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Abstracts Book

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Conference Program

Saturday.18th October, 2008

Registration	**9:30-10:00**
Opening Ceremony	**10:00-11:00**
Dr. Ayman A. Diab Dean of Faculty of Biotechnology, MSA Conference coordinator	**10:00-10:15**
Prof. Khayri Abd El Hamid President of MSA University Conference president	**10:15-10:30**
Prof. Fathy Saad 6th October governor	**10:30-10:45**
Prof. Martin J. Snowden Head of School of Science Greenwich University-England	**10:45-11:00**
Session I Medical Biotechnology **Chairman: Prof. Sherif Eldegwi** MSA University Vice president, Conference vice president	**11:00 -1:15**
Prof. Lauren Pecorino Medawy school of science, University of Greenwich **An Overview of Carcinogenesis**	**11:00-11:30**
Prof. Ibrahim Badran Professor of Surgery, Medicine School-Cairo University **Medical applications of Biotechnology**	**11:30-12:00**
Prof. Mohamed A. Saber Theodor Bilharz Research Institute **Development of recombinant DNA Vaccine against Schistosoma mansoni Infections**	**12:00-12:15**
Dr. Abeer Abdel All Department of Food Hygiene – Cairo Univeristy **Molecular characterization and antibiotic sensitivity of Staphylococcus aureus isolated from buffaloes milk with sub clinical mastitis**	**12:15-12:30**
Prof. Abdel-Rahman N. Zekri National Cancer Institute, Cairo University **Genetic profile of Egyptian hepatocellular-carcinoma associated with hepatitis C virus Genotype 4 by cDNA microarray**	**12:30-12:45**

Dr. Adel Khalil Ibrahim Faculty of veterinary medicine. Biotechnology center for services and research, Cairo University, Egypt **Comparative diagnostic investigations of Rapid test HCV screen – lateral flow, anti HCV-ELISA and Nested RT-PCR assays**	**12:45-1:00**
Dr. Abeer A. Bahnassy Cancer Biology Department, National Cancer Institute, Cairo University.	**1:00-1:15**
Coffee Break	**1:15-1:30**
Session II Pharmaceutical Biotechnology **Chairman: Prof. Lauren Pecorino** Medawy school of science, University of Greenwich	**1:30-3:45**
Prof. Solomon Habtemariam Pharmacognosy and Phytotherapy Research Labs, Medway School of Science, the University of Greenwich **Chemotherapeutic Targets, Bioassays and the Identification of Natural Pharmacologically Active Compounds: Reactive Oxygen Species**	**1:30-2:00**
Prof. Mohamed A. Saber Scientific Director of Biotechnology and Genetic Engineering Unit, Theodor Bilharz Research Institute. **Human recombinant biopharmaceutical products**	**2:00-2:30**
Dr. El-Dabaa, E. Theodor Bilharz Research Institute. **Lab scale production of human interferon Alfa 2b in E. coli**	**2:30-2:45**
Prof. Solomon Habtemariam Pharmacognosy and Phytotherapy Research Labs, Medway School of Science, the University of Greenwich **Chemotherapeutic Targets, Bioassays and the Identification of Natural Pharmacologically Active Compounds: Research Strategy**	**2:45-3:00**
Prof. Fawzia A.-F National Research Center **Assessment of Genotoxicity of the Anticancer Drugs Daunorubicin and Ifosfamide in Mice In Vivo**	**3:00-3:15**
Prof. Farag, S.H. National Research Center **Tissue cultures of Thevetia nerifolia:** **Morphogensis and Cardenolides production**	**3:15-3:30**
Lunch Break	**3:30-4:30**
Researchers and Students Poster Sessions4	**3:00-5:30**

Sunday Oct.19, 2008

Session III Agricultural Biotechnology Chairman: Prof. Ibtesam Hussein Faculty of Agriculture – Cairo University	9:30-11: 45
Prof. Aziz Rahman Greenwich University - England **The Applications of transgenesis in Biotechnology**	9:30-10:00
Prof. Ahmed Shawky General Secretary of the Biotechnology sector- ESCU **Applications of Biotechnology in Agriculture**	10:00-10:30
Prof. Mansour, A Genetics Department, Faculty of Agriculture, Zagazig University,Egypt **Activation of Bare-1 retrotransposons in barley under sorbitol stress**	10:30-10:45
Prof. CAMARA Brahima Université de Cocody, UFR Biosciences, Laboratoire de Physiologie Végétale 22 BP 582 Abidjan 22 **Screening for antifungal activity of three essential oils and one synthesis fungicide to control Black leaf streak disease (BLSD) caused by Mycosphaerella fijiensis**	10:45-11:00
Dr. Inas Fahmy Farouk Agricultural Genetic Engineering Research Institute (AGERI), GIZA, Egypt, **Investigation of transmission barriers of begomoviruses thourgh their whitefly vector Bemisia tabaci (Genn.), Insights from a study on WmCSV**	11:00-11:15
Dr. Nahed, A. A. Ibrahim Agricultural Genetic Engineering Research Institute (AGERI), ARC, Giza, Egypt **Protection of Cotton Plant (Gossypium barbadense) against lepidopteran Insects due to Colonization with Nitrogen Fixing Bacteria Expressing the Bacillus thuringiensis Toxin Gene Cry1C**	11:15:11:30
Prof. Awad, W.S. Department of Internal Medicine and Infectious Diseases, 2 Department of Clinical Pathology - Faculty of Veterinary Medicine, Cairo University **Evaluation of different diagnostic methods and various sample types for the diagnosis of Lumpy skin disease virus infection in cows with different clinical pictures**	11:30-11:45
Coffee Break	11:30-12:00

Session IV Industrial Biotechnology **Chairman: Prof. Patricia J. Harvey** School of Science Greenwich University-England	**12:00-1:30**
Prof. M. J. Snowden School of Science, University of Greenwich at Medway, Chatham Maritime, Kent, ME4 3HQ **Extending the tool box, making your polymers work for you**	**12:00-12:30**
Prof. Mahran, K.M.A Cairo University **Production and Evaluation of GST Vaccine for Protection of Sheep against Fasciola Infection**	**12:30-12:45**
Prof. Farid Bensalah Faculté des Sciences, Département de Biologie, Laboratoire de Biologie moléculaire et génétique Microbienne, Université Es-Sénia. Oran 31000, Algérie **PCR methods for identification of Thermophilic lactococci strains from the indigenous flora of fermented milk**	**12:45-1:00**
Prof. El-Behairy, A.M. Department of Parasitology, Faculty of Veterinary Medicine, Cairo University **Efficacy of excretory/ secretory and cathepsin L antigens for immunization of sheep against Fasciola gigantica infection in Egypt**	**1:00-1:15**
Prof. Taha Hussien Mubarak City for scientific research and Technology Applications Genetic **Purification and characterization of a novel thermoactive cellulase from thermophilic actinomycetes isolate**	**1:15-1:30**
Lunch Break	**1:30-2:30**

Session V Environmental Biotechnology **Chairman: Prof. Martin J. Snowden** **Head of School of Science** **Greenwich University-England**	**2:30-4:30**
Prof. Patricia J. Harvey School of Science, University of Greenwich, Chatham Maritime, Kent, ME4 4TB, UK **Challenge of growing food crops on degraded land and land contaminated with organic pollutants**	**2:30-3:00**
Prof. Ahmed Hegazi **Secretary General, Council of Environmental and development research, Egyptian Academy of Science** **Environmental problems and related biotechnology in the middle east**	**3:00-3:30**
Dr. Wael M. Lotfy **Evolutionary Origins, Diversification, and Biogeography of Liver Flukes (Digenea, Fasciolidae)**	**3:30-3:45**
Osama M. Darwesh Agricultural Microbiology Department, National Research Center, Cairo, Egypt **Biodegradation of Synthetic Azo Dyes by Bacteria**	**3:45-4:00**
Haiam M. Aboul-Ela Department of Marine Chemistry, Environmental division, National Institute of Oceanography & Fisheries, Alexandria. Egypt **Oxidative stress and DNA damage in relation to transition metals overload in Abu-Qir Bay, Egypt**	**4:00-4:15**
Patricia J. Harvey School of Science, University of Greenwich, Chatham Maritime, Kent, ME4 4TB, UK **Reducing Emissions in Manufacturing through Renewable Energy**	**4:15-4:30**
Poster Session	**4:30-5:30**
Closing ceremony **(Awards and certificates distribution)**	**5:30-6:30**

Medical Biotechnology

Presentations

An Overview of Carcinogenesis

Lauren Pecorino
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Our understanding of cancer has greatly expanded over the last decade. Cancer is ultimately a disease of the genome; agents that cause cancer affect either the regulation of genes or gene products that are involved in controlling net cell number and cell migration. Cancer education has a vital role in enabling individuals to make lifestyle changes that can reduce their risk of cancer. Cancer education can also influence policy. The knowledge of key molecular pathways that play a role in carcinogenesis is being translated into new powerful cancer therapeutics. In addition, understanding the role of infections and inflammation in cancer has led to the development of new prevention strategies (e.g. a vaccine against cervical cancer). This communication will review molecular aspects of the biology of cancer, provide an insight into how lifestyle changes can reduce cancer risk, and discuss the development of new preventative and therapeutic strategies.

