Azad University, Tehran Iran.
2. Tehran Medical Science, Islamic Azad University, Tehran, Iran.

Introduction: The gut microbiota, composed of trillions of microorganisms residing in the gastrointestinal tract, has a significant impact on human health and disease. Recent research has revealed that the gut microbiota plays a crucial role in drug metabolism and efficacy. Probiotics, live microorganisms that confer health benefits when consumed, and prebiotics, nondigestible substances that promote the growth of beneficial gut bacteria, have gained attention for their potential to modulate the gut microbiota and influence drug responses. This study aims to explore the role of probiotics and prebiotics in modulating drug metabolism and efficacy through their effects on the gut microbiota. It sheds light on the mechanisms of interaction between the gut microbiota and drugs, the impact of probiotics and prebiotics on drug metabolism, and the potential clinical implications for optimizing drug therapy.

Methods: A comprehensive literature review was conducted to identify studies investigating the role of probiotics and prebiotics in modulating drug metabolism and efficacy. Electronic databases were searched using relevant keywords, and studies published between 2013 and 2023 were included. The review encompassed in vitro studies, animal models, and clinical trials to provide a comprehensive understanding of the topic. The mechanisms underlying the interaction between the gut microbiota and drugs, as well as the effects of probiotics and prebiotics on drug metabolism, were examined.

Results: The literature review revealed substantial evidence supporting the role of the gut microbiota in drug metabolism and efficacy. The gut microbiota can metabolize drugs, leading to altered bioavailability, therapeutic efficacy, and adverse effects. Probiotics and prebiotics have been shown to modulate the gut microbiota composition and functionality, thereby influencing drug metabolism and responses. They can affect drug absorption, distribution, metabolism, and excretion through various mechanisms, such as enzymatic activity, alteration of gut barrier function, and modulation of host immune responses. Preclinical and clinical studies have demonstrated the potential of probiotics and prebiotics to enhance drug therapy in various therapeutic areas, including antibiotics, anticancer drugs, and cardiovascular medications.

Conclusion: The findings of this study suggest that targeting the gut microbiota through the use of probiotics and prebiotics represents a promising

approach to optimize drug therapy. Modulating the gut microbiota composition and functionality can influence drug metabolism, bioavailability, and efficacy, potentially leading to improved treatment outcomes and reduced adverse effects. However, further research is needed to elucidate the specific mechanisms underlying the interactions between the gut microbiota, probiotics/prebiotics, and drugs, as well as to establish optimal dosing regimens and guidelines for their use in conjunction with specific medications. The integration of gut microbiota modulation strategies into clinical practice has the potential to revolutionize drug therapy and contribute to personalized medicine approaches.

Keywords: Probiotics -Drug -Metabolism and Efficacy

The Calcium-Sensing Receptor in Health and Disease. (Review)

Alireza Akhavan,[1,*] Issa Layali,[2]

1. Microbiology group, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran
2. Microbiology group, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran

Introduction: First of all we need to know about Structure and Physiological Functions of calcium-sensing receptor or CaSR. calcium ion (Ca2+) regulates a wide range of intracellular and extracellular processes Follow that thread one of the important organs is Bone. it provides an adequate muscle and nerve function and is required for normal. Because of that is essential for life CaSR most to be to control this important thing.

Methods: A. Aggarwal et al. The calcium-sensing receptor: a promising target for prevention of colorectal cancer Biochim. Biophys. Acta (2015) https://www.sciencedirect.com/science/article/pii/S0167488915000518 U. Armato et al. The calcium-sensing receptor: a novel Alzheimer's disease crucial target? J. Neurol. Sci. (2012) https://www.sciencedirect.com/science/article/pii/S0022510X12003656 G. Breitwieser The calcium sensing receptor life cycle: trafficking, cell surface expression, and degradation Best Pract. Res. Clin. Endocrinol. Metab. (2013) https://www.sciencedirect.com/science/article/pii/S0954611103003378 G.E. Breitwieser et al. Calcium sensing receptors as integrators of multiple metabolic signals Cell Calcium (2004) https://www.sciencedirect.com/science/article/pii/S0143416003002185

Results: At all we search about CaSR in PTH release in parathyroid glands and calcium homeostasis because it has very good reaction against changes in extracellular Ca2+. However, the CaSR is expressed in numerous tissues and cell types other than parathyroid glands. Accordingly, CaSR may play important physiopathological roles beyond PTH release and extracellular calcium homeostasis . We examine CaSR in several cases 1. CaSR in Endocrine Pathology , 2. CaSR in Cardiovascular Physiopathology , 3. CaSR in Asthma , 4. CaSR in Alzheimerâ€™s Disease , 5. CaSR in Cancer. 1. Given the critical role of the CaSR in the regulation of the entire extracellular Ca2+ homeostatic system, conversion in CaSR signaling pathways are expected to make quite a significant contribution to imbalances of mineral metabolism.CaSR knockout (KO) in mice, CaSR mutations in human, as well as the use of calcimimetics and calcilytics are not just for Calcium and they used in other pathwayes. 2. Another place that CaSR has an effect is in Cardiovascular Physiopathology CaSR is expressed in several cell types in this system including the endothelium, vascular smooth muscle cells (VSMC), and even in the perivascular nerve In the past it was demonstrated that

dietary intake of Ca2+ may reduce blood pressure. 3. One of best pre-treatment for asthma do with CaSR . Asthma is characterized by airway hyperresponsiveness, bronchoconstriction, and chronic inflammation. Current treatments for asthma include drugs designed to target not the causes but the symptoms, that is, airway inflammation by corticosteroids and target this part and start treat. 4. AD is a neurodegenerative disorder associated to a progressive and irreversible loss of memoryRecent evidence suggest that CaSR could be a direct target for amyloid Î² peptides, the most likely toxins in AD 5. Cal causes cell proliferation, differentiation, and cell death predicts a role for this cation in cancer and may may contribute to cancer development. Maybe with CaSR can control cancer and cure this disease

Conclusion: So CaSR very useful for cure or treat basical disease and scientist work on these receptor for control calcium in body and cells. we hope to this method make complete soon.

Keywords: Keywords: CaSR/calcium/Alzheimer/Asthma/Cancer

The Central Mechanism of Pyruvate Dehydrogenase Inhibition in Diabetic Cardiomyopathy (Review)

Farnaz seifi,[1,*] Tahoura nazemi,[2] Mobina gharibi,[3]

1. Tehran Medical Sciences, Islamic Azad University
2. Tehran Medical Sciences, Islamic Azad University
3. Tehran Medical Sciences, Islamic Azad University

Introduction: Diabetic cardiomyopathy, a complex disease characterized by profound structural and functional alterations in the myocardium, poses a significant burden on the health of individuals with diabetes. While the intricate mechanisms underlying this disease are not fully elucidated, a constellation of factors, including oxidative stress, endoplasmic reticulum stress, microvascular dysfunction, cardiomyocyte apoptosis, cardiac lipotoxicity, and alterations in cardiac energetics, have been implicated in its pathogenesis.

Methods: To thoroughly explore the central mechanism of pyruvate dehydrogenase (PDH) inhibition in diabetic cardiomyopathy, a comprehensive literature search was conducted across PubMed, Google Scholar, and NCBI databases. This search yielded 22 relevant articles, which were carefully reviewed and analyzed to gain a deeper understanding of this topic.

Results: Among these metabolic perturbations, a robust impairment in glucose oxidation stands out as a hallmark feature of the diabetic heart. This decline in glucose utilization is attributed to a multifaceted interplay of factors, including enhanced fatty acid oxidation, mitochondrial dysfunction, and increased expression of pyruvate dehydrogenase kinase 4 (PDK4), an enzyme that inhibits PDH, the central regulatory enzyme of glucose oxidation. PDH: A Pivotal Player in Cardiac Metabolism: PDH catalyzes the oxidative decarboxylation of pyruvate, a key intermediate in glucose metabolism, to Acetyl-CoA and NADH, crucial energy substrates for cellular processes. Its regulation is a delicate balance of allosteric and posttranslational mechanisms, ensuring efficient energy production in response to metabolic demands. Inhibition of PDH: A Catalyst for Diabetic Cardiomyopathy: Studies in mice fed high-fat diets, a model of obesity and diabetes, have revealed rapid PDH inhibition in the myocardium. This inhibition, driven by increased PDK4 activity, disrupts the delicate balance of pyruvate metabolism and shifts the heart's reliance towards fatty acid oxidation, a process associated with enhanced mitochondrial pro-oxidant production. Pathophysiological Consequences of PDH Inhibition: The metabolic shift induced by PDH inhibition has profound consequences for cardiac function. First, it compromises the heart's ability to generate energy from glucose, a primary fuel for cardiac muscle contraction. Second, it promotes oxidative stress, a hallmark of diabetic cardiomyopathy, through increased mitochondrial reactive oxygen species (ROS) production. Evidence from Humans with Diabetes:

Data from individuals with type 2 diabetes substantiate the role of impaired PDH activity in the progression of diabetic cardiomyopathy. Studies employing noninvasive hyperpolarized 13C magnetic resonance imaging (MRI) have shown diminished pyruvate oxidation in the hearts of type 2 diabetic individuals with normal systolic function. This metabolic alteration is accompanied by a concomitant decline in myocardial energy levels and diastolic dysfunction, further compromising cardiac performance. Therapeutic Interventions Targeting PDH: Several therapeutic approaches have emerged as potential strategies to counteract PDH inhibition and ameliorate diabetic cardiomyopathy. These interventions include: 1. PDK4 Inhibition: PDK4 inhibitors have demonstrated efficacy in enhancing glucose oxidation in animal models of diabetes. 2. PDP Activation: PDH phosphatases (PDPs) are enzymes that reverse PDH inhibition by dephosphorylating the enzyme. Activation of PDPs has also been shown to improve glucose oxidation in animal models of diabetes. 3. IRS-2 Enhancement: Insulin receptor substrate-2 (IRS-2) is a protein involved in the signaling pathway that promotes PDP activation. Increasing the expression of IRS-2 may also be beneficial in improving glucose oxidation in diabetic cardiomyopathy.

