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5th International Conference on Biotechnology, Bio Informatics, Bio Medical Sciences and Stem Cell Applications (B3SC), September 02-03, 2016

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GICB3SC1606051

**The Apyrase Functional Properties of The 56 kD Immunogenic Protein
from Salivary Gland of Aedes aegypti**

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Abstract

Apyrase is nucleoside triphosphate-diphosphohydrolase mostly found in haematophagous arthropods which mostly able to transmit pathogen into human host. This salivary enzyme protein is responsible for inhibiting platelet aggregation in the human host while vector's blood feeding, by hydrolyzing ADP or ATP molecules. Apyrase is also known to be an allergen with high immunogenicity. Our previous study has reported that the immunogenic proteins, apyrase, was detected abundantly at 56 kDa from salivary gland of Dengue's vector Aedes aegypti. In this study, we analyzed the human immune response against 56 kDa immunogenic protein from salivary gland of Ae. aegypti by using ELISA (Enzyme Linked Immunosorbent Assay). The ability of apyrase on platelet aggregation inhibition were also further investigated. The results showed that the highest IgG (Immunoglobulin G) response was detected in sera from Dengue patients compared to healthy people from endemic area and infant. This indicate its important functional properties of 56 kDa during Dengue transmission. This could be explained by its function to inhibit the platelet aggregation during blood feeding. Results showed that human platelet aggregation was inhibited by this immunogenic protein up to 40-50% by destroying its ADP.

Key words: apyrase, immunogenic protein, salivary gland, Aedes aegypti



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**Characterization of RbcL Gene Sequences Banana Tongkat Langit (musa
troglodytarum l.) Origin Maluku Islands**

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Abstract

Characterization of rbcL gene sequences banana tongkat langit origin Maluku islands with the other group called outgroup, they are Musa fehi, Ensete glaucum, superbum and Ensete, Ensete ventricosum (NCBI) which have aims to study the nucleotide diversity, haplotype diversity, nucleotide substitution ratio and specify the variable sites. The characterization results using DNASP 5:10:01 version nucleotide diversity values obtained 0.380. Characterization haplotypes using Network version 4.6 is obtained with a total of 0.57 haplotype diversity haplotype 6 of 24 samples analyzed. Polymorphism substitution spread on banana tongkat

	<p>langit origin Maluku islands and also in outgroup. Transversion substitution is higher in the banana tongkat langit origin Maluku islands. There are 10 variable sites consisting of singleton two variants, variant tree, and four variants with varying site position</p> <p>Keywords: characterization sequences, gene rbcL, tongkat langit, the Maluku islands</p>
 <p>Yuliani GICB3SC1606054</p>	<p>Total Phenolic And Flavonoid Contents Of Asteraceae Family Leaves Extracts On Various Altitude Habitats</p> <p>Yuliani Department of Biology, Faculty Mathematics and natural Sciences, University State of Surabaya, Indonesia yuliani.ap@gmail.com</p> <p>Abstract</p> <p>Asteraceae family has various benefits as herbal medicine and phytochemical affect. It can grow in different habitats but secondary metabolites in Asteraceae depend of the environmental factor. The aims of the study was to quantitatively analyze the phenolic and flavonoid content of three kinds of plants from Asteraceae family, such as <i>Pluchea indica</i>, <i>Ageratum conyzoides</i>, and <i>Elephantopus scaber</i>, on three different kinds of habitats which differ on the altitudes. <i>Pluchea indica</i>, <i>Ageratum conyzoides</i>, and <i>Elephantopus scaber</i> leaves were obtained from three different altitude habitat: lowland (Bangkalan-Madura; 28.3 - 31.72 m asl), middle land (Trawas- Mojokerto; 727 – 937 m asl) and highland (Coban talun-Batu; 1303 – 1322 m asl). The simplicia of Asteraceae family leaves were macerated and extracted with methanol, ethyl acetate, aquades and n-butanol. The total phenolic (gallic acid/GAE) and flavonoid (quercetin/QE) contents was determined using UV-VIS spectrophotometer. The results were then analyzed by ANOVA. The results showed that the total phenolic contents of <i>P. indica</i> were showed in lowland (1,76±0,04 mg/mL) was found higher as compared to the middle-altitude land (1,45±0,03 mg/mL) and highland (1,21±0,04 mg/mL). The total flavonoid contents of <i>P. indica</i> were showed no mean difference of lowland (3,1±0,1 mg/mL), middle-altitude land (3,0±0,1mg/mL) and highland (3,2±0,1 mg/mL). The total phenolic contents of <i>A.conyzoides</i> in middle-altitude (1,66±0,1 mg/mL) was higher than highland (1,30±0,03 mg/mL) and lowland (1,25±0,02mg/mL). The total flavonoid on <i>A.conyzoides</i> in highland (3,2±0,06 mg/g dry weight) was higher than <i>A.conyzoides</i> growing in middle-altitude land (2,9±0,0 mg/g dry weight) and in lowland (2,6±0,06 mg/g dry weight). The total phenolic (1,86 ±0,03 mg/mL) and flavonoid (3,4 ±0,06 mg/mL) contents of <i>Elephantopus scaber</i> were showed in middle-altitude land was found higher as compared to the lowland and highland. The highest phenolic content was found to be in methanol extract, and the highest flavonoid content was found to be in ethyl acetate fraction of Asteraceae family.</p> <p>Keywords: Asteraceae, total phenolic content, total flavonoid, leaves extracts, altitude habitat</p>
<p>Waldemar E. Wysokinski GICB3SC1606056</p>	<p>Genes expression and Reticulated Platelets in Atrial Fibrillation</p> <p>Waldemar E. Wysokinski Cardiovascular Diseases, Mayo Clinic, Rochester, MN, U.S.A. wysokinski.waldemar@mayo.edu</p> <p>Abstract</p>

