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Yibing Hu, J Biotechnol Biomater 2017, 7:5 (Suppl)
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Sugar apoplastic transport in rice caryopsis during grain filling

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Using β-glucoronidase (GUS) and Green Fluorescent Protein (GFP) represented expression, CRISPR-associated gene editing, cross-fertilization and determination of sugar related physiological parameters in gene mutant lines and wild type plants, we aimed to investigate the function of sugar transporter OsSWEETs and OsSUTs in rice caryopsis development during grain filling. Currently, we demonstrated that OsSWEET11 play an essential role in sucrose release from maternal tissue to the maternal–filial interface. It might also induce sucrose release from the ovular vascular trace and cross cells of developing caryopsis. In addition, OsSWEET15, a homolog of OsSWEET11 in rice SWEET family, also play an important part in grain filling besides its prominent role in pollen development of rice. By contrast, the sucrose-proton symporters OsSUT1/2 which locate at the plasma membrane of cells adjacent to that of SWEETs located assume influx of sucrose from the apoplast in the caryopsis. It implies that SWEET and SUT together undertake efflux and influx of sucrose across the plasma membranes when the sugar traverses apoplastic space in developing caryopsis. These findings will hopefully elucidate the molecular mechanism of post-phloem sugar transport in rice caryopsis and facilitate the improvement of rice yield and quality by adjusting these gene's expression in the future.

Biography

Yibing Hu completed his Ph.D. in 2007, from Institute of Botany, Chinese Academy of Sciences. He is an associate professor of Nanjing Agricultural University with more than 20 papers in related journals.

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Tatsuki Kunoh et al., J Biotechnol Biomater 2017, 7:5 (Suppl)
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Green synthesis of gold nanoparticles coupled with nucleic acid oxidation

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So-called green synthesis of safe metal nanoparticles, especially gold nanoparticles (AuNPs), has increased in importance for medical and pharmaceutical applications. Thus, a variety of ecofriendly, energy- and cost-saving techniques have been developed. Here, we show that RNA prepared from Leptothrix (iron-oxidizing bacteria) cells can reduce Au(III) and spherical AuNPs eventually form when an aqueous solution of Au chloride ($HAuCl_4$ solution) is added under ambient conditions. RNA and DNA of other organismal origins have the same ability. Of the nucleosides and nucleobases, only guanosine and guanine can form AuNPs. The DNA moiety, 2'-deoxyguanosine (dG), used as a reference material, forms AuNPs when mixed with $HAuCl_4$ solution, but 8-hydroxy-2'-deoxyguanosine (8-OHdG) does not, indicating that AuNP-formation evidently depends on the reduction potential of the guanine moiety, not the sugar moiety. This finding is the first demonstration that spherical AuNPs of ca. 5 nm diameter can be obtained by simply adding guanine to $HAuCl_4$ solution at ambient temperature and no other chemicals or physical treatments are needed.

Biography

Tatsuki Kunoh is presently an Associate Professor of Graduate School of Natural Science and Technology, Okayama University, Japan. He received his BSc in Biotechnology, MSc and PhD degrees in yeast cell biology at Osaka University. He accumulated his experiences in Molecular Biology and Biochemistry in Albert Einstein College of Medicine, USA and other Universities, Japan. Currently, he is a member of the Government-granted project-Toward creating innovative applications to harness the novel functions of nano-scaled iron oxides of microbial origin in CREST supported by JST and his research focuses on the biomaterial science.

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Byungchan Ahn et al., J Biotechnol Biomater 2017, 7:5 (Suppl)
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Repetitive DNA unwinding mode of the *HIM-6* RecQ helicase

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Bloom's syndrome (BS) is caused by mutations in the BLM gene encoding the BLM helicase. The BLM protein contains a conserved RecQ helicase domain and unwinds various DNA substrates including replication forks. Cells from BS patients lack the BLM protein show defects in the response to replicative stress and contain a multitude of chromosomal aberrations. A BLM homolog (*HIM-6*) has been identified in *C. elegans* based on its close homology to human BLM. Here, we used single-molecule FRET technology to observe DNA unwinding in real time. Our results show that the *HIM-6* repetitively unwound a long forked DNA depending on ATP concentration and resolved flap and D-loop DNA, all of which are intermediates in DNA repair. Also, we found that *HIM-6* unwound at most 25 base pairs of duplex DNA in a speed of 28 nucleotides per second before returning. Besides, repetitive unwinding mode of *HIM-6* was changed to unidirectional unwinding in the presence of RPA, indicating that its unwinding mode can be modulated by partner proteins *in vivo*. This study can be used to search proteins which would modulate a *HIM-6* unwinding mode on different DNA structures such as Holliday junction and G4-quadruplex.