Conclusion: Inhibition of pyruvate dehydrogenase (PDH) plays a pivotal role in the development of diabetic cardiomyopathy. This inhibition disrupts glucose oxidation, promotes oxidative stress, and hinders myocardial function. Several therapeutic approaches targeting PDH hold promise for improving glucose utilization, mitigating oxidative stress, and ameliorating the detrimental effects of diabetic cardiomyopathy. Further research is warranted to optimize these interventions and their translation into clinical practice.

Keywords: Pyruvate dehydrogenase, Diabetic cardiomyopathy, Oxidative stress

The diagnostic application of nanoparticles for parasitic infections (Review)

Fatemeh Ataei Masjedlou,[1,*] Zahra Sobhani,[2] Mohammad Taghi Ahady,[3]

1. Department of Biology, Ardabil Branch, Islamic Azad University
2. Department of Biology, Ardabil Branch, Islamic Azad University
3. Department of Biology, Ardabil Branch, Islamic Azad University

Introduction: Introduction: Parasites, including helminths and protozoa, are considered important sources of infections that can endanger public health. Because of this, sensitive, fast, and cost-effective analysis methods are needed to identify these pathogenic agents to achieve a better quality of life. Accurate and quick diagnosis is very important for the prevention and control of parasitic diseases. Several research groups have focused on developing new, efficient, and cost-effective diagnostic techniques. Despite these efforts, diagnostic methods are still not effective due to limitations in terms of cost, sensitivity, specificity, and difficulty of use in this field. According to our topic, nanotechnology offers a new paradigm for various medical diagnostics with unique features. This systematic review aimed to investigate the use of nanoparticles in the diagnosis of parasitic infections.

Methods: Methods: In this systematic review, to collect English scientific articles, Google Scholar, Science Direct, NCBI, Springlink, PubMed, and Web of Sciences databases were used, and to collect Persian articles were referred to Magiran, Civilica, Sid, and Google Scholar databases. The keywords used to search for English and Persian articles included nanoparticles, parasite infection, diagnosis, gold nanoparticle, silver nanoparticle, parasite, diagnosis of protozoan parasite, malaria, Trichomonas vaginalis, leishmaniasis, Toxoplasma gondii, and diagnosis via nanoparticle.

Results: Results: A total of 83 articles were obtained, of which 15 articles were excluded from this study due to being non-specialized, and a total of 68 articles were selected for writing the present study. During the investigations, it was found that nanoparticles (gold, silver, chitosan, and hydrogel) have been used to detect many parasites. The names of these parasites are as follows: Plasmodium falciparum, Toxoplasma gondii, Cryptosporidium parvum, Cryptosporidium baileyi, Cryptosporidium xiaoi, Cryptosporidium ryanae, Cryptosporidium andersoni, Trichomonas vaginalis, Trichomonas hominis, Trypanosoma cruzi, Echinococcus granulosus, Giardia lamblia, Leishmania infantum, Leishmania donovani, Leishmania major, Leishmania tropica, Entamoeba histolytica, Entamoeba coli, Balantidium coli, Hymenolepis nana, Fasciolopsis buski, Enterobius vermicularis, Ascaris lumbricoides and Leptomonas seymouri. Various methods and techniques have been used for the application of nanoparticles in the detection of parasites, such as conjugation of nanoparticles with probes, conjugation of

nanoparticles with strain-specific antibodies, conjugation of nanoparticles with casein, Nano-PCR, ELISA based on nanoparticles, aptasensor based on gold nanoparticles.

Conclusion: Conclusion: Based on the results of this study, it is concluded that using nanoparticles to detect parasitic infections is an easy, fast, economical, and sensitive method. It is suggested that the use of nanoparticles in clinical studies be studied more widely.

Keywords: Keywords: nanoparticles, parasitic infections, diagnosis, diagnosis of parasitic infections

The effect of epigenetic changes on antibiotic resistance: DNA methylation (Review)

Seyed Ali Sadr Tabatabaee,[1] Maryam Mashhadi Abolghasem Shirazi,[2,*]

1. Bachelorâ€™s student, Microbiology group, Faculty of Advanced Science and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran.
2. Department of Microbiology, Faculty of Advanced Sciences and Technology, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran Molecular Virology Department, Pasteur Institute of Iran, Tehran, Iran

Introduction: Antibiotic resistance has become a global health crisis, threatening the effectiveness of our most valuable weapon against bacterial infections - antibiotics. The emergence and spread of antibiotic resistance have been extensively studied, but recent research suggests that there may be more to the story than previously thought. Epigenetics, the study of heritable changes in gene expression that do not involve alterations in the DNA sequence, is now being recognized as a potential player in the development of antibiotic resistance in bacteria.

Methods: This article uses an extensive search of PubMed - NCBI and Google Scholar databases - and the study of almost 30 articles and an analysis of the studies done in the last ten years on this issue.

Results: Epigenetic modifications, such as DNA methylation and histone modifications, can influence gene expression patterns and cellular responses to antibiotics. These modifications serve as a regulatory mechanism that allows bacteria to adapt to changing environments and survive antibiotic exposure. The dynamic nature of epigenetic modifications provides bacteria with the ability to rapidly switch between susceptible and resistant phenotypes, contributing to the high-paced emergence of drug resistance. DNA methylation, the addition of a methyl group to DNA bases, has been shown to play a role in antibiotic resistance. Methylation of adenines can influence mutation rates in bacterial genomes, leading to changes in antibiotic susceptibility. For example, methylation of specific adenines in the DNA repair gene can enhance bacterial survival under antibiotic stress by reducing deleterious mutations. On the other hand, cytosine methylation has been linked to reduced expression of resistance-conferring genes, resulting in poor survival under antibiotic stress. Histone modifications, such as acetylation and methylation, can also impact gene expression in bacteria. These modifications alter the structure of chromatin, influencing the accessibility of genes to the transcriptional machinery. Studies have shown that histone modifications can regulate the expression of genes involved in antibiotic resistance, including efflux pumps and drug targets. By modulating gene expression, histone modifications contribute to the development of antibiotic resistance in

bacteria. Several epigenetic mechanisms have been identified as potential contributors to antibiotic resistance in bacteria. These mechanisms include the activity of methyltransferases, the presence of methylated cytosines in promoter regions, and the integration of methyltransferase-encoding phages into bacterial genomes. Adaptive resistance, also known as tolerance, is a phenomenon in which bacteria acquire the ability to survive in the presence of subinhibitory concentrations of antibiotics. This form of resistance is reversible and can be lost when the antibiotic is withdrawn. Epigenetic changes have been implicated in the modulation of gene expression patterns that allow bacteria to switch between susceptible and resistant phenotypes, contributing to the development of adaptive resistance. Bacterial persistence, characterized by the presence of a small subpopulation of dormant cells that are tolerant to antibiotics, is another mechanism by which bacteria can survive antibiotic exposure. Epigenetic inheritance has been proposed as a key player in phenotypic drug tolerance in persisters; The dynamic nature of epigenetic modifications allows for the generation of a seed bank of persister cells that can survive rapidly changing environments, leading to the adaptive evolution of drug-resistant mutants. Targeting epigenetic modifications could provide a means to overcome antibiotic resistance and enhance the efficacy of existing antibiotics. Additionally, understanding the epigenetic mechanisms underlying antibiotic resistance could help in the development of new diagnostic tools and strategies for the prevention and management of antibiotic-resistant infections The dynamic and reversible nature of epigenetic modifications provides bacteria with the ability to rapidly adapt to antibiotic exposure and survive under challenging conditions.

Conclusion: Further research is needed to fully understand the complex interplay between epigenetics and antibiotic resistance and to explore the potential of targeting epigenetic mechanisms for the development of new therapeutic approaches. By unraveling the intricate connection between antibiotic resistance and epigenetics, we may be able to combat the rising tide of antibiotic-resistant bacteria and preserve the effectiveness of our arsenal against infectious diseases.