Background: Young reticulated platelet (RP) content is increased in non-valvular atrial fibrillation (NVAf). We hypothesized that platelet production and morphological features including proportion of RP is modulated by platelet predominate genes that are crucial for platelet synthesis.

Methods: Expression of platelet predominate genes that should have an impact on platelet formation and release, total platelet count and RP content were assessed in consecutive NVAf patients before and 3-4 months after catheter ablation of pulmonary veins (PVI). Results were compared to normal sinus rhythm (NSR) controls. RNA from isolated platelets were reverse-transcribed (Invitrogen), assayed against 7 genes utilizing real-time qPCR, and expressed as mean cycle threshold (ΔC_t) (ABI Prism 7700 Sequence Detection System) using beta-2-microglobulin as endogenous control. RP content was assessed by flow cytometry (thiazole orange/CD 61).Results: Over 4-fold higher percentage of RP in NVAf cases compared to controls (28.7 ± 7.0 vs. 6.7 ± 5.4 , $P < .001$) was associated with 4-fold lower expression of CFL1 gene coding for non-muscle cofilin (7.8 ± 0.9 vs 5.7 ± 1.6 , $p < .001$) and 2-fold lower expression of 5 other evaluated genes. Mucin gene (MUC6) expression could be measured only in 7 controls and in no NVAf case and is not presented in the analysis. Total platelet count was similar in cases and controls. After PVI, CFL1 gene expression increased over 2-fold; also PGRMC1 and PDZK1IP genes had expression increased when 3-4 months after PVI measured. Expression of TUBA4A gene decreased almost 2-fold after PVI. NFE2 and MYL6 genes had expression not significantly changed compared to pre-PVI values. .

Conclusion: Significantly higher content of RP in atrial fibrillation is associated with notable down-regulation of genes regulating platelet production and size



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Isolation and Characterization of Dehydration Responsive Element Binding (Dreb2a) Gene in Selected Upland Rice Accessions of Nigeria

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Abstract


DREB2A genes are transcription factors (TFs) that belongs to the APPETALA2/Ethylene Responsive Element Binding Factor (AP2/ERF) and play a key role in plant response to abiotic stress. In this study, DREB2A gene was isolated, cloned and characterized (in silico) from 25 rice accessions (10 O. glaberrima, 8 NERICA and 7 indica groups). The results revealed that DREB2A gene was present in all the 25 accessions using DREB2A gene specific primers. Comparison through alignments between coding sequence (derived from cDNA) and genomic sequence (derived from genomic DNA) revealed the position of 2 introns but of just 1 and 2 bp length respectively, though other reports from indica and japonica varieties reported the DREB2A gene to be intron less, but our findings revealed variation in length between coding sequence and genomic sequence of the same cultivar (NERICA1) by almost 3 bp length thus suggesting an intron. Coding sequence of DREB2A gene (derived from cDNA) showed 100% identity with