Biography

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Yoon-Suk Joo et al., J Biotechnol Biomater 2017, 7:5 (Suppl)
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Preparation of biocompatible shape-memory polymers using polycaprolactone and isosorbide based polyurethane blends for biomedical application

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In this study, biocompatible and biodegradable polyurethane (PU) and polycaprolactone (PCL) were blended to enhance shape memory and mechanical properties. PCL (M.W: 80,000) was used as a hard segment and PU synthesized from isosorbide, which is non-toxic and enzyme decomposition, was used as a soft segment. The obtained PU/PCL blends with weight ratios of (3/7), (5/5) and (7/3) were investigated for their thermal properties, mechanical properties and shape memory behavior. Thermal properties of blends were investigated using differential scanning calorimetry (DSC), thermal gracimetric analysis (TGA) and shape memory properties were measured using dynamic mechanical analysis (DMA). The biodegradation test performed at 37 °C in phosphate buffered solution showed a mass loss of 2-4% for the obtained PU/PCL blends after 6 weeks. Finally, MC3T3-E1 cells cultured on PU/PCL blends showed high biocompatibility.

Biography

Yoon-Suk Joo is currently pursuing Master's degree at Dankook University. His research interest is in polymers used as biomaterials and has biocompatible polyurethane synthesis.

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Suk-Min Hong et al., J Biotechnol Biomater 2017, 7:5 (Suppl)
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Preparation of high elastic polyurethanes based on polycaprolactone diol, 1,6-hexamethylene diisocyanate, isosorbide derivative and their biocompatible properties

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In this study, various chain lengths of 1' isosorbide (IC 22, IC 32, IC 52, IC 102, IC 29, IC 39, IC 59, IC 89) was prepared from isosorbide and ethylene oxide or propylene oxide in the presence of K_2CO_3. The successful synthesis of 1' isosorbide (IC 22, IC 32, IC 52, IC 102, IC 29, IC 39, IC 59, IC 89) was confirmed by ^{1}H-nuclear magnetic resonance (^{1}H-NMR). Bio-based high elastic polyurethanes were made using polycaprolactone diol, various chain lengths of 1' isosorbide and hexamethylene diisocyanate. The polyurethanes were produced by one-shot bulk polymerization without catalyst. The successful synthesis of the polyurethanes was confirmed by FT-IR and GPC. The thermal and mechanical properties were characterized by thermogravimetric analyzer (TGA), differential scanning calorimetry (DSC). The mechanical properties were measured using universal testing machine (UTM). Degradation test was performed using PBS solution and biocompatibilities of PUs were tested using C2C12 for biomedical applications.

Biography

Suk Min Hong is a Doctoral student in the Department of Nanobiomedical at Dankook University. His research interests are in polyurethanes, bio-polyurethanes, isosobides and natural polymers.

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Hyuck-Jin Kwon et al., J Biotechnol Biomater 2017, 7:5 (Suppl)
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Anti-fouling polyimide/Ag nanofiber membranes prepared by using silver (I) carbamate

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Polyimide/Ag nanofiber membranes were made by electrospinning poly (amic acid) containing a dash of silver (I) carbamate, followed by simply thermal reduction and imidization of poly (amic acid). Poly (amic acid) solutions were prepared from 3,3',4,4'-benzophenone tetracarboxylic dianhydride (BTDA) and 4,4'-oxydianiline (ODA) into dimethylformamide (DMF). Through thermal curing cycle, the silver-doped polyimide nanofiber membranes progress silver reduction. These process leads to high thermal stability, abrasion resistant and antifouling property. The polyimide/Ag nanofiber membranes were characterized by using scanning electron microscopy (SEM), X-ray diffraction (XRD), energy dispersive X-ray spectroscopy (EDS), UV-Vis, FT-IR and thermo gravimetric analysis (TGA).