Keywords: Epigenetic/DNA methylation /histone modifications

The immunogenic role of single and combination of outer membrane proteins Omp34 and BauA against Acinetobacter baumannii infection in murine model (Research Paper)

Mohammadhasan Mirali,[1,*] Iraj Rasooli,[2]

1. Shahed University
2. Shahed

Introduction: Acinetobacter baumanni is the most important agent of hospital-acquired infections low-grade but an important worldwide. This bacterium has been regarded as opportunistic pathogen that causes various types of infections, including ventilator associated pneumonia, urinary tract infection, skin and wound infections, bacteremia, and meningitis. Recombinant vaccines and specific antibodies are a new treatment strategies for such antibiotic-resistant infectious bacteria. However, a small number of bacterial surface antigens were tested that could only provide partial protection. For this reason, polyvalent (multiple) vaccines containing different antigens are needed to provide an acceptable level of protection. This study is oriented on the use of two outer membrane proteins, BauA and Omp34 as a polyvalent vaccine.

Methods: Recombinant BauA and Omp34 proteins were expressed, purified, and injected into BALB/C mice individually and in combination. Both active and passive immunizations were carried out. The mice were then challenged with a clinical isolate of A.baumannii.Then, the level of antibody in mice was measured by Indirect ELISA. The animal survival rate was also determined.

Results: Elevated antibody production was noted by ELISA in all the immunize groups. The combination of BauA and Omp34 proteins rendered good protection compared to the single administration of each protein.

Conclusion: These data indicate that antibodies to protein antigens can boost immunity and protection against A. baumannii strains. The findings are supporting use of multivalent monoclonal antibody therapy to control infections caused by A. baumannii We can therefore suggest the designed hybrid antigens as novel immunogenic candidates for developing effective subunit vaccine against A. baumanni infection.

Keywords: Acinetobacter baumunnii ., Recombinant protein., BauA ., OmpÛ³Û´., Immunogenicity ., Vaccine

The importance of EGFR (rs712829) gene polymorphism as a predictive marker for risk of lung cancer in Iranian population (Research Paper)

Milad Pezeshki,[1] Mahdi Nakhaee,[2] Jamshid Ansari,[3,*] Azam Ahmadi,[4] Saeed Ziaei,[5] Roja Valipoor,[6]

1. Development and research group of Lifeandme Company, Tehran, Iran.
2. Development and research group of Lifeandme Company, Tehran, Iran.
3. Department of Oncology, Ayatollah Khansari Hospital, Arak university of Medical Sciences, Arak, Iran.
4. Infectious Diseases Research Center (IDRC), Arak University of Medical Sciences, Arak, Iran.
5. Director of development and research group of Lifeandme Company, Tehran, Iran.
6. Department of Laboratory Medicine, Faculty of Paramedical Sciences, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran

Introduction: Lung cancer is the leading cause of cancer death globally. In Iran lung cancer is the third most common type of cancer and its prevalence is increasing rapidly. The epidermal growth factor receptor (EGFR) plays an important role in cell proliferation and signaling. The existence of rs712829 polymorphism in the EGFR gene can induce the carcinogenic process in the lung. In this study, we examined the association between EGFR (rs712829) gene polymorphism and lung cancer risk among the Iranian population.

Methods: A total of 200 patients with primary lung cancer at Ayatollah Khansari Hospital, Arak, and 200 matched healthy controls were recruited into this study. EGFR rs712829 single nucleotide polymorphism (SNP) was genotyped by PCR-RFLP techniques for this association with lung cancer risk. Finally, statistical analysis was done using the software SPSS version 16. Binary logistic regression analysis was performed to evaluate the association of polymorphism studied with the risk of lung cancer.

Results: A significant association was observed between the GG genotype (P= 0.039, OR= 5.500, CI=95%; 1.710- 11.921) and also G (P= 0.001, OR= 2.967, CI=95%; 1.557- 5.691) allele of rs712829 SNP with lung cancer risk, this was while the TT genotype and T allele of this polymorphism showed a protective role against risk of lung cancer.

Conclusion: In conclusion, EGFR rs712829 was associated with a risk of lung cancer. The rs712829 polymorphism can be used as a predictive marker for the risk of lung cancer in the Iranian population, but more studies are required to confirm the present findings.

Keywords: Predictive marker, Lung cancer, Single nucleotide polymorphism, rs712829, EGFR gene.

The importance of long non-coding RNAs in prognosis of lymphoma (Review)

Fatemeh Alipour,[1] Amir Atashi,[2,*] Mansoureh Ajami,[3]

1. Student Research Committee of School of Allied Medical Sciences, Shahroud University of Medical Science, Shahroud, Iran
2. Department of Medical Laboratory Sciences, School of Allied Medical Sciences, Shahroud University of Medical Sciences, Shahroud, Iran
3. Department of Medical Laboratory Sciences, School of Allied Medical Sciences, Shahroud University of Medical Sciences, Shahroud, Iran

Introduction: Lymphomas, leukemias and myelomas are a part of the broader group of cancers of the hematopoietic and lymphoid tissues. Lymphoma is a group of blood and lymph tissue tumors that develop from lymphocytes. The two main categories of lymphomas are the non-Hodgkin lymphoma and Hodgkin lymphoma. Long non-coding RNAs (lncRNAs) are longer than 200 nucleotides and rarely serve as templates for protein synthesis. Several studies have revealed that lncRNAs play important regulatory roles in various life-sustaining processes such as epigenetic regulation, cell cycle control, splicing, and post-transcriptional regulation. Although, the role of lncRNAs in the pathogenesis of the lymphoma has been identified, less has been discussed about its importance in the diagnosis, treatment and especially the prognosis of the lymphoma.

Methods: Published articles between 2000 and 2023 examining the role of lncRNAs in prognosis of lymphoma were identified by searching in the PubMed, Scopus and Web of Sciences databases.

Results: There is increasing evidence that lncRNAs may also play an important role in the pathogenesis of various cancers, including B-cell malignancies. They can act as scaffolds, guides, riboâ€• activators, decoy, competing endogenous RNAs and precursors for small regulatory RNAs. Several studies have used multiple lncRNAs as biomarkers to predict patient prognosis especially in diffuse large B cell lymphoma. It has been proven that six lncRNAs play a role in prognosis of lymphoma (SNHG26, PRKCQâ€□AS1, AC018521.5, RPARPâ€□AS1, AC244090.1 and AC023590.1). Upregulation of SNHG26 and RPARPâ€• AS1 was associated with poor prognosis. Lower expression of other four lncRNAs was related to poor prognosis. Also, nine lncRNAs with a prominent role in determining patient`s survival have been introduced as lncRNA-regulating epigenetic event signature (ELncSig).

Conclusion: Several lncRNAs have a decisive role in lymphoma prognosis, which can be used along with other markers such as cytogenetics and

mutation studies to determine patient survival and also to determine the optimal treatment method.

Keywords: Long non-coding RNAs (lncRNAs), Lymphoma, prognosis, survival

the new treatments of Duchenne muscular dystrophy (DMD) (Review)

Ghazale Borvaye,[1,*] dr Issa Layali,[2] Hediye geravandi,[3] zaynab kanani nejad,[4] Armina aghazade,[5]

1. department of microbiology, Islamic Azad university, medical branch, Tehran,Iran
2. Department of Biochemistry and Biophysics, Faculty of Advanced Sciences and Technology, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran
3. Department of Medicine,Ahvaz Jondishapur University of Medical Sciences, Khuzestan, Iran
4. department of Laboratory Science, Islamic azad university, borujerd, Iran
5. department of microbiology, Islamic Azad university, medical branch, Tehran,Iran

Introduction: Genetic disease Duchenne muscular dystrophy is one of the severe genetic diseases that occurs in children, and it happens due to deletion or disruption in the protein dystrophin, which is encoded by the gene located on the X chromosome. This disease mostly occurs in boys, and out of every 3500 male children, one is usually affected by this disease. Until now, there hasn't been a completely effective treatment method that has received FDA approval. However, new therapeutic approaches are being investigated and tested, which can potentially create a significant impact and slow down the progression of the disease. These approaches include the following cases. Genetic approaches, such as gene replacement therapies and micro-dystrophin gene therapy, along with steroid therapies like prednisone and deflazacort, anti-inflammatory drugs, including utrophin modulators, gene editing technologies like CRISPR-Cas9, read-through of premature stop codons using Ataluren, Eteplirsen, which works to promote dystrophin production by specific skipping of exon 51 in ineffective gene variants, are all potential treatments for Duchenne muscular dystrophy (DMD). In this article, we will try to discuss the mentioned innovative therapeutic methods but It's important to note that while these treatments hold promise, many are still in the experimental stage or undergoing clinical trials.