	<p>Pokkali reference sequence of the NCBI database (gi/377823847) and codes for 281 amino acid residues that has 58 amino acids at the AP2 DNA binding domain. DREB2A protein of NERICA coding sequence revealed a predicted molecular weight, GRAVY, stability index and Iso-electric point of 31.579 KDa, -0.670, 44.34 (unstable) and 5.87 respectively. Multiple sequence alignments of DREB2A sequence derived from 12 rice species including NERICA revealed the phylogenetic relationship and the conserved nature of the gene in rice family. In conclusion, the OsDREB2A gene in indica is orthologous to the OsDREB2A gene in NERICA accessions studied.</p>
 <p>Hanieh Shokrkar GICB3SC1606058</p>	<p>Effects of Different Enzymes on Carbohydrates Extraction from Microalgal Biomass for Bioethanol Production</p> <p>Hanieh Shokrkar Biotechnology Research Center, Faculty of Chemical Engineering, Sahand University of Technology, Tabriz, Iran h_shokrkar@sut.ac.ir sirous.ebrahimi@epfl.ch mahdizamani459@gmail.com</p> <p>Abstract</p> <p>Enzymatic hydrolysis of cellulose and starch are usually performed by cellulase and amylases enzymes, respectively. Although the enzymatic hydrolysis of starch and cellulosic material has been extensively reported, it is scarcely investigated on microalgal biomass. Especially, effects of addition of various enzymes in enzymatic hydrolysis of non-sterile, mixed microalgae culture has not been reported. The present work deals carbohydrates extraction from the mixed microalgae culture using different enzymes for bioethanol production. Among the all enzymatic treatments tested, the highest sugar yield of 99% was obtained with sequent addition of cellulase, α-amylase, and glucoamylase.</p> <p>Keywords: Alpha amylase; Glucoamylase; Bioethanol; Carbohydrates extraction; Cellulase; Mixed microalgae culture</p>
 <p>Jafar Razmara GICB3SC1606059</p>	<p>Linear encoding approach versus geometry-based techniques for protein structure comparison</p> <p>Jafar Razmara Department of Computer Science, University of Tabriz, Tabriz, Iran razmara@tabrizu.ac.ir</p> <p>Abstract</p> <p>Structural comparison of proteins is a major intellectual and practical challenge in structural biology, providing foundations for classification, functional annotation and evolutionary relationships analysis. The problem has been widely studied during last decades and several computational tools have been proposed such as CE [1] and TM-align [2]. The methods mostly use geometry of the protein structure to find an initial overlap between two structures, and then, employ an optimization algorithm to optimally align proteins. Recently, linear encoding approach has been proposed to model protein structure in sequences of structural alphabets, and then, use sequence alignment techniques to compare and align two proteins. 3D-BLAST [3], YAKUSA [4], SARST [5], and TS-AMIR [6] are the known methods developed based on this approach. Recently, we developed a similar approach to encode protein structure in a sequence of alphabets based on relative position of amino</p>

	<p>acids with respect to its previous residue. The method uses n-gram modeling technique from computational linguistics to look for an alignment between two sequences. In this paper, we introduce linear encoding approaches for protein structure comparison. We also compare the retrieval effectiveness of these methods with other geometry-based methods. The study shows linear encoding methods obtain a competitive accuracy in comparison with geometry-based techniques whereas their running time is better than the conventional methods.</p>
 <p>Kartika Senjarini GICB3SC1606060</p>	<p>Potential Use of Anopheles salivary component as future target for developing vector-based Vaccine against Malaria: molecular characterization of immunogenic protein from salivary gland of Anopheles mosquitoes</p> <p>Kartika Senjarini Department of Biology - Faculty of Mathematic & Natural Sciences, University of Jember, Indonesia</p> <p>Dwi Esti Febriyantiningasih Department of Biology, Faculty of Mathematic & Natural Sciences University of Jember, Indonesia</p> <p>Hidayat Teguh Wiyono Department of Biology, Faculty of Mathematic & Natural Sciences University of Jember, Indonesia</p> <p>Rike Oktarianti Department of Biology, Faculty of Mathematic & Natural Sciences University of Jember, Indonesia</p> <p>Christof Lenz Medical University of Goettingen, Germany</p> <p>Abstract</p> <p>Although malaria had ever been virtually eradicated from Indonesia but currently malaria is recognized as a serious re-emerging threat to public health. This disease is caused by malaria parasite which is transmitted to human host by Anopheles mosquitoes as main vector. It has been widely observed that saliva of mosquito that transmits diseases contains several factors that could enhance pathogen infection. Therefore, it should be possible to control pathogen transmission by vaccinating the host against the molecule(s) in saliva that potentiate the infection (Transmission Blocking Vaccine, TBV). However, specific component as a potential target for developing TBV in Anopheles' saliva has not yet been identified so far. Immunomodulatory factors from vector's saliva are responsible to inhibit host immune response, therefore it is very crucial to first identify these factors. This research wanted to identify the immunomodulatory factors from anopheles saliva. The immunomodulatory factors should be immunogenic, thus we used to characterize the immunogenic proteins from salivary glands as central organ to produce saliva in mosquitoes by cross reacted salivary gland extract against endemic human sera. Further proteomic analysis by Mass-Spectrophotometry has been done to further investigate these immunogenic proteins. Apart from the housekeeping proteins which were identified, there were also some proteins which play crucial role in the blood feeding process. These proteins are very likely to have important role to also transmit the pathogens into human host.</p>