Biography

Hyuck-Jin Kwon is currently pursuing his Master's degree from the College of Pharmacy at Dankook University and majoring in bio-nano fields. His research interest is in a wide range of nanomaterials and research.

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Kyung-Hyeon Yoo et al., J Biotechnol Biomater 2017, 7:5 (Suppl)
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Si- and Fe-substituted beta-tricalcium phosphate: Synthesis, characterization and *in vitro* properties

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The aim of this study was to investigate the effects of Si and Fe ions in β-TCP on the physical and chemical properties. Beta-tricalcium phosphate (β-TCP) has been known as biodegradable material for temporary medical devices. Enhancing the strength and osteoconduction properties of β-TCP is important for their applications. To modify mechanical properties and *in vitro* behavior, Si and Fe ions were substituted in β-TCP. The Si- and Fe- substituted β-TCP powder were synthesized by co-precipitation method. Crystal structure and thermal properties of Si- and Fe-substituted β-TCP were investigated by using X-ray diffraction combined with Rietveld refinement analysis and differential thermal analysis (DSC) to compare the effects of substituted elements on β-TCP. Moreover, MTT assay, alkaline phosphate (ALP) staining confirmed the cytotoxicity, cell differentiation and cell proliferation.

Biography

Kyung-Hyeon Yoo has completed her BS from Pusan National University.

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Sung-Min An, J Biotechnol Biomater 2017, 7:5 (Suppl)
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Effect of transdermal delivery of gelatins on the partial obesity in high fat diet induced obese rats

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Partial obesity is a constitutional disorder of fatty tissue deposit. It is not just a cosmetic problem due to the development of the metabolic syndromes. In the present study, we developed the new method to treat partial obesity by attachment of microneedles (MNs). In addition, the effects of gelatin on fat metabolism in adipocytes are addressed. Firstly, we applied MN to high fat diet (HFD) induced obese rats and examined rat amount of subcutaneous adipose tissue (SAT) by histological analysis and measured by micro-computed tomography (μCT) scanner. Also, expression of genes-associated with lipid metabolism is analyzed in isolated adipocytes and SAT using Q-PCR and western blotting experiments. In addition, lipolysis was measured by determining the amount of glycerol released from adipocyte. In our results, histological analysis demonstrated that the amount of SAT stored in adipocytes was reduced by MN. For the next results, we found that administration of gelatin and MN suppressed the expression levels of lipid metabolism-associated genes in both the isolated adipocytes and rat SAT. In addition, glycerol release levels which is an indication of lipolysis, was also increased in isolated adipocytes. These findings suggest that MN induces lipolysis, leading to the release of glycerol and regulates lipid metabolism and fat deposition in the AT, thereby reduces SAT in HFD induced obese rats. Our results suggest that the alteration of lipid metabolism and fat deposition through the application of MN may help to reduce SAT.

Biography

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Ye Young Shin, J Biotechnol Biomater 2017, 7:5 (Suppl)
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Pregnenolone as a new hormone therapy for female diseases targeting ERβ

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Many steroid hormones such as estrogen (E2) bind their receptors to regulate biological processes. Pregnenolone (PG) is the precursor from almost all of the other steroid hormones and is used for skin disorders and reproductive complications. However, mechanism and function of PG are not well established in the uterus. In this study, we examined the effects of PG on the activation of estrogen receptor (ER) in uterus. First, we performed computational structure prediction of PG-ER complexes and PG showed high affinity with ERβ. To study the mechanism of PG directly, Ishikawa cells were transfected with ERE-luciferase plasmid and isoforms of ERs. ERE-luciferase activity induced by PG was similar with E2 and showed high activity with ERβ plasmid. Also, the expression of ERα target genes in cells treated with PG was reduced compared to E2. In immature rat, PG negatively regulated the expression of ERβ in the uterus. These findings suggest that PG stimulates ERβ-mediated signaling in the uterus. Activation of ERβ by PG may help to overcome ERα-related female reproductive diseases such as endometriosis, breast cancer and ovarian cancer.