Methods: We use a wide variety of information that has been collected by researchers through patient samples, diverse methods, and tools. Our goal is to examine innovative therapeutic solutions for Duchenne muscular dystrophy. In addition, we evaluate the efficacy and safety of therapeutic strategies in order to improve the treatment of this disease, such as genetic therapies, steroid treatments, and so on. The integration of these materials and methods helps in designing innovative treatment options for Duchenne muscular dystrophy.

Results: All the mentioned methods in the experimental stages are inconclusive and do not definitively lead to complete disease improvement. Since Duchenne muscular dystrophy patients have a low life expectancy (about twenty to thirty years), helping reduce disease progression through new therapeutic methods can contribute to increasing lifespan and reducing disease severity.

Conclusion: Based on promising new research, we hope that by providing new treatment solutions, we can assist in improving the course of Duchenne muscular dystrophy. Generally, considering muscular, cardiac, and respiratory diseases that patients suffer from, the best therapeutic approach is prescribing various complementary medications to treat associated diseases, using assistive devices for facilitating movement, and utilizing physiotherapy and genetic therapies. It is hopeful that we can slow down the disease progression and witness improvement in the course of Duchenne muscular dystrophy patients.

Keywords: dystrophy, treatment, Duchenne,

The relationship between miRNAs and MM (Review)

Mohammad Hossein Khazaee Nasirabadi,[1,*]

1. Department of Hematology and Medical Laboratory Sciences, Faculty of Allied Medicine, Kerman University of Medical Sciences, Kerman, Iran

Introduction: The multistage disease known as multiple myeloma (MM) is defined by the formation and proliferation of monoclonal plasmacytes, which are cells that manufacture monoclonal immunoglobulin or its immunoglobulin fragments. Short (20â€“22 nucleotides), non-coding RNA molecules known as microRNAs posttranscriptionally regulate gene expression. Cell proliferation, differentiation, apoptosis, hemostasis, oncogenesis, and angiogenesis are all regulated by microRNAs. MicroRNAs are typically negative regulators of gene expression, however, there have been indications that they can also promote translation, suggesting that their roles may be far broader. Changes in the control of transcription may also affect how microRNAs are expressed during the carcinogenesis process. Oncogenes or suppressor genes encode transcription factors that regulate the expression of some microRNAs, whereas changes in the methylation state of promoters affect the expression of other microRNAs. The purpose of this study was the investigate the diagnostic and prognostic roles of miRNAs in MM.

Methods: The results of our review were based on an examination of articles that were available in the PubMed, Google Scholar, and Web of Science databases. We identified these papers using keyword searches on terms like multiple myeloma, microRNA, plasma cell malignancies, and hematological malignancies.

Results: Relapsed and/or resistant MM has been associated with decreased miR15a expression. In addition, patients with newly diagnosed MM showed greater expression of miR15a and miR16 compared to the general population. Literature findings also point to a connection between aberrant miRNA17-92 cluster expression and elevated Bcl2 protein antiapoptotic activity. The miRNA193b-365 cluster is similarly overexpressed in MM patients. Compared to the healthy population, this group of patients exhibits significantly increased levels of miR720, miR1308, and miR1246 expression. Hox9, c-Myc, Bcl2, and Shp1/2 are all regulated by the microRNAs miR146b, miR140, miR145, miR125a, miR151, miR223, and miR155, and alterations in their expression may play a role in myeloma genesis and serve as a prognostic indicator. Additionally, Myc activates miR17-92 clusters, and abnormalities in their expression are associated with the development of MM. For the first time, Neri et al. described the connection between abnormalities in microRNA-expression profiles and bortezomib resistance. Additionally, literature studies suggest that miR21 overexpression could result in resistance to apoptosis caused by doxorubicin, bortezomib, and dexamethasone.

Conclusion: For many years, researchers have worked to find novel prognostic and predictive indicators in people with hematological systemic illnesses. Even if there have been many reports on this topic, new signs still need to be discovered. MicroRNA could be one of these predictive indicators. Additional investigation is required into the abnormalities of microRNA expression in people with subsequent hematological malignancies.

Keywords: hematological malignancies, microRNA, multiple myeloma, plasma cell malignancies

The role of faecal microbiota transplantation (FMT) in the treatment of inflammatory bowel disease (Review)

Tohid Javaheri,[1,*]

1. Young Researchers and Elites Club, Islamic Azad University, Mashhad Branch, Mashhad, Iran

Introduction: The human intestine contains a large number of different microorganisms, where complex interactions between the intestinal microbiota and the host occur. Significant long-term changes in gut microbiota (dysbiosis) are associated with some gastrointestinal diseases such as inflammatory bowel disease (IBD). Fecal microbiota transplantation (FMT), also known as fecal transplantation, is the process of transferring fecal bacteria and other microbes from one healthy person to another. which can be suggested as a treatment method for IBD patients.

Methods: In this review study, a search was conducted in the electronic and scientific databases of PubMed, Google Scholar, Scopus, and ISI, and relevant articles were searched using the keywords of fecal microbiota transplantation (FMT) and inflammatory bowel disease (IBD).

Results: Definitely, conventional fecal microbiota transplantation (FMTs) for the treatment of IBD can be a targeted and important therapeutic method.

Conclusion: Recently, the results of FMT for the treatment of patients with inflammatory bowel disease (IBD) have been promising and effective. However, more extensive studies and research on this technique should be done on other microbes in the digestive system.

Keywords: Fecal Microbiota Transplantation (FMT), Inflammatory Bowel Disease (IBD), Microbiota

The Role of Fasting-mimicking Diets in Triple-negative Breast Cancer: Molecular Mechanisms and Clinical Implications (Review)

Farhad Soleimani,[1] Nasrin Karbasi Ravari,[2] Mina Soleimani,[3,*]

1. MD, Graduate of the Department of General Practice, Faculty of Medicine, Tehran University of Medical Sciences, Tehran, Iran
2. MD, Graduate of the Department of General Practice, Faculty of Medicine, Tehran University of Medical Sciences, Tehran, Iran
3. Department of Laboratory Science, Faculty of Paramedicine, Mashhad Medical Science, Islamic Azad University, Mashhad, Iran

Introduction: Breast cancer (BC) is the most common malignancy among women after non-melanoma skin neoplasms, which is increasing in most regions, especially in developing countries. The most immunogenic type is triple-negative breast cancer (TNBC), which is a malignancy with a relatively high mutation load and very aggressive, associated with poor patient survival. Although new therapeutic strategies, such as chemo-immunotherapy combinations, have significantly improved clinical outcomes, epidemiological studies have identified nutrition as essential in BC care. Also, overweight and obesity have been introduced as risk factors for the occurrence and worse prognosis of BC and TNBC, which have been considered necessary strategies in the direction of optimal body weight for prevention and help in treatment, and thus, strategies to achieve optimal body weight are essential for prevention and treatment. In this regard, alternative methods with the aim of anti-cancer, including fasting diets and diets with low and limited calories, low carbohydrates, and low protein, collectively called fasting-mimicking diets (FMDs), have been introduced as a promising therapeutic approach in BC patients.

Methods: A systematic search was conducted from 2020 to 2023 in scientific databases such as PubMed, Scopus, Google Scholar, and the World Health Organization (WHO) website. The purpose of this research was to investigate the relationship between the molecular biology of the FMD strategy and the immune environment and cancerous and healthy cells of patients with breast cancer, especially of the triple-negative type. Search terms included "fasting-mimicking diets" and "Triple-negative breast cancer".

Results: A fasting-mimicking diet can include approximately 50% fat, 40% carbohydrates, and 10% protein and provide between 50% and 90% calorie reduction per day while the body cannot detect that it is being fed. Considering that TNBC cells are susceptible to nutrient deficiency, it has been shown that Fasting/FMD changes the shape of the immune environment along with the antitumor effects of nutrient starvation in combination with standard chemotherapy and immunotherapy methods and improves the feasibility and tolerability of these treatments. FMD can protect healthy cells

from chemotherapy by reducing the toxicities associated with chemotherapy and increasing the positive response to it. Furthermore, making tumor cells more susceptible to chemotherapy and slowing down their growth in the body leads to more prolonged cell survival. FMD significantly reduces tumor development in the body. On the other hand, with a significant reduction in blood glucose and insulin concentrations, it has also reduced TNBC cancer stem cells, which play an essential role in tumor resistance to standard treatments. Most importantly, FMD significantly reduces the immunosuppressive population of myeloid cells and regulatory T cells by altering systemic and intra-tumoral immunity associated with increased cytotoxic T lymphocytes, natural killer T cells (NKT), and memory T cells. It also reduces the occurrence of immune-related adverse events (irAEs) by preventing overactivation of the immune response. On the other hand, Fasting/FMD treatment methods have proven that normalizing blood vessels in disturbed tumors can lead to the effect of drugs such as nanoparticles on tumors. Reducing the level of adenosine triphosphate (ATP) in drug-resistant cells prevents drug release, which, as a result, leads to the progress of the treatment process.