References

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Ferlay, J. et al. (2004). Globocan 2002. Cancer Incidence, Mortality and Prevalence Worldwide. IARC Cancer Base No. 5, Version 2.0 IARC Press, Lyon. http://www-dep.iarc.fr/

Development of recombinant DNA Vaccine against Schistosoma mansoni Infections

Mohamed A. Saber, Hanem M. Ehab El Dabaa, Ahmed, Tarek S. Abou Shousha1 , Hanan A Hamid, Mohamed Abbass and Mahmoud H. Romeih,

Biochemistry and Pathology1 Departments, Theodor Bilharz Research Institute, Giza 12411, Egypt (maasaber@yahoo.com)

Schistosomiasis remains a worldwide endemic cause of chronic and debilitating illness. Development of a vaccine will significantly reduce the incidence of the disease. Immunization with DNA is a new trend in vaccine development that could enhance the safety and efficacy of currently used vaccines. The immunogenicity and protective efficacy of DNA vaccines encoding the antigen SM21.7, SMFimb and SMaldo were evaluated in C57 BL/6 and Swiss albino mice. The ORF of these genes has been cloned into the eukaryotic expression vector pcDNA1/Amp under control of CMV late enhancer promoter. Different groups of mice were vaccinated intramuscularly with SM21.7-pcDNA1, SMfimb-pCDNA 1/Amp and SMaldo-pCDNA1/ Amp and boosted twice shown high and specific humeral response in comparison with control (blank pcDNA1/Amp).

ELISA has shown that the level of IgG antibody in immunized mice post-immunization was significantly higher, using the three rDNAs than in control group. Immunization with these pcDNAs conferred a significant level of protection against challenge (35 – 70 %) in experimental animals: Swiss Albino and C57BL/6 mice.

Histopathological examination of liver of vaccinated animals has revealed a decreased in the number, size and change in the cellularity of the granuloma compared to the control infected liver. In addition reductions in worm viability, worm fecundity and egg hatching ability have been observed following challenge with S. mansoni cercariae. The number of eggs in the liver and intestine was significantly reduced.

The results suggested that SM21.7, SMfimb and SMaldo might be candidates for the generation of a vaccine against schistosomes.

Molecular characterization and antibiotic sensitivity of Staphylococcus aureus isolated from buffaloes milk with subclinical mastitis

Ibrahim, A.K [1,2]; Abdel All, Abeer [3] and Awad, W.S.[4]

1 Faculty of Biotechnology - MSA University, 2 Department of Clinical Pathology, 3 Department of Food Hygiene, 4 Department of Internal Medicine and Infectious Diseases - Faculty of Veterinary Medicine, Cairo University.

Background: Subclinical mastitis is an inflammation of the udder as a result of microbial infection with no visible or palpable changes in the udder with secretion of apparently normal milk and diagnosed mainly through detection of cellular changes and bacterial culture. Mastitis is considered the most prevalent infectious disease among dairy animals being responsible for severe economic losses all over the world.

Materials and methods: A total number of 248 quarter foremilk samples were collected from 62 buffaloes. Bacteriological isolation and identification had been done according to standard protocols. Isolated strains of Staphylococcus aureus were tested for molecular characterization of 16s-RNA and Coagulase gene (coa) and potentiality of toxin production and antibiotic resistance.

Results: Performing California mastitis test revealed 60 (24.19%) out of 248 quarter foremilk samples collected from 62 hand-milked buffaloes were subclinically mastitic cases. Bacteriological examination revealed isolation of 28 (11.29%) S. aureus strains out of 248 milk samples by using the traditional method of isolation, while 34 (13.7%) strains were recovered using the modified method of isolation.

Positive amplification of both of the 16s rRNA and coa genes using separate PCR assays was obtained in 32 (94.11%) and 29 (85.29%) out of 34 S. aureus isolates. A multiplex PCR was performed on the 34 S. aureus strains to clarify the presence of enterotoxins genes sea, seb, sec, sed and see which could be detected in 4 (11.77%), 1 (2.94%), 8 (23.5%), 5 (14.7%) and 6 (17.6%) out of 34 S. aureus strains.

Antibiotic sensitivity testing was performed using antibiotic disk diffusion method for determining the resistance of the 34 S. aureus strains to amoxycillin/clavulanic acid, cloxacillin, penicillin G., tetracycline and erythromycin. Six antibiotic patterns were recorded as follows; 19 (55.9%) S. aureus strains were susceptible to all tested antibiotics, 2 (5.9%) were resistant to all tested antibiotics, 1 (2.9%) resistant to penicillin and cloxacillin and intermediate to tetracycline and erythromycin, 1 (2.9%) resistant to penicillin and intermediate to tetracycline and erythromycin, 3 (8.8%) resistant to penicillin and intermediate to tetracycline, and 8 (23.5%) resistant to penicillin only.

Genetic profile of Egyptian hepatocellular-carcinoma associated with hepatitis C virus Genotype 4 by cDNA microarray

Abdel-Rahman N. Zekri *, Mohamed M. Hafez *, Abeer A. Bahnassy **, Zeinab K. Hassan*, Tarek Mansour* and Hussein M. Khaled***

*Virology and Immunology Unit, Cancer Biology Department, **Tissue Culture unit, Pathology Department, and ***Medical Oncology Department, National Cancer Institute, Cairo University.

Hepatocellular carcinoma (HCC) is a preventable disease rather than a curable one, since there is no well-documented effective treatment modality until now, making the molecular study of this disease mandatory.

Methods: We studied gene expression profile of 17 Egyptian HCC patients associated with HCV genotype-4 infection by c-DNA microarray.

Results: Out of the 15,660 studied genes, 446 were differentially expressed; 180 of them were up regulated and 134 were down regulated. Seventeen genes out of the 180 up-regulated genes are involved in 28 different pathways. Protein phosphatase 3 (PPP3R1) is involved in 10 different pathways followed by fibroblast growth factor receptor 1 (FGFR1), Cas-Br-M ecotropic retroviral transforming sequence b (CBLB), spleen tyrosine kinase (SYK) involved in three pathways; bone morphogenetic protein 8a (BMP8A), laminin alpha 3 (LAMA3), cell division cycle 23 (CDC23) involved in 2 pathways and NOTCH4 which regulate Notch signaling pathway. On the other hand, 25 out of the 134 down-regulated genes are involved in 20 different pathways. Integrin alpha V alpha polypeptide antigen CD51 (ITGVA) is involved in 4 pathways followed by lymphotoxin alpha (TNF superfamily, member 1) (LTA) involved in 3 pathways and alpha-2-macroglobulin (A2M), phosphorylase kinase alpha 2-liver (PHKA2) and MAGI1 membrane associated guanylate kinase 1 (MAGI1) involved in 2 pathways. In addition, 22 genes showed significantly differential expression between HCC cases with cirrhosis and without cirrhosis. Confirmation analysis was performed on subsets of these genes by RT-PCR, including some up-regulated genes such as CDK4, Bax, NOTCH4 and some down-regulated genes such as ISGF3G, TNF, and VISA.

Conclusions: This is the first preliminary study on gene expression profile in Egyptian HCC patients associated with HCV-Genotype-4 using the cDNA microarray. The identified genes could provide a new gate for prognostic and diagnostic markers for HCC associated with HCV. They could also be used to identify candidate genes for molecular target therapy.

Comparative diagnostic investigations of Rapid test HCV screen – lateral flow, anti HCV-ELISA and Nested RT-PCR assays

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*The Egyptian IVF-ET center, Cairo, Egypt. # Faculty of veterinary medicine. Biotechnology center for services and research, Cairo University, Egypt.

Background : Since its discovery, HEPATITIS C virus (HCV), has been considered the major agent responsible for most cases of blood-borne hepatitis. HCV is the leading cause of chronic liver disease worldwide. An estimated 3% of the world population is chronically infected with HCV, and HCV accounts for approximately 20% of cases of acute hepatitis and 70% of cases of chronic hepatitis. Chronic hepatitis C is a major cause of cirrhosis and hepatocellular carcinoma.

Material and method : A total number of 362 patients were tested for HCV as a part of screening before starting the IVF program at the Egyptian IVF-ET center, Cairo , Egypt during October 2007. Testing samples included using the Rapid HCV Chem screening test HEALTH-CHEM DIAGNOSTICS LLC, USA. Adaltis EIA HCV AB , Italy, and Nested RT PCR Ready to go Kit Pharmacia Incorp, USA.

Results: Screening Rapid HCV Chem screening test revealed 16 positive cases with a prevalence of 4.4 % while by using ELISA assay positive cases were 13 with a prevalence of 3.6% and 3 cases were considered negative.

On testing samples by nested RT- PCR 15 samples were positive with a prevalence of 4.1% for HCV RNA including 12 detected by both previously mentioned techniques and one was negative with ELISA positive with Rapid HCV Chem screening test and 2 samples that were considered suspected cases became positively amplified by PCR.

Conclusions: Using rapid tests were quite specific as it was effectively detected all negative cases, while sensitivity may be considered very acceptable when considering both positive and suspected together as both results should be subjected for further assessment. ELISA may be more specific for detecting the Anti HCV antibodies while nested RT PCR were detecting the circulating RNA, So almost all samples that gave sharp positive or negative anti HCV antibody were positive with nested RT PCR while suspected results with anti HCV antibody needed testing with nested RT PCR

Posters

Active Immunization: A Promising Approach for Cancer Treatment

Mona A. AlQazzaz

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Traditional ways for cancer treatment are surgery, radiotherapy and chemotherapy. A novel approach for cancer treatment is immunotherapy. Immunotherapy seems to offer great promise as a new dimension in cancer treatment, but it is still very much in its infancy. Immuno therapies involving certain cytokines and antibodies have now become part of standard cancer treatment. Passive immunization against cancer proved success; monoclonal antibodies (Rituximab developed in 1997) are approved by the FDA for the use against non-Hodgkin's lymphoma.

Active immunization against cancer is still under clinical trials. Creating a vaccine against cancer is difficult because cancer cells are self-cells which may not display antigens different from the body's own antigens. Furthermore, a tumor may have different types of cells within each having different surface antigen, thus it is difficult to direct body immune cells to kill the cancerous cells.

Increasingly, cancer vaccines have been shown to be capable of improving the immune response against particular antigens. The result of this immunologic effect is not always sufficient to reverse the progression of cancer. However, cancer vaccines have been generally well tolerated, and they may provide useful anticancer effects in some situations. For example, in malignant lymphoma, a number of laboratory studies have indicated that vaccination using lymphoma-associated proteins called idio type can stimulate the immune systems of mice sufficiently to help them resist the development of lymphomas.