Biography

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Min-Jin Kim et al., J Biotechnol Biomater 2017, 7:5 (Suppl)
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Anti-inflammatory activity of *Scirpus tabernaemontani* on LPS-stimulated RAW 264.7 macrophage cells

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The stem of *Scirpus tabernaemontani*, one of the aquatic plants, has been reported to have been used as a medicinal herb, but lacks a scientific basis. Also, it is unknown whether *Scirpus tabernaemontani* extract (STE) modulate the inflammatory response in RAW 264.7 macrophage cells. The present study was therefore designed to elucidate the pharmacological and biological effects of STE on the production of pro-inflammatory cytokines and inflammatory mediators in macrophages. The results indicate that STE is an effective inhibitor of LPS-induced NO and PGE_2 production in RAW264.7 cells. And STE could effectively inhibit the LPS-induced production of pro-inflammatory cytokines such as IL-6, TNF-α and IL-1β in a concentration-dependent manner. These results suggest that STE attenuated the LPS-induced release of pro-inflammatory mediators and cytokines probably *via* suppressing the activation of MAPK (JNK, ERK and p38) and NF-κB signaling. To assess the suitability of STE for cosmetic applications, we also performed MTT assays on HaCaT keratinocytes. STE did not display any cytotoxicity in these assays. In conclusion, this study not only provides more evidence that STE exerts anti-inflammatory activity in macrophage cells, but also sheds light on the potential use of STE as an attractive candidate for treatment of various inflammation-associate disease.

Biography

Min-Jin Kim has majored in Molecular Cell Biology and has been studying biologically active materials using primarily natural materials. Currently, she is a member of the Nakdonggang National Institute of Biological Resources focusing on freshwater biological resources and is conducting research on the validity, composition analysis and practical application of freshwater biological resources for exploration, conservation and development.

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Data access and international transfer of biobanks samples – Ethical and societal perpective

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Background: Biobanks are a new scientific tool for biomedical research and currently it can be observed the rapid development of biobanking entities. One of the most common problems associated with biobanking for research purpose is ensuring the right to privacy which is connected with the effective protection of the stored samples, ensuring data confidentiality and creating appropriate procedures of data access and transfer of biological material. The aim of the research was to examine social attitudes towards biobanking, access and sharing of data and samples stored in biobanks.

Material and Method: The survey was conducted on a representative group of 600 Polish respondents through direct interviews (PAPI).

Results and conclusions: The knowledge on the biobanks for research purposes is relatively low, but social attitudes are not negative. The level of trust depends on the type of the biobanking institution, and the lower trust is given to commercial biobanks. Majority of the respondents do not accept transfer data and samples to foreign and commercial entities as well as using them for non-scientific purposes. Respondents who were willing to donate samples to biobanks present a more liberal attitude towards data access and international transfer of human tissues samples (in comparison to general population). It is important to develop a model of data/samples transfer agreement and a model of informed consent for data access and transfer of samples in order to protect the donors' rights and responsible sharing of data and samples.

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Seed-bank information systems: An international perspective

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It is conceivable that humans can live without animals but it is inconceivable that animals and humans can live without plants. Unfortunately, seeds are getting extinct caused by varied reasons such as climate change, radio activation, endangering in the wrong environment, droughts, volcanic eruptions, poor agricultural practices etc. As a panacea, seed banks have been established for prosperity and posterity. A seed bank preserves seeds as a repository for future planting in case seed reserves elsewhere are destroyed. It is similar to gene bank to guard biodiversity. Storing seeds also guards against catastrophic events like natural disasters, outbreaks of disease or war. Over the years several seed banks have been established. The best example is Svalbard Global Seed Vault, a secure seed bank located on the Norwegian island of Spitsbergen about 810 miles from the North Pole. The Global Crop Diversity Trust, the Consultative Group on International Agricultural Research (CGIAR) and the Food and Agriculture Organization of the United Nations played vital role in establishing this underground vault. This Doomsday vault is a global backup system for the planet's plant resources. There are currently about 1,400 seed banks worldwide in various countries for specific crops such as cassava, forages, beans, cowpea, soybean, yam, rice, potatoes, peanuts etc. It is worth noting that of the more than one million seed samples distributed, seed contributions from CGIAR gene banks have helped agricultural recovery after conflict and natural disasters in many countries. This paper presents an overview of major seed banks worldwide, differentiates these banks from commercial seed banks, discusses typology of these banks, and outlines strengths and weaknesses of community seed banks in developing countries.