Conclusion: Since the control of BC, especially its TNBC type, along with overweight and obesity, has become a public health issue for women worldwide due to its high morbidity and mortality, this study has shown that, based on the findings, FMD can be considered an alternative, safe and promising auxiliary approach along with drugs and other treatment methods to control and improve the care of breast cancer patients.

Keywords: Fasting-mimicking diets, Triple-negative breast cancer, Breast Cancer, and Chemotherapy.

The Role Of Probiotics In The Treatment of Bacterial Infections of The Genital Tract In Women Review Article (Review)

Mahdiyeh Nikdel,[1] Haniye Fayezi,[2,*]

1. B.sc student of Microbiology Islamic Azad University East Tehran Branch
2. M.sc student of Pathogenic Microbes Islamic Azad University North Tehran Branch

Introduction: Urinary infections are the most common bacterial infections seen in society, especially among women, and affect their daily lives. Urinary tract infections in women usually begin with vaginal infections and progress towards the urethra and bladder. Probiotic interventions are partly effective in the treatment and Prevention of genital infections. These infections can cause discomfort, burning urine, itching, and abnormal discharge. Quick treatment of these infections is crucial to prevent complications. Products containing Lactobacillus species can prevent frequent urinary tract infections. Escherichia coli is the main pathogen involved in urinary tract infections that spread from the anus to the vagina and then rise above the sterile urinary tract, thereby affecting the urinary tract. Probiotics do not cause antibiotic resistance and may have other health benefits due to vaginal recolonization with lactobacilli. However, more comprehensive research is needed to recommend probiotics as an alternative to antibiotics.

Methods: Probiotics are living microorganisms that are useful to the host when consumed in sufficient quantities. When it comes to genital bacterial infections, probiotics can help fight harmful bacteria and support the growth of beneficial bacteria. While probiotics can play a beneficial role in the management of genital bacterial infections, they should be used along with other therapies recommended by healthcare professionals. This may include antibiotics or other medications based on the type of infection. In a review of 9 clinical trials with a total of 726 patients, different strains of Lactobacillus (orally or suppositories) were used and showed different effectiveness in preventing recurrent urinary tract infections.

Results: In recent years, several clinical trials have been conducted to investigate whether specific lactobacilli(oral or intra-vaginal) species combined with antibiotics can be effective in treating or preventing vaginal infections.Antibiotics kill pathogenic agents while Lactobacillus GR - 1 and RC-14 inhibit the growth and adhesion of pathogens of the genitourinary tract, reduce vaginal inflammation and strengthen immune defenses, all of which can make the combined treatment of probiotics with antibiotics more effective. Studies have shown that probiotics can help prevent and treat genital bacterial infections in women.Probiotics introduce good bacteria into the vaginal flora, which can help restore normal balance and fight harmful

microorganisms.This can lead to reduced symptoms of infection and promote overall vaginal health.

Conclusion: In short, probiotics offer a promising approach to the management of bacterial infections of the genital tract in women. Their ability to restore the normal balance of bacteria and support vaginal health makes them a valuable complement to traditional therapies. By choosing the right probiotic strains and including them in a comprehensive treatment plan, women can potentially get rid of these uncomfortable infections.

Keywords: Probiotics, Urinary Tract Infections , Lactobacillus , Bacterial Vaginosis

the role of probiotics in the treatment of colorectal cancer before and after surgery review article (Review)

Haniye Fayezi,[1,*]

1. M.sc student of Pathogenic Microbes Islamic Azad University North Tehran Branch

Introduction: Colorectal cancer is a common and devastating disease that affects millions of people around the world. Colorectal cancer develops in the colon or rectum. It usually begins as small, non-cancerous polyps that gradually turn into cancerous masses. Colorectal cancer risk factors include age, family history, some genetic conditions and lifestyle factors such as diet and physical activity. Research shows that probiotics may have a positive effect on colorectal cancer patients by modulating the gut microbiota and enhancing immune system response. These effects could potentially inhibit tumor growth and improve treatment results. Administration of probiotics before surgery in patients who undergo gastrointestinal surgery can reduce postoperative infectious complications.

Methods: Inclusion criteria included studies of patients with CRC who underwent chemotherapy, radiotherapy, open, laparoscopic or robotic surgery for colorectal cancer with curative intent. Studies included randomized controlled trials with a comparator group, a control group, or a placebo group. Primary outcomes included reduction in duration, severity, and incidence of antibiotic-associated diarrhea, chemotherapy-associated diarrhea, and especially probiotic-associated infection.

Results: The findings suggest that probiotics are very important for the prevention and treatment of CRC. The intervention of probiotic bacteria during surgery can prevent postoperative complications in patients with colorectal cancer and reduce the overall infection rate after surgery and can be a valuable adjunctive treatment in colorectal cancer surgery. The effectiveness should be confirmed by more clinical trials in the future and the most valuable ways to prevent CRC should be investigated. When aggressive tumors form, probiotics can cooperate with surgery and chemotherapy to treat them, reduce the complications associated with surgery and chemotherapy, improve the effectiveness of chemotherapy and improve the quality of life of patients. Some studies suggest that probiotics may prevent CRC metastasis.

Conclusion: The use of probiotics to prevent CRC surgical inflammation is promising. It was found that the combination of more than one microorganism, such as Lactobacillus and Bifidobacterium, improves treatment and improves surgery. A systematic review and meta-analysis of studies show that preoperative probiotic administration may have an effect in reducing postoperative complications, including general infectious complications, in

patients undergoing colorectal cancer surgery without any significant side effects. Therefore, probiotics may be considered a useful adjunct to routine care after colorectal cancer surgery. The administration of probiotics in patients with CRC not only reduces the risk of postoperative infection, but also reduces the tumor incidence in the long term and also improves the general quality of life. Considering the diversity in the use and types of probiotics, more research is necessary to create an optimal treatment protocol.

Keywords: Colorectal Cancer, Probiotics, Gastrointestinal, Microbiota

The science behind probiotic bacteria isolated from honey samples and their effect on lipid profiles Review article (Review)

Haniye Fayezi,[1,*]

1. M.sc student of Pathogenic Microbes Islamic Azad University North Tehran Branch

Introduction: Probiotics are live microorganisms that, when consumed in adequate amounts, confer health benefits to the host. These beneficial bacteria are commonly found in fermented foods and can also be taken as supplements. Probiotics play a crucial role in maintaining the balance of our gut microbiota, which has a far-reaching impact on our overall health. Bacteria isolated from honey samples contain bacterial strains that show probiotic potential. Natural honey can help increase HDL and lower LDL cholesterol levels, as well as reduce the risk of cardiovascular disease. Elevated triglyceride levels are another significant contributor to an unhealthy lipid profile. Excessive triglycerides in the blood can increase the risk of heart disease and stroke. The good news is that natural honey has been shown to help regulate triglyceride levels, keeping them within a healthy range and promoting a balanced lipid profile.

Methods: While the exact mechanisms behind honey's impact on lipid profiles are not yet fully understood, researchers believe that its antioxidant and anti-inflammatory properties play a significant role. Antioxidants help reduce oxidative stress and inflammation in the body, which are key factors in the development of cardiovascular diseases. Probiotics can change the composition of bile acids, which increases cholesterol metabolism and decreases cholesterol, reducing the total cholesterol burden of the body.

Results: Several scientific studies have been conducted to evaluate the effectiveness of isolates in honey to reduce cholesterol levels. These studies show promising results that may indicate that some probiotic strains in honey can help lower cholesterol. Administering specific bacterial strains from honey samples led to a significant reduction in total cholesterol and LDL cholesterol levels in mice. Similar findings were observed in human studies, suggesting the potential application of these results in humans. Research is needed to determine optimal strains, dose, and duration of treatment. In addition, the effectiveness of these probiotics may vary among individuals for reasons in the composition of the gut microbiota. It is important to check with a healthcare professional before introducing probiotics into your diet, especially if you have a medical condition that requires you to take medications that could interact with these supplements.

Conclusion: With its potential to reduce LDL cholesterol, increase HDL cholesterol, and regulate triglyceride levels, incorporating natural honey into

diet may contribute to a healthier lipid profile. The evaluation of different bacterial honey isolates as probiotics and their efficient roles in cholesterol reduction is an intriguing field of study. Scientific evidence suggests that certain strains present in bacterial honey isolates can positively influence cholesterol levels through various mechanisms. While further research is needed to fully understand the optimal use of these probiotics, their potential in promoting cholesterol reduction offers hope for individuals seeking natural ways to improve their cardiovascular health.