Electron microscopy: Preparation of biological samples, interpretations and common artifacts.

Ayman M. Ghallab
Professor of Cell biology and Histology, Faculty of Dentistry,
MSA University

Very small soft tissue specimens (less than 1mm^3) are obtained and immediately fixed in the primary fixative by immersion in 2.5% glutaraldhyde in 0.1 M sodium cocodylate buffer solution at pH 7.4 from 2 to 24 hours in a refrigerator at 4ºC. After 2 rinses in buffer, the specimens will be post-fix the specimens in the secondary fixative by immersion in 1% osmium tetraoxide in 0.1 M sodium cocodylate buffer solution at pH 7.4 for 2 hours in room temperature. Wash specimens again in cacodylate buffer solution to remove excess fixative. Dehydrated specimens in ascending grades of ethanol (from 50-90%) for 15 minutes then in absolute alcohol for 15 minutes (2 changes). After dehydration, the specimens are placed in propylene oxide for 30 minutes at room temperature (2 changes) as it quickly replaced the dehydrating agent and then diffused out of the tissues and allowed easy infiltration of the epoxy resin. The specimens are impregnated in a mixture of propylene oxide and epoxy resin (1:1). The vials containing the specimens were shaken to mix their component, and placed on a specimen rotator for 1 hour or longer (over night). The mixture is replaced with pure epoxy resin and the vials were left overnight on rotator. The specimens are embedded in epoxy resin in better equipment electron microscope (BEEM) capsules and left for polymerization to occur at 60 ºC for 24 hours. Sectioning is carried out using ultramicrotome and glass knives. One µm (1000 nm) thick sections (semi-thin sections) are obtained and mounted in a drop of water on glass slides and stained by toluidine blue and examined with light microscope, to detect the proper area for ultra-thin sections. Ultra-thin 70 - 90 nm sectioning are carefully cut, using ultramicrotome and glass or diamond knives from selected blocks, and mounted on copper grids. These sections are stained with uranyl acetate and lead citrate to increase the contrast between the different cellular components before electron microscopy examination. The ready sections are examined carefully and photographed using transmission electron microscope (TEM). The negatives are developed and photographs are printed.

Many artifacts may meet the electron microscope researcher. Degradation of cellular contents may be due to inadequate fixation. Swelling of cellular contents may be due to sudden drastic changes in the environment of the tissue. Shrinkage of cellular contents may be due to delayed and prolonged dehydration. Presence of air bubbles in the resin block avoided by prolonged stirring. Presence of stain aggregates may obscure cellular fine details. Artifacts due to sectioning and hazy printing are also common.

During interpretation of electron micrograph, be sure that you can see a normal intact cell before judging on an abnormal alteration in another cell.

Pharmaceutical Biotechnology

Presentations

Chemotherapeutic Targets, Bioassays and the Identification of Natural Pharmacologically Active Compounds: Reactive Oxygen Species

Solomon Habtemariam

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High level of reactive oxygen species generated either by abnormal physiological processes, exogenous factors or reduced level of antioxidant defences are known to induce oxidative damage to biological macromolecules. There is now overwhelming evidence to suggest that such oxidative macromolecular and cellular damage may lead to the development of a variety of disease conditions including cancer, aging, atherosclerosis, ischemic injury, inflammation and neurodegenerative diseases [1]. Since antioxidant compounds could reduce the risk of these disease conditions, numerous recent studies gave special attention to the search of natural antioxidants, mainly phenolic compounds, for use as dietary supplements, food preservatives and medicine. Our own work in this field has identified several novel natural products with potent protective effect against biological macromolecules such oxidative DNA damage and also cell death [2-7]. In the present communication, some selected chemotherapeutic targets and promising natural products identified from our studies are discussed.

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Lab scale production of human interferon Alfa 2b in E. coli

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Recombinant human interferon alfa (rhIFN α) is one of the major therapeutic recombinant proteins approved for a wide variety of uses, including use in patients with some types of carcinomas and leukemias, genital warts, and hepatitis B and C viruses. Hepatitis C infection represents a major national health problem in Egypt. Production of interferon α with affordable costs will have an impact on the treatment strategy in Egypt.

This work aimed to establish and optimize lab scale production of rhIFN-α2b protein in prokaryotic expression system: E. coli. The open reading frame sequence encoding the mature active human IFN-α2b protein have been isolated and cloned from the human genomic DNA with selective proof reading PCR process. The cloned sequence have been characterized and cloned into different pET expression vectors. Expression of Native and fusion IFN-α2b proteins have been tried in different strains of E. coli using different strategies. Successful expression have been optained after resolving of problems related to RNA 2ndry structure and rare argining codon usage. IFN-α2b was produced in E.coli as non-soluble inclusion bodies (IBs). High density cell culture fermentation has been optimized (60 g wet weight bacteria /liter, 2.8 g IBs /liter). The IBs have been Solubilized using 6M guanidinium hydrochloride. Oxidative refolding of IFN-α2b protein to its native tertiary structure using dilution method have been optimized (240 µg folded IFN-α2b /ml folding reaction). The refolded IFN-α2b protein was concentrated and purified from other bacterial proteins and solubilizing agents using differnt chromatographic procedures. The purified refolded IFN-α2b protein proved exact molecular weight monomeric protein, exact N terminal amino acids sequence with removal of N terminal methionine by E. coil, proper isomerization of the two disulfide bonds and proper refolding to its native structure.

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Chemotherapeutic Targets, Bioassays and the Identification of Natural Pharmacologically Active Compounds: Research Strategy

Solomon Habtemariam

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Though herbal remedies with a holistic orientation to health have effectively been used by mankind for thousands of years, there is recognition that such therapies could have potential risks. The lack of scientific evidence to justify the use of herbal medicines, lack of standardisation, etc, have been the subjects of intense debates and research in recent years. In this regard, the safety, efficacy and quality issues of common European herbal drugs have not been exceptions. As part of the current ongoing effort to provide scientific evidence for these medicines, we have been routinely screening plants with claimed traditional medicinal uses. Once pharmacological activity is detected in our in house bioassay batteries, crude herbal extracts further go through a systematic bioassay-directed fractionation procedures leading to the isolation and characterisation of active principles. Hence, we are not only providing scientific evidence for the claimed uses but also identify active components for standardisation of crude herbal drugs. We are also using theses strategies as a means of discovering new drugs. In this mini-talk, our research strategy is highlighted by using some key specific examples ranging from neurodegenerative disease targets to infectious diseases [1-6].

Key References

Patents (1994-Present): United States Patent 6313099, GB 9903823.4, WO/1998/032761, etc.

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Assessment of Genotoxicity of the Anticancer Drugs Daunorubicin and Ifosfamide in Mice *In Vivo*

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Daunorubicin (DNR) and ifosfamide (IFO) are two anticancer drugs used in the treatment of different neoplastic diseases. Male Swiss mice were injected with the different doses of DNR and IFO intraperitoneally to investigate their genotoxicity in somatic and germ cells. The doses were 1, 3 and 5mg DNR/kg body wt. and 8, 16 and 24mg IFO/kg body wt. as single doses. The repeated doses were 1mg DNR/kg body wt. and 8mg IFO/kg body wt. for three consecutive days. Samples collected after 1, 7 and 14 days after treatments. Both anticancer drugs induced chromosomal aberrations (in somatic and germ cells), SCE's and sperm shape abnormalities, which were highly significant and in a dose dependent manner 1 day after treatments. The chromosomal aberrations were decreased with increasing the time of recovery. However, the tetraploid cells in mouse bone marrow were increased. Both drugs increased the percentage of DNA fragmentation in mouse spleen cells as measured by diphenylamine (DPA) assay, and confirmed by agarose gel electrophoresis. In conclusion, our results indicate that the anticancer drugs DNR and IFO are genotoxic drugs in mouse somatic and germ cells and in consequence induction of secondary malignancies should be taken into account as diverse side effect of them.

Key Words: Daunorubicin- Ifosfamide- Chromosomal Aberrations- SCE's- Sperm Shape Abnormalities- DNA Fragmentation.

Tissue cultures of Thevetia nerifolia: Morphogensis and Cardenolides production

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Tissue cultures were established from leaf, stem and root of the plant Thevetia neriifolia. Plant growth hormones influenced the morphogenetic of the cultures. The explants gave multiple shootlets on Murashige and Skoog's (MS) supplemented with 2,4-dichlorophenoxyacetic acid (2,4-D) (1mg/l)+ Kinetin (K) (3mg/l), rootlets on MS+1-naphthaleneacetic acid (NAA) (1mg/l) and callus formation was achieved on MS+1mg/l 2,4-D + 3mg/l Kin . Multiple shootlets, rootlets and calli cultures synthesized levels of thevetin B, neriifolin, peruvoside and digitoxigenin and their concentrations varied with different growth regulators.

Posters

Spectrophotometric Determination of Domperidone and Risperidone in Pharmaceutical Formulations using Alizarin Derivatives

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New spectrophotometric procedures have been established for the quantitation of domperidone (DMP) and respiridone (RPD). The procedures are based on the reaction between the examined drug and alizarin (I), alizarin red S (II), alizarin yellow G (III) or quinalizarin (IV) producing ion-pair complexes which can be measured at the optimum wavelength. The optimization of the reaction conditions is investigated. Beer's law is obeyed in the concentration ranges 0.5–28 µg mL−1, whereas optimum concentration as adopted from Ringbom plots was 1.0–26 µg mL−1. The molar absorptivity, Sandell sensitivity, detection and quantification limits are also calculated. The correlation coefficient was ≥ 0.9990 (n=6) with a relative standard deviation (R.S.D.) of ≤ 1.2, for six determinations of 1.0 µg mL−1. The methods are successfully applied to the determination of domperidone and respiridone in their pharmaceutical formulations.