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Pharmacoinformatic approach for discovery of better drug combination with currently available drug against Leishmaniasis

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Hypoxanthine phosphoribosyl transferase (HGPRT; EC 2.4.2.8) is a central enzyme in the purine recycling pathway of all protozoan parasites. Protozoan parasites cannot synthesize purine bases (DNA/RNA) which is essential for survival as lack of de novo pathway. Thus, its good target for drug design and discovery as inhibition leads to cessation of replication. PRTase (transferase enzyme) has common PRTase type-I folding pattern domain for its activities. Genomic studies revealed the sequence pattern and identified highly conserved residues catalyzed the reaction in protozoan parasites. A recombinant protein has 24 kDa molecular mass (rLdHGPRT) was cloned, expressed and purified for testing of guanosine monophosphate (GMP) analogous compounds *in vitro* by spectroscopically to the rLdHGPRT, Lysates protein and MTT assay on *Leishmania donovani*. The predicted inhibitors of different libraries were screen into FlexX. The reported inhibitors were tested *in vitro*. The 2'deoxyguanosine 5' diphosphate (DGD) (IC_{50} value 12.5 µM) is two times more effective when compared to guanosine-5' diphosphate sodium(GD). Interestingly, LdHGPRT complex has showed stable after 24ns in molecular dynamics simulation with interacting amino acids are Glu125, Ile127, Lys87 and Val186. QSAR studies revealed the correlation between predicted and experimental values has shown R_2=0.985. Concludes that inversely proportional to their docked score with activities. It is predicted that patients suffering from both HIV and visceral leishmaniasis (VL) may benefit if they are treated with acyclovir in conjunction with first-line anti-leishmanial therapies such as Miltefosine and AmBisome.

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Role of biotechnology in cancer diagnosis and control

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Despite the huge advances in cancer diagnosis and treatment, it is still the second leading cause of death in the world. Recent advances in medical biotechnology have increased researcher's knowledge of molecular events of Cancer and have created new hopes in early diagnosis and treatment of cancer. Changes in the genome and proteome of the cells disturb the normal cellular control mechanisms. Using biotechnology methods these molecular errors can be determined and appropriate treatments can be selected. In this paper, the biotechnology techniques are explained and the advantages of each of them in the diagnosis and treatment of cancer are discussed. These techniques include gene mapping, *in situ* hybridization (ISH), microarray analysis and cell culture. ISH is a method for detecting RNA and DNA inside tissues and cells using labeled probes. This method is useful in identifying genes related to the incidence and progress of cancer. Microarray technology provides the possibility of examining the tumor behavior in the living tissue and drug resistance of the patient. Cell culture is used to investigate the effects of genes involved in the incidence of cancer on cultured cells. Gene mapping is a method for determining the location of genetic markers on the related genome. This method is also used in early diagnosis of cancer and identifying high risk cancer patients. Having knowledge about molecular events of cancer can be very helpful in choosing an effective treatment and its results can be more effective and accurate than conventional methods of cancer detection and treatment.

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Effect of solvent system on the extraction of phenolic compounds and antioxidant capacity of *Gloriosa superb* L.