Keywords: Honey; Probiotics; Cholesterol; Cardiovascular disease

The skin microbiome (Review)

Alireza farahnak,[1,*]

1. Biology department Science and art University of Yazd

Introduction: The skin is the human bodyâ€™s largest organ, colonized by a diverse milieu of microorganisms, most of which are harmless or even beneficial to their host. Colonization is driven by the ecology of the skin surface, which is highly variable depending on topographical location, endogenous host factors and exogenous environmental factors. The cutaneous innate and adaptive immune responses can modulate the skin microbiota, but the microbiota also functions in educating the immune system. The development of molecular methods to identify microorganisms has led to an emerging view of the resident skin bacteria as highly diverse and variable. An enhanced understanding of the skin microbiome is necessary to gain insight into microbial involvement in human skin disorders and to enable novel promicrobial and antimicrobial therapeutic approaches for their treatment.The skin is an ecosystem composed of 1.8 m2 of diverse habitats with an abundance of folds, invaginations and specialized niches that support a wide range of microorganisms. The primary role of the skin is to serve as a physical barrier, protecting our bodies from potential assault by foreign organisms or toxic substances. The skin is also an interface with the outside environment and, as such, is colonized by a diverse collection of microorganisms â€” including bacteria, fungi and viruses â€” as well as mites1â€“7. As we describe, many of these microorganisms are harmless and in some cases provide vital functions that the human genome has not evolved. Symbiotic microorganisms occupy a wide range of skin niches and protect against invasion by more pathogenic or harmful organisms. These microorganisms may also have a role in educating the billions of T cells that are found in the skin, priming them to respond to similarly marked pathogenic cousins.The perception of the skin as an ecosystem â€” composed of living biological and physical components occupying diverse habitats â€” can advance our understanding of the delicate balance between host and microorganism. Disruptions in the balance on either side of the equation can result in skin disorders or infections. Perturbations affecting the hostâ€“microorganism relationship can be endogenous (for example, genetic variation that selects for a specific microbial community) or exogenous (for example, hand washing). To further our understanding of health, disease and infection of the skin, microbiologists, immunologists and dermatologists have partnered with genomic scientists to develop a more complete characterization of the skin microbiota and how it interacts with the host. The physical and chemical features of the skin select for unique sets of microorganisms that are adapted to the niche they inhabit.

Methods: 1. Probiotics and Prebiotics: Consuming probiotics and prebiotics can help support a healthy skin microbiome by promoting the growth of

beneficial bacteria. 2. Topical Probiotics: Using skincare products containing live probiotics can help restore and maintain a healthy balance of bacteria on the skin. 3. Gentle Cleansing: Using gentle, pH-balanced cleansers can help to maintain the natural balance of the skin microbiome. 4. Moisturizing: Using moisturizers with ingredients that support the skin microbiome, such as ceramides and fatty acids, can help provide a healthy environment for beneficial bacteria. 5. Sun Protection: Protecting the skin from UV radiation can help maintain a healthy skin microbiome, as sun damage can disrupt the balance of bacteria on the skin. 6. Diet: Consuming a balanced diet rich in fiber, fruits, and vegetables can support a healthy skin microbiome. 7. Stress Management: Managing stress can help support a healthy skin microbiome, as stress can impact the diversity and balance of bacteria on the skin. 8. Regular Skin Examinations: Regularly examining the skin for any changes or abnormalities can help identify and address any disruptions to the skin microbiome.

Results: The skin microbiome refers to the diverse community of microorganisms, including bacteria, fungi, and viruses, that inhabit the skin. Studies have shown that the skin microbiome plays a crucial role in maintaining skin health and preventing disease. It acts as a protective barrier, helps to regulate the immune system, and may even influence skin conditions such as acne, eczema, and psoriasis.Research on the skin microbiome has revealed the complexity and variability of microbial communities across different individuals and body sites. Factors such as genetics, environment, lifestyle, and skincare products can influence the composition of the skin microbiome.Understanding the skin microbiome can lead to the development of personalized skincare treatments and interventions that target specific microbial imbalances and promote skin health. Ongoing research is focused on uncovering the mechanisms by which the skin microbiome influences skin health and disease, as well as identifying potential therapeutic strategies to modulate the skin microbiome for beneficial effects.

Conclusion: Molecular approaches to characterizing microbial diversity have dramatically changed our view of the skin microbiome, subsequently raising many important questions about the hostâ€“microorganism relationship and its relevance to skin disease. Although it is now clear that several dominant organisms (that is, Staphylococcus and Propionibacterium spp.) constitute a large proportion of the skin microbiota, little is understood about the rare or transient organisms making up the balance. It is unclear what factors drive variation in these organisms, and how fluctuation is associated with skin disease.Another outstanding question is whether indigenous skin microorganisms provide some benefit to the host, and whether they are truly symbiotic, or commensal. In a recent example of host and microorganism joining forces to combat invasion by pathogens, the commensal skin bacteria S. epidermidis was demonstrated to inhibit nare colonization and biofilm formation by S. aureus102. A subset of S. epidermidis express the glutamyl endopeptidase protein (encoded by the esp gene), which can synergize with

the human AMP Î²-defensin 2 (also known as Î²-defensin 4A) to interfere with S. aureus colonization. This example raises several important points for consideration, including the possibility of the host and the microorganism evolving together. Furthermore, as our arsenal of antimicrobial weapons falls short in the battle against S. aureus and other potential pathogens, perhaps therapeutics derived from microorganisms themselves will offer promise as viable alternatives.

Keywords: skin , microbiome , microbiota , Symbiotic

The therapeutic effects of resveratrol in cancer treatment (Review)

Mahya Fekri,[1,*] MohammadSaleh Safari,[2] Hossein Rezvan,[3]

1.
2. PhDStudent, Department of Pathobiology, Faculty of Veterinary Sciences, Bu-Ali Sina University, Hamedan, Iran
3. Department of Pathobiology, Faculty of Veterinary Sciences, Bu-Ali Sina University, Hamedan, Iran

Introduction: Cancer and its complications are considered a clinical problem all over the world and it is the second cause of death. Putting some food items in the diet has a preventive or therapeutic effect against cancer. Research has shown that substances such as resveratrol (3,5,4â€²-trihydroxy-trans-stilbene), which contains polyphenol compounds, are useful in the healing process of inflammatory diseases, including cancer. Therefore, we will examine resveratrol, which is a phytoestrogen. Resveratrol is a natural stilbene and a non-flavonoid polyphenol, that possesses anti-oxidant, anti-inflammatory, cardioprotective, and anti-cancer properties.

Methods: By searching keywords such as the therapeutic effects of resveratrol and the effects of resveratrol in cancer in reliable databases such as Pubmed, Google Scholar, and Embase, the search was conducted and after studying and reviewing related 50 articles during the years 2016 to 2023, the desired information was obtained and presented in this review article.

Results: Resveratrol acts as an antioxidant and destroys free radicals from the body. Also, sensitizing cancer cells to chemotherapy agents, leads to a decrease in drug resistance and mutagenicity of cells in cancer.

Conclusion: Considering the various properties of resveratrol, it can be pointed out the positive effect of this substance in the improvement and prevention of diseases such as cancer, diabetes and cardiovascular problems. As a result, resveratrol needs more study and investigation.

Keywords: resveratrol; cancer therapy; apoptosis

The use of CAR T cell therapy in treatment of B cell malignancies (Review)

Mohammad Hossein Khazaee Nasirabadi,[1,*] Amir Hami,[2]

1. Department of Hematology and Medical Laboratory Sciences, Faculty of Allied Medicine, Kerman University of Medical Sciences, Kerman, Iran
2. Department of Medical Library & Information Science, Faculty of Management and Medical Information Sciences, Kerman University of Medical Sciences, Kerman, Iran

Introduction: Hematological cancers are typically treated primarily with chemotherapy, radiation, and hematopoietic stem cell transplantation (HSCT). However, improvements in immune-targeted therapy for tumors, such as chimeric antigen receptor T (CAR-T) cell therapy provided a new approach to treating cancer. So, this study aimed to examine CAR T cells' use to treat B-cell malignancies.

Methods: Our review's findings were derived from analyzing publications in the PubMed, Google Scholar, and Web of Science databases. We located these articles by conducting keyword searches using terms like CAR-T cell, immunotherapy, hematological malignancies, and B cell malignancies.

Results: One of the most crucial target antigens in B-cell malignancies, such as B-ALL and NHL (non-Hodgkin lymphoma), is CD19. Anti-CD19 CAR-T cell therapy has significantly changed the treatment landscape for B cell malignancies in recent years, producing quick and long-lasting responses in patients with R/R B-ALL and NHL. Four anti-CD19 CAR-T cell treatments have so far received FDA approval to treat R/R B-ALL and NHL. Despite the anti-CD19 CAR-T therapy's excellent clinical outcomes, CD19 antigen loss is frequently seen. In R/R BALL and NHL, alternative targets for CAR-T cell therapy have been investigated. Also, CD20 is overexpressed in over 90% of B cell lymphomas, making it an interesting target for these cancers. Over the past few years, rituximab, an anti-CD20 monoclonal antibody, has demonstrated an excellent effect on NHL. Anti-CD19 and anti-CD20 CAR-T cell combination therapy was studied to treat R/R DLBCL in order to avoid antigen escape, and it was found to be both efficient and safe. Most B cell malignancies, including B-ALL and DLBCL, have significant levels of CD22 expression, so it is an ideal target for CAR-T cell therapy in R/R B-ALL and DLBCL since it is restrictedly expressed on normal B cells while not expressed on hematopoietic stem cells. Patients with R/R B-ALL and R/R DLBCL who had not responded to prior antiCD19 CAR-T cell therapy have shown excellent success in multiple clinical trials using the anti-CD22 CAR-T cell therapy. Nevertheless, the side effects of CAR-T cell therapy, which include cytokine release syndrome (CRS), infections, cytopenia, and CRS-related coagulopathy, could be severe or even fatal.