Reactions on 3-acetylindole: Synthesis and Pharmacological activity of some new 1-benzyl and 1-benzoyl-3-heterocyclic indole derivatives

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Indoles and their derivatives constitute an important class of therapeutic agents in medicinal chemistry. Bromoacetyl indoles 2a,b were prepared and allowed to react with glycine to give 3a,b, which cyclized via their reaction with ammonium thioglycolate to give thio-imidazolidinone derivatives 4a,b. acid hydrolysis of the latter yielded 2,4-dioxoimidazo-lidinone derivatives 5a,b. on the other hand, oxidation of 2a,b with selenium dioxide gave the corresponding carbomethyl acetate derivatives 10a,b. heterocyclization of 10a,b with o-phenylenediamine gave quinoxaline derivatives 11a,b. Compounds 4a,b, 5a,b and 11a,b were used as a key compounds for preparation of condensed heterocyclic derivatives and have been evaluated as antibacterial and anti-inflammatory.

Antioxidant activity of Tanacetum vulgare L.

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Tancetum vulgare, commonly known as Tansy, is an European medicinal plant [1] with uses in traditional medicine ranging from anthelmintic, tonic, stimulant to an emmenagogue [2, 3]. In the course of our systematic screening of herbal products for antioxidant activity, we have identified the ethanol extract of Tansy leaves with potent radical scavenging activity. Fractionation of the crude extract with solvents of increasing polarity (i.e. hexane, chloroform, ethyl acetate, butanol and water respectively) identified the ethyl acetate fraction with the highest activity towards DPPH free radical scavenging. Further activity-directed purification of the active fraction using repetitive column chromatography resulted in the identification of the antioxidant principles (DPPH scavenging activity ranging from IC50 = 3.50µg/ml to 12.50µg/ml). The therapeutic potential of the active principles and Tansy is now being studied through other antioxidant assays [4].

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Agricultural Biotechnology

Presentations

Activation of Bare-1 retrotransposons in barley under sorbitol stress

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LTR-retrotransposons and other repetitive DNA elements are directly or indirectly responding to a wide variety of stresses by increasing or decreasing its copies. This effect is specific for different retrotransposons or stresses. The Bare-1 retrotransposon members are actively transcribed in vivo in barley. Bare-1 family was reported to respond to sharp microclimatic divergence specially drought. Sorbitol has been used widely to mimic the effects of drought. A potential osmotically-stressed action has been ascribed to sorbitol, but invivo evidence of this remains elusive. In the present work, the effect of sorbitol was compared in both Copia and Gypsy groups of retrotransposon using specific primers for both groups. One step RT-PCR analysis showed that sorbitol exerted a strong influence upon Copia elements group after 4, 24 and 34 hours of sorbitol treatment. When Bare-1 specific primers were used to amplify Copia cDNA products, it revealed unique strong DNA bands at the same time points. The immunobloting of Bare-1 Gag protein specific antibody showed no specific increase after these treatments. Hence, sorbitol, has the capacity, in barley plant, to increase the transcriptional activity of Copia elements specially Bare-1 retrotransposon.

Screening for antifungal activity of three essential oils and one synthesis fungicide to control Black leaf streak disease (BLSD) caused by *Mycosphaerella fijiensis*

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Banana is an importance food for the populations in Côte d'Ivoire. Black leaf streak disease caused by Mycosphaerella fijiensis is present in all al areas where bananas or plantains were grown. Smallholders, because of the size of the surfaces and also for lack of financial resource cannot use fungicides of synthesis against Black leaf streak disease (BLSD). They could have recourse to plants extracts which they can have in their immediate environment to fight against fungi present in their farm. Also the commercial farmers could use these same extracts to produce biological banana which is more appreciated on the international markets. The present study was led with an aim of determining antifungal effect of three essentials oils of certain Ivorian plants, compared with synthetic fungicide (Impulse) against Mycosphaerella fijiensis, a fungus responsible of Black leaf streak disease (BLSD) in Côte d'Ivoire. Those essential oils were added to PDA medium in different doses. Ocimum gratissimum essential oil showed high fungi toxicity at all concentration. As for two other essential oils and fungicides of synthesis, they had an increasing activity according to concentrations used. Some essentials oils of Ivorian flora are biological struggle method efficient against Black leaf streak disease (BLSD).

Key words: biological struggle method, essentials oils, synthetic fungicide, Mycosphaerella fijiensis, Ivorian flora, bananas and plantains.

Investigation of transmission barriers of begomoviruses thourgh their whitefly vector Bemisia tabaci (Genn.), Insights from a study on WmCSV

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To investigate the cellular mechanisms of transmission and the molecular interactions between begomoviruses and its whitefly vector, acquisition and translocation of WmCSV by Bemisia tabaci were studied. A whitefly transmissible WmCSV isolate from Sudan and 4 different non transmissible mutants carrying a single amino acid change in the capsid protein at position 133, were used in the translocation experiments. B. tabaci nonvirulifeorus insects were feed on infected watermelon plants for 48 h AAP then transferred for 48 h to non-host plants, to subsequently inoculate healthy watermelons. Transmission was taken as an evidence for a viable interaction between virions, the gut membrane and the salivary glands. Fresh, dissected organs from viruliferous whitefly feeding on wild type or mutant virus were examined by PCR to determine presence of virus. For the transmissible, wild-type a virus pathway similar to luteoviruses/aphids interactions and to Tomato yellow leaf curl virus TYLCV translocation in B. tabaci, was found. Virus DNA was detected in the midgut and in the hemocoel as well as in the salivary glands of B. tabaci for both the transmissible and non- transmissible mutants. In Trialeurodes vaporariorum (a non-vector of geminiviruses), wild type WmCSV was not capable of crossing the gut wall and hence not detected in hemocoel or salivary glands. In these non-vector whitefly insects, the gut wall represents the essential epithelial barrier to virus passage. Both transmissible and the non-transmissible virus mutants were capable of crossing the midgut (PCR studies), while different observations were made with glands - primary salivary glands (PSG) and accessory salivary glands (ASG). At these organs, virus mutants were detected, however, in all cases there was no virus transmission. Consequently, virus localization studies concentrated especially on these organs.

The whitefly circulative non-propagative transmitted Geminiviruses, to be translocated; the ingested virus has to cross two cellular barriers; the gut epithelial cells, to be released into the haemocoel and, the salivary glands, to be re-injected for plant infection. To elucidate this putatively receptor-mediated process and to reveal the sites of endocytosis, insects fed on plants infected with WmCSV were subjected to immunolocalization studies using electron microscopy. Ultrathin sections of insect organs embedded in different resins such as Epon 812, LR White or Lowicryl, were subjected to immunolocalization experiments. Transmission Electron Microscopy (TEM) observations demonstrate that the specific labelling using WmCSV antiserum was concentrated in the microvilli lining the gut wall of the epithelial cells of the food canal (the descending midgut and the filter chamber) which would point to a putative virus storage site allowing further internalisation for delivery to the haemocoel. A highly specific labelling in the primary salivary glands PSG, especially in the electron lucent and in multilamellar vesicles was observed. This labelling intensity as well as specificity was not observed in examinations of the accessory salivary glands (ASG). Hence, for translocation of WmCSV in B. tabaci insects, the primary salivary glands represent the major epithelial barrier. These organs therefore play the most decisive role for a successful vector transmission of begomoviruses by Bemisia tabaci.

Protection of Cotton Plant (Gossypium barbadense) against lepidopteran Insects due to Colonization with Nitrogen Fixing Bacteria Expressing the Bacillus thuringiensis Toxin Gene Cry1C

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Nitrogen fixing bacteria NMO10 was engineered to harbor cry1C gene for insecticidal activity against Lepidopteran insects and named tNMO10. The tNMO10 bacteria used in this work is naturally colonizing the phylloplane of cotton plant leaves. Cotton Plant leaves were inoculated with tNMO10 bacteria. Bacterial colonization of the plant leaves was examined by electron microscopy. Transmission electron microscopy (TEM) revealed the presence of tNMO10 bacterial cells within leaf epidermal cells, inter cellular spaces and inside the cells up to 40 days. Colony forming units (CFU) measurements were determined. Bioassays against cotton leaf worm S. littoralis were performed in the lab where the 2nd and 3rd instars were fed on cotton leaves sprayed with tNMO10 bacteria. The bioassay showed very high toxicity against the 2nd and 3rd instars S. littoralis larvae. On the plant level, ten specific real time PCR primers with a 51 bp conserved amplicons were designed. These conserved sequences represented the nif H, D, K and glnB genes, in addition to the upstream activator sequence (UAS). Real time PCR analysis showed high expression folds of the nif and glnB genes inside the treated leaves with tNMO10. However, the expression level of UAS region was slightly lower. Cotton plant leaves treated with tNMO10 showed higher expression of nif H, D, K and glnB genes than that found in the leaves treated with the parent strain NMO10. In addition, nitrogenase activity was measured by acetylene reduction assay, and the results proved that the level of nif H, D, K and gln B gene expressions were positively correlated with nitrogen fixation in the cotton plant leaves. In conclusion, the tNMO10 bacterial strain caused a protection of the cotton plant against the Lepidopteran insects as well as exhibiting high potency in nitrogen fixation.

Evaluation of different diagnostic methods and various sample types for the diagnosis of Lumpy skin disease virus infection in cows with different clinical pictures

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Background: Lumpy skin disease (LSD) is an acute, subacute, chronic, or inapparent viral infection affects all ages and breeds of cattle caused by Lumpy skin disease virus (LSDV) which is a member of genus Capripoxvirus, subfamily Chordopoxvirinae, family Poxviridae. The disease causes significant economic loss due to hide damage, decreased milk production, weight gain, mastitis, infertility in males and females, decrease semen quality and death.