<p>Khaldi Amina GICB3SC1606055</p>	<p>FIC Test performance on multi-resistant bacteria isolated from different environments</p> <p>Khaldi Amina Laboratoire de Bioconversion, Génie Microbiologique et Sécurité Sanitaire, Faculté SNV, Univ. Mascara-29000-Algérie amkhaldia@hotmail.com</p> <p>Maghdouri N Laboratoire de Bioconversion, Génie Microbiologique et Sécurité Sanitaire, Faculté SNV, Univ. Mascara-29000-Algérie</p> <p>Tir touil A. Laboratoire de Bioconversion, Génie Microbiologique et Sécurité Sanitaire, Faculté SNV, Univ. Mascara-29000-Algérie Laboratoire de Recherche sur le système biologique et géomatique Faculté SNV, université Mustapha Stambouli Mascara-Algérie</p> <p>Mouri N, Meddah B Laboratoire de Bioconversion, Génie Microbiologique et Sécurité Sanitaire, Faculté SNV, Univ. Mascara-29000-Algérie Laboratoire de Recherche sur le système biologique et géomatique Faculté SNV, université Mustapha Stambouli Mascara-Algérie</p> <p>Abstract The emergence of multi-resistant bacteria (BMR) represents a major health problem worldwide. Among these bacteria, the most encountered are those that express beta-lactamase (ESBL) extended spectrum. The alternative therapy implementation represents an alternative solution to fight against this health risk. The purpose of this study is to investigate the bacterial diversity, antimicrobial resistance, types of beta-lactamases and evaluate the antibacterial effect of the extract of <i>A. halimus</i> on pathogens resistant bacteria isolated from clinical infection, food and environmental. 115 pathogenic strains were isolated from different samples (<i>Staphylococcus aureus</i>, <i>E. coli</i>, <i>Salmonella sp</i>, <i>Clostridium sp</i>), respectively. All isolates are strains of beta-lactamase. The three <i>Atriplex halimus</i> extracts, essential oil, hydrometanolic and acetate have a low return linked to the characteristics of the plant itself. The extracts showed higher antibacterial activity. The essential oil exerts an antagonistic effect on all strains pathogenic with 200 ul / ml while the extract of hydrometanolic acetate and showed an inhibitory effect at a concentration of 300 mg / ml depending on the strain tested. the results suggest that the extracts of <i>Atriplex halimus</i> could be a potential treatment alternative for resistant bacteria.</p> <p>Keywords <i>Atriplex halimus</i> extract, beta-lactamase, an antibacterial activity.</p>
<p>Khaldi Amina GICB3SC1606055</p>	<p>Screening of the multi-resistant bacteria isolated from Food, Clinical infection and Environment Water in west region of Algeria</p> <p>Khaldi Amina Bioconversion Laboratory, Engineering Microbiological Safety and Health, Univ. Mascara-29000-Algeria amkhaldia@hotmail.com</p>

	<p style="text-align: center;">Zennaf I. Bioconversion Laboratory, Engineering Microbiological Safety and Health, Univ. Mascara-29000-Algeria</p> <p style="text-align: center;">tir touil A. Bioconversion Laboratory, Engineering Microbiological Safety and Health, Univ. Mascara-29000-Algeria</p> <p style="text-align: center;">Abstract</p> <p>The bacteria quickly evolve not only changing but also by acquisition of exogenous genetic material. Resistance by mutation accumulation is assumed to present a minimum risk of releases of genes while the resistance exogenous gene acquisition has a strong diffusion potential as it is in most cases carried by mobile genetic elements. Thus, the food chain has a role in the transmission of resistant bacteria and some arguments prove its reality for some pathogens such as animal foods that could be a vector of the resistance of beta lactamases expanded spetre (ESBLs).Our aim was to investigate multiresistance bacteria (Enterobacteriaceae and Staphylococci) and characterize beta lactams from various origins samples: food (milk and milk products, meat), nosocomial infection (infection of wounds and urinary tract infection) and water (sewage, lake).The first results clearly indicate that 95.45% of isolates are mutirésistantes 80% contain ESBL. This suggests that the transfer of resistance gene between strains of animal origin, vegetable, or commensal is possible and could act on the intestinal microflora of man by disrupting the microbial balance, thus favoring the colonization of the intestine by pathogenic or opportunistic bacteria mutirésistantes. We believe that by working educate users physicians, veterinarians and breeders about the risks of the emergence of bacterial resistance while not questioning the appropriate antibiotic therapy, adusive and doses administered.</p> <p>Keywords: ESBL bacteria Emergence, Resistance</p>
<p>Khaldi Amina GICB3SC1606055</p>	<p style="text-align: center;">Screening of the multi-resistant bacteria isolated from Food, Clinical infection and Environment Water in west region of Algeria</p> <p style="text-align: center;">Khaldi A Laboratory of Bioconversion Microbiological Engineering and Sanitary Safety (LBMESS), University of Mascara-29000, Algeria amkhaldia@hotmail.com</p> <p style="text-align: center;">Tir touil Meddah A. Laboratory of Bioconversion Microbiological Engineering and Sanitary Safety (LBMESS), University of Mascara-29000, Algeria</p> <p style="text-align: center;">Meddah b Laboratory of Bioconversion Microbiological Engineering and Sanitary Safety (LBMESS), University of Mascara-29000, Algeria</p>