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Gloriosa superba Linn. (Family: Colchicaceae), commonly known as Malabar glory lily; Kalihari; Glory lily is grown in semi-shade open areas. The species is distributed throughout temperate zone of India, Burma, Malaysia, SriLanka at an altitude of 2100 m above sea level. In India, it is found in southern parts to the mid hill zones of Himachal Pradesh, Jammu Kashmir, Uttar Pradesh and Uttarakhand. The species is brilliant wavy-edged yellow and red flowers. The plants have reported richest sources of colchicine and gloriosine. Recently, colchicine is reported prime importance for its possible use in cancer treatment. The species has been reported to use in the Indian and Chinese system of medicine for its analgesic, anti-inflammatory, antimicrobial and antitumor properties. In addition, it is used in the treatment of snake bite, skin diseases, fever, inflammation and respiratory disorders by local communities. The rhizome and its paste is used for the treatment of colic, paralysis, chronic ulcer, bruises, sprains and considered useful in promoting labor and expulsion of placenta. The essential oil of the species is used in cosmetic industries. Therefore, rhizome portion of *Gloriosa superba* was sampled and analyzed for polyphenolic and antioxidant capacity in different solvent system and for harnessing maximum potential. Results revealed a significant variation ($p<0.05$) in analyzed parameters among solvent systems. Total phenolic content ranged between 0.54-1.35 mg GAE/g; flavonoid 0.66-185 mg QE/g; flavonol 0.33-1.03 mg QE/g and tannins 1.08-3.47 mg TAE/g dry weight and maximum exhibited in methanolic solvent. Similarly, antioxidant activities were determined *in vitro* assays varied significantly (ABTS 2.67-4.09; NO 2.26-4.05; DPPH 1.24-4.58 and OH 0.14-041 mM AAE/100 g dry weight). Among different solvent types, methanolic extract was recorded best for harnessing maximum antioxidant potential; however, highest reducing antioxidant power (0.54 mM AAE/100 g dry weight) was found in acetone. Total phenolic content showed significant ($p<0.05$) positive relationship with flavonoid ($r=0.905$); tannin ($r=0.914$) and antioxidant activity (ABTS-$r=0.967$; NO-$r=0.994$; $p<0.01$; OH-$r=0.927$; $p<0.05$, respectively). Likewise, flavonol showed strong correlation ($p<0.01$) with tannin ($r=0.978$) and hydroxyl radical scavenging antioxidant activity ($r=0.971$). Tannin positively correlated ($p<0.05$) with antioxidant activity (ABTS-$r=0.892$; NO-$r=0.914$; OH-$r=0.971$; $p<0.01$, respectively). The results of the present study are indicative of the fact that the species possess polyphenolic content and antioxidant activity and therefore, can be a source of natural antioxidant. Solvents with moderate polarity such as methanol and acetone showed higher polyphenolics and antioxidant activity, therefore, can be utilized for harnessing maximum polyphenolics content.

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Utilization of yeast industry wastewater (YIW) as a fermentation medium for the production of bioethanol

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The utilization of yeast industry waste water (YIW) to produce ethanol by *Saccharomyces cerevisiae* was studied. Ethanol production was investigated in batch liquid culture at different modes of operations after optimizing process parameters. The maximum ethanol production after 48 hours was 41.86 g/l. The yeast growth ceased after 48 hours of fermentation as CFU was declined and the sugar concentration was accumulated. In sequential production of ethanol in two stages bioreactor system, the maximum ethanol production from the first stage was 42.87 g/l while the maximum ethanol production from the second stage without sugar addition was 39.86 g/l. This scheme of production lasted for 10 days with a steady productivity accomplishment. In conclusion, YIW is a promising substrate for the bio-ethanol production, with additional benefits of its use regarding environmental and economic aspects.

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kLa gas-liquid mass transfer coefficient simulation using CFD in helical ribbon impeller

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In the present study a CFD simulation (Computational Fluid Dynamics) applied to non-newtonian fluids was developed in order to characterize the gas-liquid mass transfer in a 10 L bioreactor equipped with a helical ribborn impeller. The kLa mass transfer coefficient was estimated Based on CFD results. The operating conditions chosen were defined by typical settings used for culturing fungi organism. Turbulence, rotating flow, bubbles breakage and coalescence were simulated by using the k-e, MRF (Multiple Reference Frame) and PBM approaches, respectively. The numerical results from different operational conditions are compared by evaluating its effect on kLa. Interested by these simulated results CFD simulations are qualified as a very promising tool not only for predicting gas-liquid hydrodynamics but also for finding design requirements that must be implemented to optimize an aerobic bioprocessing useful for non-newtonian applications which are characterized by the constrain of achieving relatively high stirring conditions and avoiding cellular damage due to hydrodynamic conditions.