Materials and methods: A total of 55 dairy cows in a single dairy farm were examined for lumpy skin disease. The examined animals were classified according to clinical signs into 3 groups. The first group comprised of 25 cows showing clinical signs, the second group comprised of 9 cows showing fever only and the third group comprised of 21 apparently normal in-contact cows showing no clinical signs. From the 25 infected cows, skin biopsies, blood in heparin and in EDTA and blood without anticoagulant for serum separation were collected. Whereas, from those cows (30) showing fever and the apparently normal in-contact animals showing no clinical signs, blood in heparin and in EDTA and blood without anticoagulant were collected. The collected skin biopsies were used for virus isolation, PCR and Dot blot, while the blood in heparin was used for virus isolation, whereas the blood in EDTA was used for PCR and Dot blot, in addition to blood without anticoagulant for serum separation and application of Indirect ELISA.

Results: From cows with clinical signs, Lumpy skin disease virus was isolated from skin biopsies and blood in percentages of 72 and 20%, respectively. While from cows showing fever, virus isolation was successful from blood in percentage of 33.3%. Both of polymerase chain reaction (PCR) and dot blot hybridization (DBH) detected viral DNA of LSDV in all skin biopsies collected from cows with clinical signs in percentage of 100%. Detection of viral DNA was successful in blood collected from all cows with clinical signs in percentage of 100% using PCR, whereas a detection rate of 84% was obtained by DBH. PCR detected viral DNA in blood samples collected from feverish cows in percentage of 77.8%, whereas DBH detected viral DNA in blood samples in percentage of 66.6%. Both of PCR and DBH detected viral DNA in blood samples collected from in-contact cows in percentage of 19.1%. Detection of antibodies against LSDV using iELISA in serum samples collected from cows with clinical signs and those with fever in percentages of 56 and 11.1%, respectively, whereas all in-contact cows had no antibodies against the virus. From all cows under investigation virus isolation was successful in percentage of 32.7% when the sample type was skin biopsy, whereas when the sample type was blood, the virus isolation was successful in percentage of 14.5%. While detection of viral DNA from all cows using PCR and DBH was successful in percentage of 45.5% when the sample type was skin biopsy, whereas when the sample type was blood, the detection of viral DNA was successful by using PCR and DBH in percentages of 65.5 and 56.4%, respectively. Antibodies against LSDV were detected in the sera of all cows under examination in percentage of 27.3%.

Posters

Construction of Genetic Linkage Map Showing Chromosomal Regions Associated with Some Agronomic Traits in Cotton

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Cotton is the world's leading fiber crop and the second most important oil seed crop. In Egypt, plant breeders have made major contributions to the productivity of this crop; however, this has led to decreasing the genetic variation among Egyptian cotton varieties. Enhancing the productivity of cotton could be addressed through improving different agronomic traits including early flowering and maturation (earliness). In the present investigation, an interspecific cross (G. barbadense x G. hirsutum) was performed between two genotypes, Giza83 (late flowering) and Deltapine (early flowering) to develop F2 segregating population. Analysis of segregation among the 71 F2 individuals was performed using 3 RAPD, 10 SSR, 6 AFLP primer combinations. Twenty four AFLP primer combinations were used in bulked segregant analysis for flowering time. Linkage analysis and map construction were performed using Map Manager. The map showed 22 linkage groups with 140 markers covered a total length of 1556.7 cM. The average length of linkage groups ranged from 1.4 to 649.5. Single point analysis was used to identify the genomic regions controlling traits for plant height, number of nodes at flowering time, bolling date, days to flowering and number of bolls. In total, 30 significant QTL were identified for the five traits on ten linkage groups, among these 11 QTL for plant height, 8 for number of bolls, 4 QTL for each of days to flowering and bolling date and 3 QTL for number of nodes at flowering time. This work represents the first linkage map for the intercross between Giza83 and Deltapine showing chromosomal regions associated with some agronomic traits.

Keywords: Cotton, linkage map, molecular markers, QTL, Agronomic traits.

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Applications of laser microbeam cell surgery and Agrobacterium tumefaciences systems in melon (*Cucumis melo* L.)

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In the current investigation, the application of laser microbeam cell surgery (based on visible laser at 441.5 nm focused to less than 0.5 µ) as a new transformation system in melon has been studied and compared with transformation via Agrobacterium tumefciences as well as a combine of laser microbeam cell surgery and A. tumefaciences treatment. The three transformation treatments have been carried out on the hypocotyls proximal zone explants of melon cv. Shahd El-Dokki with the plasmid pISV2456 that harboring gus-intron and bar genes. The treated explants were regenerated on shoot regeneration medium MSBA1 composed of MS supplemented with BA at concentration of 1 mg/l and 250 µg/l bialaphos. The obtained shoots were transferred to the elongation medium then, to the rooting medium. This study aimed to estimate the frequency of transformation using Agrobacterium-mediated transformation system as a successful common method for gene transfer in Melon (Cucumis melo L.), establish transformation system by laser microbeam cell surgery as a new technology for gene transfer in Melon, where it facilitates the incorporation of exogenous DNA into cells of hypocotyl through puncturing holes in the cell wall and cell membrane, estimate the frequency of transformation by using a combined treatment between Agrobacterium-mediated transformation system and laser microbeam cell surgery to study the efficiency of this method in the transformation in Melon (Cucumis melo L.), compare the regeneration process and the transformation frequency of the three methods and to confirm the presence of the transgene in the putatively transgenic plants by molecular analysis in every methods. Melon transformation was carried out using A. tumefaciens strain LBA4404/pISV2678. In the case of Laser mediated gene transfer in melon, the laser energies were enough to puncture a tiny submicrometer self-healing holes, momentarily made in the cell wall and membrane. After the holing process of the cell wall and membrane of the plasmolized cells, the exogenous DNA enters the cell quickly. In the case of the combined treatment, the explants cultivated with Agrobacterium after treating with laser. Results showed that there was no significant difference of shoot regeneration between both Agrobacterium and laser microbeam transformation techniques, while laser microbeam technique showed higher percentage than the Agrobacterium technique (75.94. and71.83, respectively). Furthermore, they revealed higher percentage than the combine treatment as it was 67.74 %. Histochmical GUS assay and molecular analysis proved the existence and the expression of the gus-intron gene. However, the presence of the bar gene has been detected by the molecular analysis. PCR assay was performed to confirm the presence of the transgenes. All the three transformation treatments showed PCR-positive with different percentage, indicating that the two genes were successfully transferred to the explants during the three methods. It was observed that the obtained shoots from Agrobacterium and laser treatments individually revealed 23.33% PCR-positive as out of 30 tested shoots,(i.e., 7 were positive) for PCR. On the other hand, the combined treatment represents 20% PCR-positive as out of 30 tested shoots (i.e., 6 were positive). To summarize, the new technique based on visible laser at 441.5 nm focused to less than 0.5µ proved to be an efficient, safe strategy for gene transfer in melon as compared with the well-established A. tumefciences technique. Moreover, the combined laser and Agrobacterium showed a successful modality as well.

Stress activation of Genomic Retrotransposon

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Retrotransposon are mobile genetic elements; most are largely quiescent during development, becoming more active under stress conditions. These elements have spread throughout the genome by a process termed retrotransposition, consisting of transcription of an element into RNA, reverse transcription into cDNA, and reinsertion of the copied element into a new genomic location. A feature common for many retrotrasposon is their activation by stress conditions. Activation of retrotransposable elements can be induced by various stresses. In particular, LTR retrotransposons, which found in most plant species, are characterized by a high level of variability in the LTR sequences involved in transcription, and have evolved by gaining new expression patterns mostly associated with responses to diverse stress stimuli. Most of the plant LTR retrotransposons that have been investigated produce larger pools of transcripts in response to stress, biotic as well as abiotic. Moreover, this Epigenetic activation of these mobile elements alter the expression of the adjacent genes. The new insertions in or next to coding regions generate mutations that can lead to changes in gene expression and thus reshaping the genome both structurally and functionally. Thus, activation of LTR retro-transposable elements can play an essential role in plant development and evolution.

The Safety and Wholesomeness Assessment of Genetically Modified Foods

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Global sustainable demands new tools to increase yield, relieve environmental stresses and enhance the quality and quantity of food. Genetically modified crops increased yield and reduce the need for pesticides and fertilizer. Genetically modified food can development vaccines produced in transgenic plants, plants enriched with vitamin A or iron, better fatty acid profiles, better digestibility for animals, aluminum and manganese tolerance. Genetically modified plants capable of growing in extreme environments offer a real opportunity to improve nutrition in developing countries. However, genetic engineering of plans and animals may potentially cause them to unexpectedly contain substance harmful to consumers.

The advent of genetically engineering technology for producing novel foods have focused attention on the need more appropriate methods for assessing the wholesomeness of complex novel foodstuffs. Therefore, microbiological, nutritional and toxicological investigations continue to be used in evaluating potential hazards which might result from application of molecular biology and biotechnology in development of new foods.

The concept of substantial equivalence has been used as a basis for determining what safety testes are needed before putting a genetically modified product on the market and whether product labeling is required. Substantial equivalence is used to address the safety of food components derived from genetically modified crops and is on comparison of the phenotypic and focuses on compositional characteristics of the parent crop and the genetically modified crops.

On the basis of the recommendations of the FAO/WHO, three categories of genetically modified crops can be considered: (1) no obvious difference between the assessed products and it's natural counterpart, regarding it appearance, taste, or selected chemicals and nutritional properties, It is assumed to be equivalent. Only a molecular characterization of the genetic insert is sufficient. (2) genetically modified crops which have the same composition as the parent crops with the exception of a well defined trait should be test for a safety assessment of the toxicity of the expressed protein(s) and their products . (3) genetically modified crops which are different from the natural counterpart, an extensive evaluation including bioavailability and wholesomeness studies are required.