	<p style="text-align: center;">Abstract</p> <p>Exerting pressure on microorganisms, misuse of antibiotics is the main epidemiological factors responsible for the emergence of multidrug-resistant bacteria (BMR) by several mechanisms, including enzyme inhibition among which the β-lactamases. Along with the widespread use of β-lactams, β-lactamase bacteria have evolved towards diversification, broadening their spectrum of activity, and shared among many species of bacteria. In the present study, 80 samples were analyzed from three sites, Food samples, clinical infection and environment Water. In Total 115 strains were isolated from different sampling with large dominance of Gram-negative represented by 70% against 30% of Gram-positive bacteria. In the Gram positive bacteria, Staphylococcus aureus was the most frequently isolated with 23%. Among the Gram negative bacteria, E. coli and Klebsiella sp, Salmonella sp were the organisms most frequently found with a prevalence of 20%, 15% and 12% respectively. However Shigella sp and Providencia sp were found at 10% and 08% in different samples. In other Gram negative bacteria Pseudomonas aeruginosa was isolated at 12%. Our results indicate that all strains isolated and identified in various sites were multi-resistant to antibiotics. From different specimens (Food, clinical infection and environment water), 50% of Staphylococcus aureus strains isolated are presumed MRSA. In the Gram negative bacteria and from Enterobacteriaceae 79.46% isolated strains producing ESBL.</p> <p>Keywords: β-lactamase, Environment, Food, clinical infection, Multi-resistant bacteria</p>
 <p>Fazel Gorjipour GICB3SC1606062</p>	<p>Allogeneic mesenchymal stem cells from fetal adnexa for cardiac regeneration: hopes for a scalable cell-based therapy for an age-related adverse conditions</p> <p style="text-align: center;">Fazel Gorjipour Cellular and Molecular Research center, Iran University of Medical Sciences, Tehran, Iran fgorjipour@gmail.com</p> <p style="text-align: center;">Seyed Javad Hajimiresmaiel Department of Cardiology, Faculty of Medicine, Iran University of Medical Sciences, Tehran, Ira mirsmaili@yahoo.com</p> <p style="text-align: center;">Hamidreza Pazoki-toroudi Physiology Research Center and department of Physiology, Iran University of Medical Sciences, Tehran, Iran hrptoroudi@gmail.com</p> <p style="text-align: center;">ABSTRACT</p> <p>Myocardial infarction and subsequent heart failure are the leading causes of mortality and morbidity in adults worldwide. Usually cardiac remodeling after ischemia and insufficient perfusion leads to multiple organ failure and death. Treatment with mesenchymal stem cells has shown promise in postponing the adverse outcomes following myocardial ischemia. However, there exist concerns regarding the impairment of regenerative and proliferative capacity of MSCs by advanced age of the donor. This is really important in age-related disorders including cardiovascular conditions and limits the efficacy of autologous or allogeneic transplants from aged donors. Recently, MSCs have been widely isolated from fetal adnexa including umbilical cord, amnion and amniotic fluid. These cells</p>

are identical to MSCs from bone marrow and adipose tissue which are currently the dominant sources of these cells for clinical application. Furthermore, they lack the disadvantage of aged donors and are categorized as fetal stem cells which are superior to adult stem cells in their differentiation potential, regenerative capacity and proliferation. These offer a good opportunity for the biotech industry to prepare off-the-shelf preparations of mesenchymal stems cells (MSCs) for clinical trials of myocardial infarction. These cells could be prepared from fetal adnexa which are usually disposed after childbirth without significant technical difficulties compared to bone marrow aspirations or liposuction which both are relatively complex and risky operations. Preclinical studies have proven that they are immune system modulator and are effective in improving the outcomes following experimental myocardial infarction and heart failure models. Further studies are required to address the challenges for use of these products in clinical practice.
Keywords: mesenchymal stem cells; fetal adnexa; myocardial infarction, heart failure; stem cell therapy; amnion



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GICI16062051

Detection Of Biofilm Formation In Clinical Stains Of Staphylococcus Aureus Associated To Healthcare Infections

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Abstract

The burden of disease caused by *Staphylococcus aureus* continues to grow; this organism has the ability to form biofilm and it is also a frequent cause of medical device and implant-related infections. The objective of this study was to evaluate the biofilm-forming ability of a collection of clinical isolates of *S. aureus*. In a total of 240 *Staphylococcus* spp. isolated from catheters, retrieved at five services (neonatology, internal medicine, pneumology, pediatric and neurology), only 50 (20.83%) strains were identified by conventional microbiological methods as *S. aureus* species; these strains were screened by microtiter plate assay for detection of biofilm formation. Of the 50 clinical isolates, 16 (32%) were non adherent, 20(40%) weakly, 10 (20%) moderately and 4(8%) strongly adherent. The quantitative method of microtiter plate can be involved as a simple, rapid, inexpensive and reproducible assay to assess biofilm formation which is further an important feature of pathogenicity of *S. aureus* in the clinical setting.

Key words: Microbial biofilm, *Staphylococcus aureus*, catheter, microtiter plate assay



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The relationship between family support & glycemic control in diabetes type 2

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Abstract

Background & Aim: one of the most important aims of diabetic patient's care is glycemic control. Glycemic control in these patients is influenced by different biological, mental & social factors. Family support is the most important source of social support in the patients and influence on glycemic control is much more than other factors because the most part of care of these patients is done at home.