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Complete chloroplast genome sequences of cacao (*Theobroma cacao* L.) useful for phylogenetic analysis and DNA barcoding

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Cacao (*Theobroma cacao* L.) is known as main material for chocolate industry worldwide. Indonesia is recognized as the third largest cacao producer in the world with the total production in 2014 reached 709.331 tonnes. In order to understand cacao genomic, we conducted chloroplast genome sequencing generated by an Illumina Miseq platform. Chloroplast plays a crucial role in sustaining life on earth. The availability of chloroplast sequences could enhanced our understanding of chloroplast biology, conservation, diversity, and the genetic basis by which chloroplast transgenes can be engineered to enhance plant agronomic traits. The size of chloroplast genomes of cacao ranged from 160,619 bp to 160,649 bp. Cacao chloroplast sequences encoded 114 genes, consisted of 80 protein coding genes, 30 tRNA genes and four rRNAs genes. Based on chloroplast sequences, we conducted phylogenetic analysis of 12 cacao genotypes that successfully separated bulk and fine types. The dendrogram resulted in this study proved the utility of chloroplast sequences for phylogenetic analysis. Some variations demonstrated through the number and structure of repetitive sequence in cacao chloroplast sequences. Identification of repetitive sequence by REPuter program exhibited that cacao possessed 18 repeats and three repeat structures (forward, palindrome and reverse). In addition, we have developed three indel-based barcode markers which were designed based on the polymorphic regions of *trnK-UUU-rps16, rps16* intron and *trnA-UGC-rrn23*. The result obtained herein would give new insight regarding chloroplast genome structure in cacao, which would be useful to resolve phylogenetic relationships and development of DNA barcode markers.

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Alcohol exposure suppresses neural crest cells generation and differentiation during early chick embryo

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It is now known that excess alcohol consumption during pregnancy can cause fetal alcohol syndrome (FAS) in which several characteristic craniofacial abnormalities are often visible. However, the molecular mechanisms of how excess ethanol exposure affecting cranial neural crest cells (CNCCs), the progenitor cells of the cranial skeleton, is still not clear. In the study, we investigated the effects of ethanol exposure on CNCCs migration both in early chick embryo and *in vitro* explant culture. First of all, we demonstrated that ethanol treatment caused alizarin red-stained craniofacial developmental defects including parietal defect. Second, the immunofluorescent staining with neural crest special markers indicated that CNCCs generation was inhibited by ethanol exposure. And, double immunofluorescent staining's (Ap-2α/PHIS3, HNK1/BrdU and AP-2α/c-caspase3) revealed that ethanol exposure inhibited CNCCs proliferation and increased apoptosis. In addition, it inhibited NCCs production by repressing the expression level of key transcription factors which regulate neural crest development by altering expression of Epithelial-mesenchymal transition (EMT)-related adhesion molecules in the developing neural crests. In sum, we have provided experimental evidence that excess ethanol exposure during embryogenesis disrupts CNCCs survival, EMT and migration, which in turn causes defective cranial bone development.

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Genome sequencing, assembly, annotation and analysis of methicillin-resistance of *Staphylococcus aureus* strain SO-1977 reveals genes responsible for antibiotic resistance

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Background: *Staphylococcus aureus* is a ubiquitous bacterial pathogen and a leading cause of morbidity and mortality worldwide. The epidemiology of infections is influenced by rapid and widespread emergence of multidrug-resistant methicillin-resistant *S. aureus* (MRSA). *Staphylococcus aureus* (MRSA) is a major cause of nosocomial infection in Sudan. The relatively small genome size and rapid evolution of antibiotic resistance genes in the species have been drawing an increasing attention in public health. To extend our understanding of the species and use the genome data for comparative genomic studies, we sequenced the whole genome of Methicillin-resistant of *Staphylococcus aureus* strain SO-1977 isolated from Sudan.

Methods: Genomic DNA was sequenced using the Illumina MiSeq. The complete genome was annotated and the presence of antimicrobial resistance genes was identified.

Result: The draft genome of MRSA strain SO-1977 consisted of 2,827,644 bp with a G+C content of 32.8 %, 2,629 predicted coding sequences (CDSs) and 55 RNAs. The final assembly contained 151 contigs of N50 contig length of 62,783 bp and the largest contig assembled measured was 146,886 bp. Comparative studies of the MRSA strain SO-1977 and MRSA 252 through RAST server showed a total of 20 were annotated to antibiotic resistance genes. Interestingly, one gene related to methicillin resistance and four-genes related to Tetracycline resistance were found only in SO-1977 strain.