Substantial equivalence is not quite enough to assure the safety of genetically engineered foods, because of the insertion of a foreign gene, unpredictable metabolic changes may occur that may generate unexpected hazardous that require thorough testing to be detected. No food can be excluded from rigorous testing on the basis of comparing selected characteristics. Therefore these tests are necessary (1) short term animal testing with through laboratory analysis of the effects on the condition of the animal. For detection of immediate harmful effects. (2) rigorous long term animal testing is necessary for detection of slow acting harmful substances (3 rigorous human testing over long periods of time as animal testing is not a fully reliable means for detecting harmfulness to humans. (4) human allergy testing is necessary for reliable assessment of allergenicity.

In view of the potential health impacts due to the use of genetic engineering in agriculture and food production, NCRRT has established a research program in assessing and in identification of genetically modified foods and feeds and irradiated genetically modified foods and feeds.

Use of Phage Cocktail Isolated from Egyptian Soil to Control Brown Rot disease of Potato

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Soil samples, taken from the root zone of potato plants, collected from different locations of Dakhlia and Damietta Governorates in Egypt, were used for isolation of lytic phages active against virulent strain of Ralstonia solanacerum (the causative of brown rot disease of potato). Four phages were isolated and designated as RSP4, RSP5, RSP6 and RSP7. These phages had clear plaques with different shapes and diameters. All the four isolated phages were tailed phages belonged to the order Caudovirales. The phage RSP4 had short tail, so it belongs to the Podoviridae family. The other three phages had long flexible non-contractile tails, so, they belong to the Siphoviridae family. The four isolated phages were polyvalent; they can infect more than one bacterial species. They can infect virulent isolates of R. solanacearum, Pseudomonas aeruginosa and Erwinia amylovra. No lysogenic bacteria appeared after incubation these phages for one week. Greenhouse and field experiments were conducted to reveal the effectiveness of phage cocktail that was composed of mixture of the four isolated phage (RSP4, RSP5, RSP6 and RSP7). The results indicated that phage cocktail resulted in significant increase in plant height and increase in tuber weight at harvest time. Also, Phage cocktail significantly reduce disease incidence and percentage of infected tubers (total of infected tubers at harvesting time and after 60 days of storage). Furthermore, in the field experiment, phage cocktail in field experiment caused significant increase in number of tubers/ plot and significant decrease in non-marketable tubers % at harvesting time.

Improving growth and secondary metabolites of Ocimum basilicum

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Aseptic nodes with a pair of axillary buds obtained from two weeks old seedling explants (cultured in free hormone media) cultured on Murashige and Skoog medium supplemented with 7 g/l Agar, sucrose at 30g/l or glucose at(20, 30, 40 g/L) and BA at concentrations of (0.0, 5, 10, 15, 20 mg/l) for six weeks. Data revealed that using BA at 5 mg/l significantly gave the heaviest value of shoots fresh weight and dry weight when compared with the others BA concentrations. Fantastic increase was obtained by using BA at concentration at 5 mg/L which significantly gave the highest value of essential oil percentage 0.58 % (about three times than the open field plants 0.19%). Most of the main components concentrations increased in vitro culture than the open field plants (in vivo). MS medium supplemented with BA at 5 mg/L increased the concentrations of Cineol, Linalool, Terpeniol and Methyl Chavicol to (15.25, 65.39, 2.30 and 4.27 %) when compared with the open field plants as it was (4.47, 34.63, 2.01 and 0.38) respectively. Data revealed that using sucrose at 30 g/L gave the highest value of shoots fresh weight (6.98 g) and dry weight (1.73 g) than all glucose concentrations. It was clear that using sucrose at 30 g / L gave the highest value of essential oil percentage as it was 0.60 % than all other treatments and the open field plants as it was 0.19 %. And the highest value for the main component of the essential oil as it was (13.62, 55.48, 2.32, and 3.98) for cineol, linalool, Terpeniol and methyl Chavicol respectively.

High resolution comparative conserved blocks of chicken chromosome 28 and human chromosome 19.

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Comparative mapping between the human and chicken genomes has revealed a striking conservation of synteny between the genomes of these two species, but the results have been based on low-resolution comparative maps. To address this conserved synteny in much more detail, a high-resolution chicken-human comparative map was constructed from human chromosome 19 (HSA19) compared to chicken chromosome 28 (GGA28).

A combination of screening Bacterial Artificial Chromosome library (BAC) and EST mapping has allowed putting more than 10 genes on the map. In addition, a highresolution comparison of GGA28 with HSA19 identified at least 7 conserved blocks, indicating the presence of inter- and intra-chromosomal rearrangement breakpoints in the bird lineage after the separation of birds and mammals. These results improve our knowledge of the evolution and dynamics of the vertebrate genomes and will aid in the clarification of the mechanisms that underlie the differentiation between the vertebrate species.

Pulmonary Hypertension Syndrome (PHS) In Broilers: Validation And Fine-Scale Mapping Of Quantitative Trait Loci Affecting PHS Using Advanced Intercross Line.

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Pulmonary hypertension syndrome (PHS) is one of the major quantitative traits that affects both of production and welfare in chicken. In this study, all the work was carried out at Wageningen university, animal breeding and genetics group, we confirmed and fine-mapped QTL for PHS-related traits on chicken chromosomes 2 and 4 using an advanced intercross line (AIL) derived from a cross between two genetically different broiler dam lines originating from the White Plymouth Rock breed. Combined linkage disequilibrium and linkage analysis (LD/LA) was used to refine the position of these two PHS related QTL previously identified in a total genome scan of generation 2. In total 47 microsatellite markers were used at an average marker spacing of 2 cM. The use of a high marker density in combination with the combined LD/LA analysis on generation 7 and 8 of the AIL, resulted in the reduction of the size of the confidence interval on GGA4 from the original 50-60 cM to around 10 cM.

Key words : broiler, pulmonary hypertension, validation, fine mapping

Industrial Biotechnology

Presentations

Extending the tool box, making your polymers work for you

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The application of polymeric systems to the world of biotechnology and pharmaceutical science relies heavily on the delicate structure-function inter-relationship which exists for all polymer based assemblies. This talk aims to show how polymer architecture may be manipulated to optimise the performance characteristics of a typical macromolecular system used in the production of drug carrier and drug delivery systems. The careful use of blends of monomers in well defined ratios will be examined and the influence of polymer composition on formulation design will be reported. The importance of having robust techniques for the quantitative analysis of the composition of co-polymer systems will also be discussed along with some examples of such analysis using Raman and NMR spectroscopy. Finally the talk will consider how hydrophobic modification of a typical polysaccharide can result in a polymer which has very different rheological and drug binding ability compared to the parent macromolecule. A detailed description of the chemistry involved in bringing about the hydrophobic modification will be provided.

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Production and Evaluation of GST Vaccine for Protection of Sheep against *Fasciola Infection*.

Mahran, K.M.A., Safaa Yassin, Raafat, A.A, Mousa, W.M.A., Ibrahim, A.K. and Awad, W.

Glutathione S-transferase (GST) in Fasciola gigantica was isolated by affinity chromatography by which highly purified enzyme was obtained. The GST was evaluated as vaccine in combination with Freund's complete adjuvant and Freund's incomplete adjuvant (FCA/FIA) in sheep against F. gigantica infection. Four groups of sheep of 3 animals each were used. Group (A) was the control negative group. Group (B) was the control positive group. Group (C) was the GST group. Group (D) was the GST and challenge group. The sheep of group (B) and (D) were challenged with 125 metacercaria of F. gigantica. Evaluation of the prepared GST was done by clinicopathological, histopathological and parasitological examinations. ELISA was used for detection of anti-GST antibody titre. All sheep were slaughtered 20 weeks after challenge. After vaccination, the anti-GST antibody titre raised to protect the sheep against F. gigantica. The results indicated that GST caused a delay in egg production, a decrease in EPG (egg per gram) and a decrease in liver fluke. Also, improvement in the anemia and liver damage induced by the F. gigantica was recorded.

PCR methods for identification of *Thermophilic lactococci* strains from the indigenous flora of fermented milk

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Lactic acid bacteria (LAB) are widely used in food industry and their growth performance is important for the quality of the fermented product. By combining results from conventional isolation methods and molecular investigation of 16S rDNA and lactococcal/enterococcal-specific genes, we identify at strain level catalase negative gram positive Thermoresistant cocci isolated from traditional 'leben', a 24-h fermented milk in arid area of west Algeria, in order to isolate new strains of potential interest in milk fermentation and assess their diversity within the wild microbial population. 40 strains phenotypically related to streptococci could be identified as belonging to the species Lactococcus lactis ssp. lactis, Enterococcus faecalis, Enterococcus faecium, and other Enterococcus species. No Streptococcus thermophilus strain was isolated. Ten different phenotype group were recognised, and the species content of these group were in some cases different from the expected features usually given in genus and species descriptions. In particular, 3 atypical lactococci, able to grow in 6.5% NaCl, at 42°C and showing a resistance to thermal stress were isolated. Selective SB medium was found to be a reliable technique, alternative to molecular techniques, allowing the discrimination of most enterococci from lactococci. New starter strains displying unusual properties for their species could be isolated from traditional 'leben' produced in isolated Algerian region. Study of more of this type should provide starter strains for innovation product. This study proposes a simple and reliable isolation method could be used at a first level to isolate number of such strains in different geographical area.

Keywords: Streptococci, thermotolerant wild lactococci , enterococci , indigenous lactic acid bacteria , arid area , 16S rDNA.

Efficacy of excretory/ secretory and cathepsin L antigens for immunization of sheep against Fasciola gigantica infection in Egypt

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Background: Fasciolosis is caused by two trematode species affecting liver, Fasciola hepatica (temperate liver fluke) and F. gigantica (tropical liver fluke). It is a well-known parasitic disease of great veterinary importance causing great economic losses in livestock production, in addition to its public health importance and considered as an emerging human disease.