Materials & Method: This is a cross-sectional study, that 230 diabetic patients who referred to Endocrinology and Metabolism Center Iran University of Medical Sciences were selected continuously. A self-reported questionnaire of "Diabetes Social Support- Family Version" was used for gathering information. Data were analyzed by SPSS version 15 by using Chi-square and Pierson regression tests. **Result:** results showed that there was an inverse meaningful correlation between family support & HbA1c and 68.4% of patients who received much more support from their family had lower HbA1c level. ($r = -0.56$, $p = 0.000$) **Conclusion:** results showed that family support lead to glycemic control in patients with type 2 diabetes. Therefore it is suggested that family members of diabetic patients should be engaged treatment plan.

Key words: family support, diabetes type 2, Glycemic control.



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A Model for Managing Medical Image Data on the Cloud



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Abstract

Due to the increasing demand on Hospital Information System (HIS) resources and the high cost of constructing independent information platform especially for medium to small hospitals, large scale clusters which are based on cloud computing technologies have been very popular to use in order to have a quality information platform that best suits the hospital budget. In this paper, we propose an enhanced model that provides a solution for hospital information systems. This model provides new features that will enhance the efficiency of data retrieval of medical

	<p>images and the costs of processing these images in the cloud. Keywords: Cloud Computing, Healthcare cloud, DICOM protocol server, Hospital Information System, Cloud of HIS architecture</p>
 <p>Amer Al-Badarneh GICHNDM1606059</p>	<p>An Adaptive Role-Based Access Control Approach for Distributed E-Health Systems</p> <p>Amer Al-Badarneh Jordan University of Science and Technology, Irbid 22110, Jordan amerb@just.edu.jo</p> <p>Hassan Najadat Jordan University of Science and Technology, Irbid 22110, Jordan najadat@just.edu.jo</p> <p>Enas Essa Jordan University of Science and Technology, Irbid 22110, Jordan enasissa82@yahoo.com</p> <p>Abstract Securing and protecting electronic medical records (EMR) stored in a cloud is one of the most critical issues in e-health systems. Many approaches with different security objectives has been developed to adapt this important issue. This paper proposes a new approach for securing and protecting electronic health records against unauthenticated access with allowing different hospitals, health centers and pharmacies access the system, by implementing role-based access control that could be applied smoothly in cloud health systems.</p> <p>Keywords— EMR; security; privacy; role-based access control; cloud computing</p>
 <p>Hamidreza Aghababaeian GICIAPHLR1606064</p>	<p>Workplace Violence towards Pre-Hospital Emergency Care Personnel: A Questionnaire Survey in Iran</p> <p>Hamidreza Aghababaeian Department of Nursing, Dezful University of Medical Sciences, Dezful, Iran hamidrezaaghababaeian@yahoo.com HAMIDAGHABABAEIAN@gmail.com</p> <p>Mehrdad Maghami Department of Nursing, Dezful University of Medical Sciences, Dezful, Iran</p> <p>Ladan Araghi Ahvazi Department of Nursing, Dezful University of Medical Sciences, Dezful, Iran</p> <p>Ehsan Bahrampor Department of Nursing, Dezful University of Medical Sciences, Dezful, Iran</p> <p>Abstract Background: International studies on workplace violence against pre-hospital personnel have mainly reported that emergency medical personnel experience concerning levels of workplace violence. The current study evaluated workplace violence against Iranian pre-hospital emergency personnel. Method: This cross-sectional study was conducted with 144 Iranian pre-hospital emergency personnel to evaluate workplace violence against them. Data was gathered through a 6-part</p>

	<p>questionnaire which included demographic properties, reports of physical and Psychological violence (include verbal, cultural or racial, sexual abuse), reaction to the violence, and reasons for the violence. Then data was analyzed with SPSS software (ver. 18).Result: In the 12 months prior to the study, 34.7% of participants were exposed to physical violence, 67% verbal and 20% experienced cultural or racial abuse. Additionally, while no sexual abuse was recorded, There was a strong correlation between physical violence and verbal abuse ($p=0.0001$). significant statistical relationships existed between shifts worked and the prevalence of violence ($P = 0.001$, respectively) and The difference between the mission place and the prevalence of violence was significant ($p = 0.01$) Also, Most perpetrators of violence against pre-hospital emergency personnel were male ($P = 0.001$).The most prevalent reason for violence, according to personnel, was people's lack of knowledge of pre-hospital emergency staff duties. The most common reaction to violence was to invite the attacker to relax. In addition, no regulations are in place nor have there been any educational courses made available to pre-hospital personnel in the past. Conclusion: Based on the study results, it is recommended that Educational courses be conducted to increase general knowledge of emergency personnel's duties and to improve the personnel's knowledge on how to prevent and/or counter violence. Keywords: workplace violence, physical violence, Psychological violence, Pre-hospital emergency care, emergency medical services</p>
 <p>Magdalena Potempa GIC16062051</p>	<p>Assessment of dietary habits and level of knowledge about principles of nutrition among parents of children attending Primary Schools in the area of Silesian and Opole Voivodeship (Europe, Poland)</p> <p>Magdalena Potempa Student Research Cycle at the Chair of Patophysiology and Endocrinology, School of Medicine with the Division of Dentistry in Zabrze, Medical University of Silesia, Poland magdalenapotempa@o2.pl</p> <p>Pawel Jonczyk Student Research Cycle at the Chair of Patophysiology and Endocrinology, School of Medicine with the Division of Dentistry in Zabrze, Medical University of Silesia, Poland pawel_jonczyk@o2.pl</p> <p>Michal Janerka Student Research Cycle at the Chair of Patophysiology and Endocrinology, School of Medicine with the Division of Dentistry in Zabrze, Medical University of Silesia, Poland michal.n.janerka@gmail.com</p> <p>Abstract</p> <p>Proper rules of dietary habits should be present in most of households and known by every adult people, particularly among parents raising their children and educating them how to eat healthy. Regular nutritional habits are an elementary factor to achieve good growth and human health. Our main assumption of this research was to determinate through anonymous questionnaire the level of knowledge of proper nutritional habits among parents of children attending some primary Schools in Poland (Silesian and Opole Voivodeship). This research is a follow-up of our previous study, which were focused on the assessment of dietary</p>