Conclusions: This study is the first to report on the whole genome sequence of a Sudanese MRSA isolate. Antibiotic resistance genes found in the genome indicate the presence of antibiotic resistance mechanism prior to the usage of antibiotics. The finding of this study would help to understand the evolution of resistance mechanism and dissemination of the resistance genes of MRSA

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Trichostatin A inhibits radiation induced lung epithelial mesenchymal transition (EMT) in lung adenocarcinoma cancer cells A549

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Radiotherapy is used to treat tumors of different origins and nature. Lung cancer patients significantly dependent on radiotherapy for treatment but often lead to side effects including pneumonitis and fibrosis. It is interesting that radiation induces TGF-ß1 signaling and induces the epithelial-mesenchymal transition (EMT), is a process by which epithelial cells changes to mesenchymal cell by losing cell polarity, cell-cell adhesion and gains enhanced tumor progression capability. Our study investigated the inhibitory effect of Trichostatin A (TSA), a natural derivate isolated from genus *Streptomyces* of bacterial species, has been shown to inhibit TGF- ß1 signaling pathway, upon radiation induced lung EMT and we tried to understand the molecular mechanism using lung cancer cells A549 as a model of EMT study. The cancer cells were irradiated at 8Gy of X-ray using LINAC. The cells were divided into five treatment group untreated control (C), radiation alone (R), radiation combined with TSA (R+T) and TSA alone. Radiation induced lung EMT in A549 cells were evidenced by decreased expression of epithelial markers E-cadherin and increased expression of N-cadherin and vimentin. A marked increase in phosphor-Erk½ was observed within short span in western blot analysis. Snail protein-the master factor for EMT, which will translocate into nucleus was shown elevation after radiation treatment. Radiation group increased the migration of cancer cells whereas TSA treatment reduced the migration of cancer cells. In addition, TGF-ß1 signaling activates Smad signaling expression is elevated in radiation group and data is supported by the increased m-RNA expression of E-cadherin and snail genes. This effect was reversed by TSA treatment. In addition to this as supportive evidence we did docking which showed good interactions between snail and the TSA. Our report suggests that, TSA is effective in inhibiting TGF-ß1 pathway induced by radiotherapy.

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Biodiesel production from edible oil wastewater sludge with bioethanol using nano-magnetic catalysis

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Currently, most sludge from the wastewater treatment plants of edible oil factories is disposed to landfills, but landfill sites are finite and potential sources of environmental pollution. Production of biodiesel from wastewater sludge can contribute to energy production and waste minimization. However, conventional biodiesel production is energy and waste intensive. Generally, biodiesel is produced from the transesterification reaction of oils with alcohol (i.e. Methanol, ethanol) in the presence of a catalyst. Homogeneously catalyzed transesterification is the conventional approach for large scale production of biodiesel as reaction times are relatively short. Nevertheless, homogenous catalysis presents several challenges such as high probability of soap formation in the presence of water and free fatty acids and difficulty of separation and reusability. The current study aimed to reuse wastewater sludge from the edible oil industry as a novel feedstock for both monounsaturated fats and bioethanol for the production of biodiesel. Preliminary results have shown that the fatty acid profile of the oilseed wastewater sludge is favorable for biodiesel production with 48% (w/w) monounsaturated fats and that the residue left after the extraction of fats from the sludge contains sufficient fermentable sugars after steam explosion followed by an enzymatic hydrolysis for the successful production of bioethanol [29% (w/w)] using a commercial strain of *Saccharomyces cerevisiae*. A novel nano-magnetic catalyst was synthesized from mineral processing alkaline tailings, mainly containing dolomite originating from cupriferous ores using a modified sol-gel technique. Both the catalytic properties and reusability of the catalyst were investigated. A maximum biodiesel yield of 64% was obtained, which dropped to 52% after the fourth transesterification reaction cycle. The proposed approach has the potential to reduce material costs, energy consumption and water usage associated with conventional biodiesel production technologies. It may also mitigate the impact of conventional biodiesel production on food and land security, while simultaneously reducing waste.

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