Material and methods: The execratory/secretory (E/S) antigen prepared from adult Fasciola gigantica flukes collected from the bile ducts of cattle. The cathepsin L antigen released by F. gigantica adult worms was separated from E/S antigen using chromatography technique. Immuno-characterization of F. gigantica E/S and purified cathepsin L using SDS-PAGE and immunoblotting was done. Four groups of sheep were used in immunization trial against Fasciola gigantica infection using the two prepared antigens. The degree of protection was evaluated by parasitological, histopathological examinations and assessment of humoral and cellular immune responses using ELISA and Lymphocyte proliferation assay.

Results: Immunization using E/S antigen revealed a reduction in fluke burden by 45 %, anti-fecundity effect in percentage of 60% and reduction in egg viability by 36%, and thus, a protection rate of 47% (the mean of the 3 aforementioned effects) was achieved by immunization using E/S antigen. Immunization using purified cathepsin L revealed a reduction in fluke burden by 62%, anti-fecundity effect in percentage of 73% and reduction in egg viability by 45%, and thus, a protection rate of 60% was achieved by immunization using cathepsin L antigen, in addition to enhancement of humoral and cellular immune responses and has given satisfactory diminishing of hepatopathological sequelae.

Conclusions: Cathepsin L antigen appeared to be more immunoprotective than E/S antigen, so there is a need for reliable, cost effective production and commercialization of this antigen as a vaccine to reduce competitiveness against chemical treatment of fasciolosis in Egypt.

Purification and characterization of a novel thermoactive cellulase from thermophilic actinomycetes isolate

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An alkaline thermoactive cellulase from thermophilic actinomycete was purified 25.18-fold with a 2.3% yield and a specific activity of 24.83 U mg-1 protein. It was optimally active at pH 8 and 60°C. and was stable from pH 6 to 9 with more than 80% activity remaining after incubation at room temperature for 12 hour. The molecular mass of cellulase was determined. The activity of the enzyme was significantly inhibited by bivalent cations (Ag3+ and Hg2+, 1.0 mM each) and activated by Mn+2and Na+. Thermostability, pH stability, good hydrolytic capability, and stability in the presence of detergents, surfactants, organic solvents and chelators make this enzyme potentially useful in laundry detergents.

Posters

Characterization of Immobilized Nitrate Reductase from *Pseudomonas* sp.

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Nitrate reductase was purified from Pseudomonas sp. SH7 and immobilized by different immobilization methods via entrapment in sodium alginate, agar and sol-gel. It was found that, the sol-gel retained the highest activity (3.5U/ml) while sodium alginate retained (2.8U/ml), but agar method gave about (1.2U/ml).

It was found that, the immobilized nitrate reductase by sol-gel method had the ability to reduce nitrate to nitrite in soil sample contaminated with 0.5 mM GTN and the enzyme gave a high reduction rate after one hour of reaction ,with a broad pH range from 6.5-10, wider temperature range. The result showed that the enzyme lost 50% of its activity when it was exposed to 80oC for 15 min., but it retained its activity when it was stored at 4˚C after three month storage period.

Key word: Nitrate reductase, Enzyme, Immobilization, Sol-gel

New cold-Adepted and thermostable amylase from new isolate of thermotolerant bacteria

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Anew thermotolerant bacteria was isolated from Awsiem (Giza) (Egypt) soil. This isolate produced amylase. This amylase had an apparent molecular mass of 90 kDa as estimated by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis and zymogram activity staining. The partial purified enzyme was active in low and high temperature and had a maximal activity on starch at pH 9 and 80°C. The enzyme was stable at pH 9 for 72 h and retained half of its activity after incubation at 80°C for 120 min at pH 9. The Km and Vmax values, the effect of metal ions, solvents and detergents and The hydrolysates of soluble starch by the enzyme were determinated. These properties indicated a possible use of this amylase in detergent, and in other industrial applications.

Screening, characterization of thermostable cellulase enzyme from the new thermophilic actinomyces isolated from Egypt

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Abstract:- The new strain grow hetertrophically under aerobic condition at optimally on carboxymethyl cellulose at 50°C and pH 8.0. This strain was found to utilize cellulose as carbon source during batch cultivation and produce extracellular cellulase . The cured enzyme is optimally active at 60°C and pH 8.0. The cellulase from this strain is fully thermostable at 60°C for 24 hour. The molecular mass for the enzyme and zymogramme staining and the effect of metal ions and detergents were determinated .

Synthesis and in vitro antitumoral activity of diazepine and diazocine derivatives

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Benzodiazepine and diazocine derivatives are an important class of heterocyclic compounds which possess a wide range of therapeutic and pharmaceutical properties. Derivatives of 1,5 benzodiazepine , 1,4 naphthodiazepine and 1,5 naphthodiazocine derivatives were evaluated for their in vitro anticancer activity toward cell lines of nine different types of human cancers by the National Cancer Institute (NCI) for their anticancer activity following the known in vitro disease –oriented anti tumor screening program, which is based upon use of multiple panels of 54 human tumor cell lines.

Some of these compounds demonstrated inhibitory effect on the growth of a wide rang of cancer cell lines generally at different concentration.

Environmental Biotechnology

Presentations

Challenge of growing food crops on degraded land and land contaminated with organic pollutants

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The International Energy Agency in 2007 projected that the world's primary energy needs would grow by 55% between 2005 and 2030, to reach 17.7 billion tonnes of oil equivalent, and that CO2 levels would increase to 42 Gt in 2030, up 57% from 2005. Figures such as these have resulted in increased attention1 being focused on the role that agriculture might play in meeting our energy requirements, since plants provide a cost-effective route for capturing solar energy as well as sequestering CO2. However, agriculture will also need to meet the increased demand for food as the world's population grows from 6.5 billion today to 8.3 billion in less than 30 years' time. Yields of maize, wheat and rice continue to increase at 1.1 per cent per year but the world's population is growing faster at 1.2 per cent per year. On top of this, the demand for animal feed is rising as the demand for meat increases with rising incomes. Current global agricultural land is 4.96 GHa, and meets a global food consumption of ca 25 EJ. On the other hand, global fossil energy demand is 487 EJ, but global arable land and pasture is only ca 1.6 GHa. Furthermore, 65 per cent of all soil on Earth shows signs of degradation such as erosion, desertification or salinisation. Over 300 million hectares of former agricultural land is now reported to be too degraded to produce food, and a further 10 million hectares become degraded or damaged every year. On top of this, the amount of land used for agriculture has to remain stable if we are to protect wild spaces, uncultivated land and biodiversity. These figures highlight the

urgent need to translate our understanding of the effects of growing crops on degraded land and land contaminated with organic pollutants into practical solutions for meeting the world's food, feed and energy demands.

Global food consumption	25 EJ
Global fossil energy use	488 EJ
Global arable + cropland	≤1.6 Gha
Global agricultural land	4.97 Gha

The focus of our work has centered on understanding the interactions between plants and organic contaminants in polluted soils. Mechanisms for controlling the uptake and sequestration of toxic organic compounds in plants are still relatively unknown. Lipophilic organic compounds with a log Kow >4 have a high potential for retention to plant root surfaces as well as soil organic matter. Their presence hinders water from spreading homogeneously in soil and once they are absorbed to the outer walls of root surfaces, cause plants to develop symptoms akin to water stress, ie reduction in root growth rate, increased cell wall lignification of roots, and reduced development of vessels. Roots also develop a markedly thickened endodermis, which may also help to retain and prevent the transport of organic pollutants into upper plant parts. Peeling root crops exposed to soil polyaromatic hydrocarbons will reduce substantially (up to 97% in the case of PCBs) the load in carrots but evidence for the penetration of lower molecular weight PAHs deep into the root tissues from the carrot surface has also been found2. These data indicate that crops grown in soils contaminated with organic pollutants will show impaired food quality and reduced yields unless

remedial action is taken. Agricultural measures such as diluting the concentration of toxic organic pollutants in soil with non-toxic organic matter may reduce the level of pollutant uptake and improve yields by reducing the tendency for drought-like symptoms to develop. However the use of drought resistant (genetically-modified) crops will enable contaminated soils to be brought into agricultural productivity and enable crops that sequester CO2 during growth to be used as renewable energy resources

Evolutionary Origins, Diversification, and Biogeography of Liver Flukes (*Digenea, Fasciolidae*)

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Fasciolid flukes are among the largest and best known digenetic trematodes and have considerable historical and veterinary significance. Fasciola hepatica is commonly implicated in causing disease in humans. The origins, patterns of diversification, and biogeography of fasciolids are all poorly known. We have undertaken a molecular phylogenetic study using 28S, internal transcribed spacer 1 and 2 (ITS-1 and ITS-2) of nuclear ribosomal DNA, and mitochondrial nicotinamide dehydrogenase subunit 1 (nad1) that included seven of the nine recognized species in the family. The fasciolids examined comprise a monophyletic group with the most basal species recovered from African elephants. We hypothesize fasciolids migrated from Africa to Eurasia, with secondary colonization of Africa. Fasciolids have been conservative in maintaining relatively large adult body size, but anatomical features of their digestive and reproductive systems are available. These flukes have been opportunistic, with respect to switching to new snail (planorbid to lymnaeid) and mammalian hosts and from intestinal to hepatic habitats within mammals.