	<p>habits among children going to Primary Schools (in the age od 6-13 years old). Our last study consisted of nearly 1000 respondents living in rural and urban areas. Th e results ware alarming – approximately 20% of all studied children have overweight and the same percent revealed obesity. Proper body mass was shown only among 40% of populated study group. These findings persuaded us to go ahead and broaden this results. We want to know, which factors determine this disturbances most. Thnaks to our present resarch we would have a possibility of a wider analysis of the thema connected with diet. We could analyse the results looking at the nutritional principles having at family home – the most important factor in creating children dietary habits. Our results of present study are still in progress. We alread have about 1000 questionnaires sent to the parents and now we are preparing the results. We trurly hope that the esearch will be interesting and could improve the knowledge about society orientation about nutrition. Key words: proper dietary habits, knowledge, awareness, parents of children</p>
 <p>Madoui Bachir El Mouaz GIC16062052</p>	<p>Ecological And Systematic Study Of Fleas Wildlife And Their Impact On Health In The North-East Of Algeria</p> <p>Madoui Bachir El Mouaz Laboratory "Ecology of terrestrial and aquatic Systems "Badji Mokhtar Annaba University" madoui_mouaz@yahoo.fr madoui.mouaz@yahoo.fcom</p> <p>Ali Bouattour Pasteur institute Tunis of Tunisia</p> <p>Bouslama Zihad Laboratory "Ecology of terrestrial and aquatic Systems "Badji Mokhtar Annaba University"</p> <p>Abstract Parasites have been studied for a long time, most of the knowledge concerning parasites of ecological interest, medical or veterinarian. So despite their ubiquity in the living world, the role of parasitic infections in natural populations is still poorly controlled. Our study was conducted during two-year period, between January 2010 and December 2011 in the North-eastern of Algeria. The objective of this study is on the one hand, to study the characterization and population dynamics of fleas parasitizing wild and domestic fauna of the region and also detect different pathogens present in the fleas to evaluate the risk of transmission of these agents by using molecular biology techniques (DNA extraction, PCR, sequencing) for the detection of Bartonella spp and Rickettsia spp. Key words: Fleas, siphonaptera, parasite, pathogenic agents, PCR, Bartonella spp, Rickettsia spp.</p>



Hosein Rohani
GIC16062053

Development and reliability testing of a health action process approach inventory for healthful diet among type 2 diabetes patients

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Abstract

Introduction: dietary management of Type 2 diabetes among patients is one way to prevent or delay the long term effect of the condition. Research is urgently required in developing evidence-based behavioral interventions for improving dietary behavior of diabetes patients. One model that has been used to understand the mechanisms underlying healthful diet is the health action process approach (HAPA). The purpose of this study was to adapt and pilot-test a HAPA-based inventory that reliably captures salient, modifiable healthful diet determinants for individuals with diabetes.

Methods: Initially, 8 outpatients with diabetes reviewed the inventory and provided verbal feedback regarding comprehension, item relevance, and potential new content. Then an expert panel evaluated the items by assessing content analysis. Next exploratory factor analysis (EFA) was performed to indicate the scale constructs. In addition criterion validity was assessed by pearson correlation. Consequently reliability analyses including internal consistency and test-retest analysis were carried out. **Result:** In all a sample of 121 diabetes patients participated in the study. A seven-factor solution emerged as a result of an exploratory factor analysis explaining 81.14% of the variance observed. Preliminary assessment of criterion validity of the HAPA inventory showed significant, large-sized correlations between behavioral intentions and both outcome expectancies and action self-efficacy, and small to moderate correlations between self-reported nutritional style and the volitional constructs of the HAPA model. Additional analyses indicated satisfactory results for internal consistency (Cronbach's alpha ranging from 0.65 to 0.95) and intraclass correlation coefficients (ranging from 0.71 to 0.92). **Conclusion:** Scales for measuring HAPA variables were valid and reliable for use with T2DM patients. Further examination with minority persons is warranted.