Conclusion: CAR-T immunotherapy has emerged as a crucial new strategy for treating several hematological disorders due to its safety and controllability, While the efficiency, cell persistence, and side effects become barriers to the widespread application of this strategy.

Keywords: CAR-T cell, immunotherapy, hematological malignancies, B cell malignancies

Therapeutic potential of exfoliated mesenchymal stem cells from human dental pulp (Review)

Fatemeh Sadat Shojaeddin,[1] Faramarz Khosravi,[2,*]

1. Bachelorâ€™s student. Department of Microbiology, Faculty of Modern Science and Technologies, Tehran Medical Science, Islamic Azad University, Tehran Iran.
2. Tehran Medical Science, Islamic Azad University, Tehran, Iran.

Introduction: Human mesenchymal stem cells (hMSCs) are multipotent cells, which express specific cell surface marker spectrum, have multi-lineage differentiation potential and have exhibited immunomodulatory properties by secreting cytokines. These cells can be obtained from multiple tissues, therefore Human Dental Pulp Stem Cells (hDPSCs) were selected to investigate ,cause are easy accessible, neurotrophic and originated from the embryonic neural crest, which distinguishes them from other mesenchymal stem cells . Dental MSCs were first isolated from dental pulp of the extracted third molar and till now they have been purified from various dental tissues, including pulp tissue of permanent teeth and exfoliated deciduous teeth. To date, several subpopulations of dental-derived stem cells have been identified, including dental pulp stem cells (DPSCs), periodontal ligament stem cells (PDLSCs), stem cells from apical papilla (SCAP), stem cells from human exfoliated deciduous teeth (SHED), dental follicle stem cells (DFSCs), and gingival mesenchymal stem cells (GMSCs). Interestingly, the majority of dental-derived stem cell subpopulations exhibited the expression of key pluripotency markers, including Nanog, Oct4, Sox-2, SSEA-3, and SSEA-4 this suggests their potential to differentiate into multiple developmental lineages, despite the relatively low expression levels of these markers. Moreover, dental stem cells do not express haematopoietic and lymphocytic markers such as CD14, CD34, CD45, and human leukocyte antigen-DR (HLA-DR; <2%). Amongst many potential candidate stem cell types, dental pulp stem cells appear to be the most promising cell lineage due to ameliorate AÎ²-induced damage in vitro models by releasing neuroprotective factors such as BDNF, GDNF and NGF among other neurotrophins.

Methods: A comprehensive literature review was conducted to identify studies investigating the role of Therapeutic Potential of exfoliated mesenchymal stem cells from Human Dental Pulp. Electronic databases were searched using relevant keywords, and studies published of PubMed - NCBI and Google Scholar databases- which have done on this issue between 2013 and 2023 were included. The review encompassed in vitro studies, animal models, and clinical trials to provide a comprehensive understanding of the topic.

Results: In the assessment of Alzheimerâ€™s disease (AD) mouse models, Mita et al. (2015) showed that SHED-CM improved cognitive function and attenuated AÎ²-induced inflammation, thus protecting the neurons against AÎ² toxicity. The study also found that SHED-CM suppressed glutamate-induced neuronal death in primary cerebral neurons derived from mouse embryos. Moreover another study of permanent middle cerebral artery occlusion (pMCAO) in rats showed that SHED-CM promoted the migration and differentiation of endogenous neuronal progenitor cells (NPCs), reduced infarct volume, stimulated vasculogenesis, and subsequently improved motor function recovery . Recent studies have shown the ability of hDPSCs to differentiate into endothelial cells and their angiogenic potential and they were found to secrete vascular endothelial growth factors (VEGF) and generate visible blood vessels in three-dimensional- (3D-) printed HA constructs. The high plasticity of hDPSCs makes them an ideal stem cell source for stem cell-based therapy. Additionally, dental MSCs have a remarkable potential to treat Neural and glandular diseases such as spinal cord injury (SCI) and diabetes which It has been demonstrated that dental MSCs could facilitate functional improvement after SCI in animal models ,further, in a mouse model of streptozocin-induced diabetes, SHED-CM has been shown to promote the proliferation of pancreatic Î²-cells and enhance insulin secretion.

Conclusion: MSCs have multi-lineage differentiation potential, these cells can be obtained from multiple tissues. Easy accessibility, and multi-lineage differentiation potential make dental MSCs distinct from the other hMSCs and an effective tool in stem cell-based therapy. To date, several subpopulations of dental-derived stem cells have been identified, which Amongst many potential candidate dental stem cell types, (DPSCs) appear to be the most promising cell lineage in the treatment of AD and neural disease. Dental MSCs have been a precious stem cell source in regenerative medicine have a great therapeutic application potential in various diseases like SCI and diabetes which has been proved in a mouse model. We are hopeful to see brilliant results in human model in near future.

Keywords: Stem cells â€“ Dental MSCs â€“ Multi-lineage differentiation â€“ Diabetes â€“ spinal cord injury (SCI).

Thrombosis with thrombocytopenia syndrome caused by Covid-19 vaccine (Review)

Mahsa Taheri,[1,*] Mobina Nakhaei Shamahmood,[2] Younes Sadeghi-Bojd,[3]

1. Student Research Committee, School of Allied Medical Sciences, Birjand University of Medical Sciences, Birjand, Iran.
2. Student Research Committee, School of Allied Medical Sciences, Birjand University of Medical Sciences, Birjand, Iran.
3. Student Research Committee, School of Allied Medical Sciences, Birjand University of Medical Sciences, Birjand, Iran

Introduction: The common reported adverse effects of COVID-19 vaccination consist of the injection siteâ€™s local reaction followed by several non-specific flu-like symptoms. However, recent reports of thrombosis with thrombocytopenia syndrome (TTS) associated with adenovirus vector vaccines have raised concern. Objective: This is narrative review to investigate TTS after the Covid-19 vaccine.

Methods: Studies of TTS after ChAdOx1 nCoV-19 or Ad26.COV2 vaccine were searched in PubMed, Scopus, Embase and Web of Science databases until August 2022. Summary effects between studies were observed regarding incidence, presentation, site of thrombosis, diagnostic findings, and clinical outcomes.

Results: TTS, also known as vaccine-induced immune thrombotic thrombocytopenia, is a reaction associated with exposure to the ChAdOx1 nCoV-19 and Ad26.COV2 vaccine, which may result in thrombocytopenia and thrombotic events. There are several case series of patients diagnosed with TTS, but the overall incidence is rare. TTS is characterized by exposure to one of the aforementioned vaccines 4â€“30 days prior to presentation, followed by thrombosis, mild-to-severe thrombocytopenia, and a positive platelet factor-4 (PF4)-heparin enzyme-linked immunosorbent assay (ELISA). Thrombosis typically involves atypical locations, including cerebral venous thrombosis and splanchnic vein thrombosis. Evaluation should include complete blood count, peripheral smear, D-dimer, fibrinogen, coagulation panel, renal and liver function, and electrolytes, as well as PF4-heparin ELISA if available. Consultation with hematology is recommended if suspected or confirmed. Treatment may include intravenous immunoglobulin and anticoagulation, while avoiding heparin based agents and platelet transfusion.

Conclusion: Health care providers should be familiar with the clinical presentations, pathophysiology, diagnostic criteria, and management consideration of TTS. Early diagnosis and quick initiation of the treatment may help to provide patients with a more favorable outcome.

Keywords: TTS, Covid-19, Vaccine.

Title: NORAD: Orchestrating Cellular Equilibrium in Disease Dynamics (Review)

sahar ghyasi,[1] fatemeh ahmad pour,[2] ali asghar kiani,[3] shahla rahmani,[4] mahsa loran,[5,*]

1. MSC student of hematology department of laboratory science school of Alied Medical sciences kermanshah university of medical science
2. nutritional health Research Center Lorestan University of medical Sciences
3. Associate Professor of Laboratory Hematology and Blood Banking School of Allied Medical Sciences Lorestan University of Medical Science
4. MSC student of hematology department of laboratory science school of Alied Medical sciences kermanshah university of medical science
5. MSC student of hematology department of laboratory science school of Alied Medical sciences kermanshah university of medical science

Introduction: 1. Introduction: NORAD, standing tall as a molecular scaffold, is introduced with an emphasis on its molecular architecture, functional significance, and pivotal contributions to maintaining genomic stability and overall cellular homeostasis. This foundational section sets the stage for a deeper dive into NORAD's multifaceted roles.