Biodegradation of Synthetic Azo Dyes by Bacteria

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The aim of this study is to identify several indigenous microbes potent in azo dye biodegradation and to better understand the conditions necessary to enhance the biodegradation process. Bacterial isolates were obtained by enrichment cultures technique from 8 textile industrial wastewater and 2 soil samples collected from textile and dyeing plants at New Borg El-Arab, Cairo, Kafr El-Dawar and El-Mehalla El-Kubra regions. The isolation of microbial consortium involved in dyes bioremoval was done on mineral salts medium (MSM) supplemented with the dyes. The microbial consortia were able to decolourize dyes under anoxic and anaerobic conditions. Hundred and fifty bacterial isolates were obtained from the enrichment cultures. Each isolate was checked for the ability to decolourize Direct Violet (DV) and Reactive Red (RR) dyes. The study revealed that no decolourization can take place by any isolate under aerobic conditions. However, the percentage of decolourization by isolates reached 90.0 and 96.4 % of the original colour of DV and RR dyes after 9 days under anoxic conditions. Twenty-five isolates were identified as the most efficient in colour bioremoval. Based on the morphological and biochemical analysis of these isolates. Two were long rod spore former identified as Bacillus sp.. Six isolates were short rods identified as Pseudomonas sp., and seventeen belonges to family of Enterobacteraece. The degradation of dyes is usually judged by the formation of aromatic amines. Most of the isolates under anoxic conditions were found to produce aromatic amines from the tested dyes.

Keywords: degradation, textile dyes removal, bioremediation, bacteria.

Oxidative stress and DNA damage in relation to transition metals overload in Abu-Qir Bay, Egypt

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The aim of the present study is to evaluate the relationship between transition metals overload (especially Fe and Cu) in Abu-Qir Bay, Egypt and several biomarkers of oxidative stress. Levels of Catalase (as U/mg protein), and lipid peroxidation (as Malondialdehyde [MDA] concentration), have been measured in liver tissues of fishes living in the bay. Moreover, the levels of DNA damage (as the number of apurinic/apyrimidinic [AP] sites/1x105 bp) in liver and gills tissues were estimated. Concentrations of Fe and Cu in fishes (Mugil cephalus) liver tissues were found significantly higher in samples from the polluted area (Abu-Qir Bay) as compared to samples from the reference area (Sidi-Barrani coast): Fe: 407.2 ± 188.58 µg/g wet wt vs. 216.11 ± 68.95 µg/g wet wt; p=0.01, Cu: 54.03 ± 20.20 µg/g wet wt vs. 17.77 ± 13.84 µg/g wet wt; p=0.0001. This increase could account for the observed increase in MDA concentration (15.77 ± 18.31 vs. 2.5 ± 1.6 nmol/L; p=0.035), and the elevated number of AP sites (13.98±7.37 vs. 0.3718 ± 0.5683 AP site /1x105bp; p= 0.001). Similarly, the activity of Catalase enzyme implicated in the cellular defense was also significantly elevated (58.31 ± 12.26 vs. 28.47 ± 4.02 U/mg; p=0.032). Altogether, the results of this study indicated a clear relationship between the pollution degree of marine environment and both biochemical and molecular responses of the piscine system which in turns reflects an important role of pollution with transition metals (Fe & Cu) in marine toxicology.

Key words: catalase, lipid peroxidation, AP sites, marine pollution, Mugil cephalus

Reducing Emissions in Manufacturing through Renewable Energy

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Analysis of the impact of rising energy use In China and India has recently led the International Energy Agency to conclude that the world's energy needs could grow by 55% between 2005 and 2030, to reach 17.7 billion tonnes of oil equivalent, with fossil fuels –oil, gas and coal – dominating the fuel mix (80%). CO2 levels would increase commensurately to 42 Gt in 2030, up 57% from 20053. Against this background, and with the realisation that a coherent EU energy policy was needed the European Council last year agreed to a common strategy for energy security and climate change, which included a commitment to source 20% of the EU's energy from renewables by 2020 (covering electricity, heat and transport) and a 20%/30% GHG emissions reduction depending on wider international effort. For the UK, this has been translated into a target of 15 per cent of final energy consumption to be accounted for by energy from renewable sources in 2008.

Renewable energy is an integral part of the UK's longer-term aim4 of reducing CO2 emissions by 60% by 2050 compared with 1990 levels under the Kyoto protocol. Currently around 60% of the UK's energy consumption is as electricity and heat; a further 31% is consumed in transport and the remainder as feedstock. In 2002, the Renewables Obligation (RO) was imposed on electricity suppliers to achieve a target of 10% of electricity supply from renewable energy by 2010 compared to 1.8% in 2002, and the Renewable Transport Fuel Obligation was announced in 2005 to ensure that 5% of all road vehicle fuel should be supplied from sustainable renewable sources by 2010. Despite these targets, by 2006 electricity supplied from RO eligible sources stood at only around 4% of the UK's total electricity, whilst the targets for biofuels in road transport, a central plank of the programme to combat climate change, are likely to be readjusted downwards to 4%.

The focus of our work has centred on measures that could be adopted to reduce CO2 emissions and energy requirements in the region. The use of Combined Heat and Power (CHP) could cut energy requirements, greenhouse gas emissions and costs incurred by a range of manufacturing industries by as much as 50%, and if delivered using engines that burnt liquid biofuels instead of fossil fuels, would reduce emissions to zero provided the fuel used was vegetable oil and not biodiesel. This is because production of the latter uses the fossil fuel methanol for transesterification and produces an energy-rich ‚waste' product, glycerol. By the same token, conversion of plant oil to biodiesel for use in the road transport industry should be discouraged. However to meet demands for food and fuel will require modifications to existing supply chains, the establishment of ‚biomaterial handling stations' and introduction of new biotechnologies to process food wastes and agricultural residues to liquid and gaseous biofuels sustainably

Posters

Biotechnological interventions for developing agricultural production Biofuels

Motaz M. Elewa

Because of the raising global concerns about Climate Change, fossil fuel shortage and its booming prices; alternative energies – from Renwables to Biofuels – started to grab the attention of the global strategies because of its lesser environmental impact and sustainability. Researchers are developing the agricultural production of Biofuels like; ethanol and biodiesel from different resources like; sugar crops, grains, oilseeds, lignocellulosic materials, algae and cyanobecteria through biotechnological interventions to solve different problems like Food Vs. Fuel and biodiversity issues.

Environmental Impacts of Modern Gene Technology

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In the light of the general consensus that modern gene technology is required for improving human life and help keep our environment clean, genetically modified organisms (GMOS) and GM foods are now available in the international market. Yet, the sale of these products is being permitted without proper assessment of their risks and without adequately informing the public. In fact very little data is released either for or against any special health or environmental risks posed by these products. Some scientists argue that GMOs and GM foods are not substantially different from existing organisms and foods and pose no special risks. Meanwhile, others express fear of the radical changes being made, to the GMOs, by gene technology that never happen in nature by traditional breeding. Current regulations require only minimal safety testing for some GMOs and GM foods; in no case do regulations require evaluation of long term impacts on health, biodiversity and environment. This article is concerned with impacts of gene GMOs on a number of environmental aspects concerned with biodiversity crises and the problems of species extinction and genetic resources depletion. Another major topic is the role of gene technology in combating pollution and its possible functions in cleaning up the environment. The article further touches on the ethical aspects that has been raised since the introduction of GMOs and GM food and also on the principles of safety and risk assessment of modern approaches that involves gene technology processes.

The impact of water contamination with diazinon on stress-proteins HSP70 induction in Oreochromis niloticus.

Nagwa Elnwishy and Dalia Sabri

The research investigated the use of stress proteins HSP70 in fish as a biomarker to evidence the chronic exposure to pollution. Equal male tilapia Oreochromis niloticus was exposed to LC10 (0.28 mg/L) (G1) and LC33.5 (1.87mg/L) (G2) of diazinon, commonly used and detected Organophosphorus insecticide in Egypt, for 30 days. Both were recovered for 7 days (G3, G4) respectively. All groups were compared to control fish of equal size (G5). HSP70 inductions of blood samples analysis using SDS/PAGE and molecular marker (214 - 6.8kDa) was identified in all groups. Results revealed an induction of HSP70 proteins (71 and 77 kDa) in G1, the induction was removed by the recovery in G3, while 78.16 kDa was induced in G2; the induction intensity was decreased in G4. The results suggest that expression of HSP70 in tilapia is sensitive to the chronic exposure of diazinon contaminations in the aquatic ecosystems, which can reflect the cellular responses of fish to the stress of water pollution.

Utilization of medicinal plants waste for fungal growth and textile dye removing

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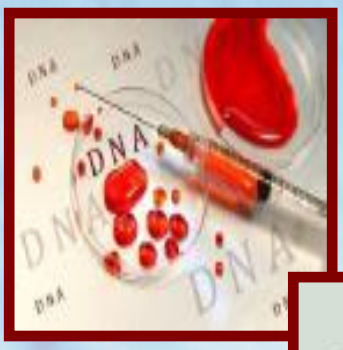
There are great environmental concerns to develop new and efficient ways to remove azo-dyes from wastewater. Among these ways abiotic and biotic agents were tested for removal of dyes. Cultivate of Aspergillus niger growth and the bioremoval of four textile dyes using several medicinal plants wastes has been studied.

Three wastes of distillation medicinal aromatic plants namely; garlic (Allium sativum L.), jasmine (Jasminum officinale L.) and thyme (Thymus basilicum) in addition to wheat bran (Triticum aestivum L.) were used as growth media for Aspergillus niger. This fungus is used for textile dye bioremoval. The plant waste supported good growth of fungi in rather short incubation time (7 days).

The aim of this study is to adopt low-cost technology for removal of some textile dyes by biotic or abiotic agents. Four commercial dyestuffs; direct violet, direct green, reactive red and acid red were included in this study. It was found that color bioremoval of the various dyes within 72 hours of incubation using Aspergillus niger biomass varied from 40.2 to 99.6% of the original dye color. This finding was dye-dependent. In absence of fungi, the tested abiotic sorbents (wheat bran, jasmine, garlic and thyme) showed comparatively low removal capacity amounting < 60% in the majority of treatments. The bioremoval efficiency by fungi obviously raised up to > 90%. These findings confirm the role of fungi in decolorization of textile dyes.

Biotechnology



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