Key words: health behavior, behavioral research, measurement, diabetes mellitus

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Invasive fungal infections diagnosed at laboratory of medical parasitology and mycology of the chu of Annaba. Algeria.

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<p>Noureddine Boulenouar GIC16062055</p>	<p style="text-align: center;">Effect of Punica Granatum Fruit Rind Extracts on Fusariumoxysporum f. sp. Albedinis</p> <p style="text-align: center;">Noureddine Boulenouar Biological Sciences Department, Science Institute, NourBachir University, El-Bayadh, 08000, Algeria Phytochemistry and Organic Synthesis Laboratory, Tahri Mohamed University, Bechar, 08000, Algeria noureddine.boulenouar@gmail.com</p> <p style="text-align: center;">Nasser Belboukhari Bioactive Molecules and Chiral Separation Laboratory, Tahri Mohamed University, Bechar, 08000, Algeria.</p>

	<p>Abdelkrim Cheriti Phytochemistry and Organic Synthesis Laboratory, Tahri Mohamed University, Bechar, 08000, Algeria</p> <p>Abderrazak Marouf Biological Sciences Department, Science Institute, Salhi Ahmed University Center, Naama, 45000, Algeria</p> <p>Abstract</p> <p>The date palm “Phoenix dactylifera” represents the principal components for the saharian ecosystems. It gives for these desertic regions the microclimates to cultivate vegetables and fruits. The date palm has numerous biotic and abiotic enemies. The most dangerous enemy, especially in South-West of Algeria and Morocco, is Bayoud disease caused by the fungus “Fusarium oxysporum f. sp. albedinis”(Foa). Till know, there is no efficient treatment for this disease. Punica granatum is known for its benefits. Its fruits rind contains many secondary metabolites with proven physiological effects. We focus in this study to evaluate the effect of four extracts (methanol, ethyl acetate, dichloromethane, hexane) on the radial growth of Foa. The antifungal tests were realized with two concentrations: 0.05 and 0.1% (w/v) using the radial growth method. The antifungal tests had demonstrated that the best effect was presented by dichloromethane extract (0.05 and 0.1%) with radial growth decrease (13.70% and 29.94%), respectively. The important effect of dichloromethane extract reflects that this extract contains compounds that can be used for the treatment of Bayoud disease.</p> <p>Key words: Phoenix dactylifera, Bayoud disease, Punica granatum, antifungal, radial growth</p>
 <p>Hasan Shahbazi GIC16062056</p>	<p>A survey on Relationship of Spirituality with the Perception of suffering and Quality of Life in Patients with Type 2 diabetes</p> <p>Hasan Shahbazi PhD Student, Department of Health Education, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, Iran sh.hasan333@gmail.com</p> <p>Ghajari H M.Sc. Department of Health Education, Faculty of Health, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.</p> <p>Shakerinejad Gh Associate Professor of Health Education, Jihad-E-Daneshgahi Khuzestan, Ahvaz, Iran.</p> <p>Ghofranipour F Professor, Department of Health Education, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, Iran.</p> <p>Lotfizadeh M Assistant Professor, Department of Community Health, Shahrekord University of Medical Sciences, Shahrekord, Iran</p> <p>Abstract</p>

Background: Spirituality can be an important source of coping with the disease, reduce feelings of suffering and improving quality of life in patients with chronic diseases. **Objectives:** The purpose of this study was to determine the Relationship of Spirituality with the Perception of suffering and Quality of Life in Patients with Type 2 diabetes. **Materials and methods:** This was a descriptive-correlation study. Participants were 145 patients with type 2 diabetes of rural health clinics and valiasr hospital in khorramshahr city which were selected via stratified random and available sampling methods. Data collection tools were version of 29-item of the spiritual questionnaire (Parsian and Dunning), Experience and Perception of Suffering Questionnaire (Schulz) and version of 26-item of the Quality of Life Questionnaire (World Health Organization). Data were analyzed with using of SPSS version 16 software and by using Pearson's correlation, T-test, ANOVA, Post Hoc and Stepwise Regression analytical statistics. **Results:** The spirituality average scores were 79/41±15/82, Perception of Suffering average scores 54/89±2/14 and Quality of Life 74/44±1/65. There was a significant negative relationship between spirituality and feeling of suffering ($p<0.05$) and significant positive relationship between spirituality and quality of life ($p<0.0001$). **Conclusion:** A strong correlation between spirituality with quality of life and, Suffering in patients with type II diabetes, demonstrate the roles and responsibilities of healthcare providers, including physicians and nurses and patient's family in Meeting the varied spiritual and religious needs of patients Along with therapeutic actions. Paying attention to improve spiritual health also is important in education programs for these patients. **Keywords:** Spirituality, Suffering, Quality of Life, Type 2 diabetes.

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