Methods: Conducted an extensive review of current literature using scholarly databases like PubMed, ScienceDirect, and IEEE Xplore to identify recent studies on NORAD. Focused on papers elucidating NORAD's functions across diverse diseases.

Results: NORAD in Cancer: Navigating through the landscape of cancer, we scrutinize NORAD's impact on disease progression. Elevated NORAD levels emerge as influential factors in tumor development, proliferation, and metastasis. This segment scrutinizes NORAD's nuanced roles across various cancer types and explores its potential as a diagnostic beacon. NORAD in Cardiovascular Diseases: Our journey extends to the cardiovascular arena, where NORAD's influence on oxidative stress and inflammation within blood vessels takes center stage. The exploration of NORAD's cardiovascular roles not only sheds light on heart health promotion but also hints at novel therapeutic possibilities. NORAD in Inflammatory Diseases: In the realm of inflammatory diseases like arthritis and colitis, NORAD's regulatory prowess within inflammatory pathways is dissected. Understanding NORAD's impact on inflammation not only broadens our comprehension of disease mechanisms but also hints at potential therapeutic targets. NORAD in Neurological Diseases: Recent revelations thrust NORAD into the spotlight in neurological diseases such as Alzheimer's and Parkinson's. Delving into NORAD's contributions to neuronal health and its potential in preventing neuro-pathological changes expands our understanding of its neurological implications. NORAD in Metabolic Diseases: Turning our attention to

metabolic diseases, we explore NORAD's effects on glucose homeostasis and lipid metabolism. Unveiling NORAD's intricate dance in maintaining metabolic balance presents promising avenues for therapeutic exploration in metabolic disorders.

Conclusion: In conclusion, our holistic exploration underscores NORAD's pivotal position as a central regulator across diseases. NORAD's versatility positions it as both a promising therapeutic target and a potential diagnostic biomarker. This nuanced understanding lays the groundwork for future research endeavors and clinical applications.

Keywords: NORAD, long noncoding RNA, cancer, cardiovascular diseases, inflammatory diseases, neurological dise

Unraveling the Regulatory Role of microRNAs and Long Non-coding RNAs in Peripheral Blood Mononuclear Cells of Autoimmune Diseases (Review)

Hadis Rahimi,[1] Shadi Nazarifard,[2] Gholamreza Shahsavari,[3,*]

1. Student research committee, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Student research committee, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Department of Biochemistry, School of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran

Introduction: Introduction: Autoimmune diseases represent a diverse group of conditions marked by immune system dysregulation. PBMCs, pivotal in immune surveillance, offer valuable insights into the molecular landscape of autoimmune disorders. This section provides an overview of autoimmune diseases, emphasizing the significance of studying PBMCs and the emerging roles of miRNAs and lncRNAs in immune regulation.

Methods: Methods: The systematic review employed a comprehensive literature search strategy, targeting articles in PubMed, Scopus, and Web of Science. Selection criteria favored studies elucidating miRNA and lncRNA expression in PBMCs of autoimmune diseases, employing robust methodologies. Data extraction, synthesis, and critical analysis were performed to organize findings and identify research gaps.

Results: MicroRNA Regulation in Autoimmune Diseases: This section focuses on miRNA expression profiles in PBMCs associated with specific autoimmune diseases. For instance, the overexpression of miR-146a and miR-155 in SjÃ¶gren's syndrome and primary SjÃ¶gren's syndrome, respectively, suggests their potential as disease-specific biomarkers. The dysregulation of miR-146a in rheumatoid arthritis PBMCs indicates its role in the pathogenesis. 4. Long Non-coding RNAs in Autoimmune Disorders: The role of lncRNAs in autoimmune diseases is explored, highlighting their involvement in immune cell activation and signaling pathways within PBMCs. Elevated expression of lncRNA IFNG-AS1 in rheumatoid arthritis patients suggests its regulatory impact on inflammatory responses. The upregulation of LOC100652951 and LOC100506036 in T cells of rheumatoid arthritis patients underscores their potential as biomarkers. 5. Integrative Analysis and Future Directions: An integrative analysis synthesizes findings, emphasizing the interconnected regulatory networks orchestrated by miRNAs and lncRNAs in PBMCs. Research gaps, limitations, and future directions in the field are critically discussed, guiding subsequent investigations.

Conclusion: Conclusion: This comprehensive review provides a nuanced understanding of the regulatory roles of miRNAs and lncRNAs in PBMCs of autoimmune diseases. Insights gleaned from these molecular interactions hold promise for advancing diagnostic approaches and therapeutic interventions in the realm of autoimmune disorders.

Keywords: microRNA, Autoimmune Diseases, Mononuclear Cells

Urinary Exosomes; Innovative insight into diagnosis and treatment of renal diseases (Review)

Banafsheh Yalameha,[1] Reza Rahbarghazi,[2,*]

1. Student Research Committee, Tabriz University of Medical Sciences, Tabriz, Iran Department of Biochemistry and Clinical Laboratories, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran
2. Department of Applied Cell Sciences, Faculty of Advanced Medical Sciences, Tabriz University of Medical Sciences, Tabriz, Iran

Introduction: Exosomes, endosomal-based nano-sized vesicles, are involved in cell-to-cell intercommunication. Exosomes are produced under physiological and pathological conditions with prominent distribution in biofluids. In the urinary system, urinary exosomes (UEs), with an average diameter of 20-100 nm, are excreted by renal tubules epithelial cells, glomerular podocytes, and epithelial cells of the genitourinary tract (bladder and prostate). These exosomes harbor several signaling biomarkers, including membrane proteins, transcription factors, and microRNAs. UEs serve as immune effectors for the protection of the urinary tract against bacterial infection via carrying multiple innate immune proteins.

Methods: In this study, several sources were searched in numerous databases including PubMed/Medline, Scopus, and Google Scholar using keywords including; exosomes, urinary exosomes, biomarker, renal diseases, etc.

Results: Recent findings have confirmed the potential diagnostic properties of UEs in different abnormalities, such as renal tissue injuries. It is thought that rapid and accurate urine assay in terms of UE biomarkers may facilitate non-invasive diagnosis and develop prosperous management programs for patients suffering from kidney disorders. Besides, changes in the UE molecular signature can help us in the comprehension of the various renal diseases. The molecular composition of UEs displays their cellular origin, making them a promising source of biomarkers for kidney dysfunction and structural damage.

Conclusion: Despite recent progress in the detection of patient-specific UE proteome and transcriptome, UE research is still in its infancy, and multi-omics analysis is becoming an increasingly important area of study. The combination of exosomes and multi-omics analysis may provide an in-depth understanding of cellular changes and the essence of disease.

Keywords: Urine; Exosomes; Biomarkers; Kidney Disease; Diagnostic

Using artificial intelligence to diagnose hematological neoplasms (Review)

Mobina Nakhaei Shamahmood,[1] Mahsa Taheri,[2] Mahtab Sayadi,[3,*]

1. Student research committee, school of Allied medical science, Birjand university of medical science, Birjand, Iran
2. Student research committee, school of Allied medical science, Birjand university of medical science, Birjand, Iran
3. Cellular and Molecular Research Center, Birjand University of Medical Sciences, Birjand, Iran.

Introduction: Morphological examination is essential for the diagnosis of hematological diseases. However, traditional manual operation is time-consuming and labor-intensive. Artificial intelligence (AI) is now systematically finding its way into hematological cancer diagnostic and The future of clinical diagnosis and treatment of hematological diseases will inevitably involve the integration of artificial intelligence (AI)-based systems into routine practice to support the decision-making of hematologists.. The aim of this study was to investigate the use of artificial intelligence for better and easier diagnosis of hematological neoplasms.

Methods: for this systematic review study we searched in PubMed, Google Scholar, Scopus, Embase, Medline, and Cochrane databases until October 2023. Also A search was carried out in Medline and in MedRxive and BioRxive and 21 articles related to this topic were used.

Results: Today, the use of artificial intelligence in hematology laboratories is limited. Approved devices are mainly limited to the morphological analysis of blood smears. Digital imaging has made it possible to use faster, more efficient and standardized methods to perform morphological analyzes of peripheral blood smears and classify blood cells, which will be of great use in the diagnosis of hematological neoplasms. However, this technology is far from gold standard. However, even the best tool can become unusable if it is used inadequately or the results are misinterpreted. Therefore, to fully evaluate and correctly apply newly developed AI-based systems, a hematologist must have a basic understanding of general machine learning concepts.

Conclusion: AI-based technologies have evolved rapidly over the last five years, producing a range of narrow AI applications that can be used at all stages of patient management in hematology from analyzing peripheral blood differentials to gene profiling. In the future, we envision a scenario in which AI-based algorithms could help integrate complex data with practical applications in patient care in an efficient and innovative way. Such a model is still a long way off, but it certainly deserves discussion and further research.

Keywords: Artificial intelligence,Hematological diagnostics,Neoplasms