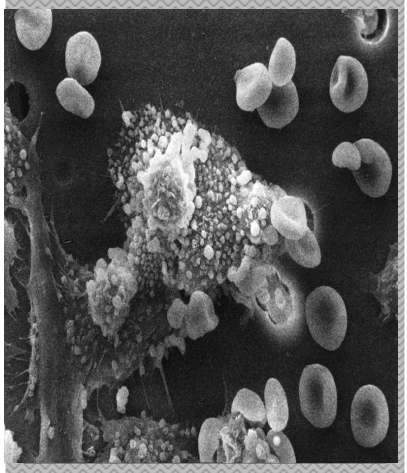

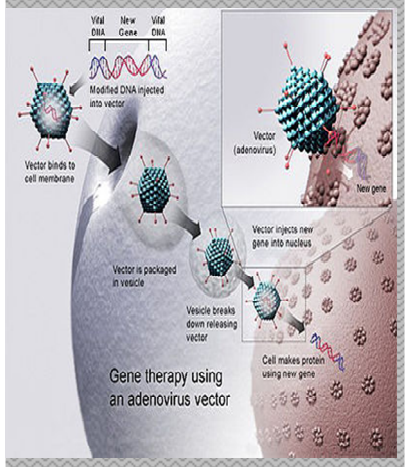

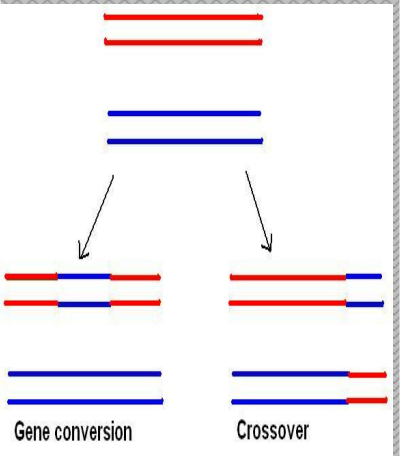

EMGEN Newsletter

Vol. 4, Issue 6, March, 2012

INSIDE THIS ISSUE:

Eastern Mediterranean Health Genomics and Biotechnology Network (EMGEN) was created in 2004 with collaboration of representatives of selected center of excellence in (health related) molecular biology, biotechnology & genomics in the Eastern Mediterranean region by recommendations and efforts of WHO/EMRO.

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Article

Nanospider Technology for the Production of Nylon-6 Nanofibers for Biomedical Applications

An article entitled "Nanospider Technology for the Production of Nylon-6 Nanofibers for Biomedical Applications" aims to explain the production of Nylon-6 nanofiber mat incorporated with 5,5-dimethyl hydantoin (DMH) as an antimicrobial drug from formic acid. The study was carried out by Dr. Mohamed H. El-Newehy; he is working as Petrochemical Research Chair, Chemistry Department, College of Science, King Saud University, Riyadh, Saudi Arabia; and the paper was published in Journal of Nanomaterials 2011, Article ID 626589,

Dr. Mohamed El-Newehy

Electrospinning is widely approved as a method to fabricate submicron polymer fibers. Electrospinning is a fiber-forming procedure, where the high voltage is used to produce an electrically charged jet of polymer solution or liquefy from the needle.. Nanospider is an adjusted electrospinning approach which requires the use of a high-voltage electrostatic field to produce an electrically charged stream of polymer solution or melt. The innovatory concept of the Nanospider is based on the probability of producing nanofiber from a thin layer of liquid polymer. In addition, Nanospider can process a wide range of polymers in diameters of 50–300 nm into nonwoven webs. Extensively, polymer-based drug-delivery systems are used to optimize the therapeutic properties of drugs and to give them safer, effective, and reliable. The main benefits of the fibrous conveyors are that they offer site-specific delivery of drugs to the body. Furthermore, more than one drug can be encapsulated clearly into the fibers. Due to the high outside area and porous construction of the electrospun fibers, they have applications in many fields such as medicine, biosensors (Frey and Baeumner 2006), allergic solar cells (Zhao et al. 2006), tissue engineering (Wutticharoenmongkol et al. 2006), photonics (Telemeco et al. 2005), nano composites (Tomczak et al. 2005), catalysts (Lee et al. 2005), and antimicrobial materials and membranes (Dersch et al. 2005).

The focus of this paper is the encapsulation of 5,5- dimethyl hydantoin as an antimicrobial drug into electrospun nylon-6 nanofiber using Nanospider technology as a modified electrospinning approach. The examinations base on, Scanning Electron Microscope (SEM), UV-Vis Spectrophotometer, Thermo gravimetric Analysis (TGA) and FT-IR Spectroscopy.

Cultures of several micro-organism were used in the study included: *Escherichia coli*, *Pseudomonas aeruginosa*, *Aspergillus niger*, and *Aspergillus flavus*. The release of 5,5-dimethyl hydantoin (DMH) from the electrospun nylon-6 mat was determined by placing a known mass of the material (2mg) in 3mL buffer of pH 7.0 at 37℃. The morphology of the obtained electrospun nylon-6 nanofiber containing drug using SEM showed that nylon-6 nanofiber have an average diameter of around 15–328 nm.

The cover thickness ranged from 40 to 50µm. As well, the fibers acquired had cylindrical morphology and no fiber bundles, showing that the distance between the functioning electrode and gathering electrode 18 cm was sufficient for proper evaporation of the solvent. The encapsulation of DMH in electrospun nylon-6 nanofiber is prosperous and was established using FTIR spectra and TGA. The thermogram of electrospun nylon-6 nanofiber showed that the electrospun nylon-6 nanofiber including drug was demeaned in three steps. The first step appears for the evaporation of the residual absorbed water at the temperature range of 30–100°C.The second step at the temperature range of 100–200°C, which represents the degradation of DMH. The third step at the temperature range of 200–475°C, which acts for the degradation nylon-6. Moreover, the TON for the nylon-6 was found to be 401°C, and leaves a residue of 3.4% at 475°C.

The benefits of the electrospinning method are that it could be applied for a wide range of pharmaceutical compounds either functional or nonfunctional. It could be used for more than one drug at the identicle time. Furthermore, it is possible to be electrospun as layers. The microphotograph of the electrospun nylon-6 nanofiber including drug showed routine fiber diameter containing DMH entrapped on it.

Antimicrobial analysis results acquired from the disc method in the present study revealed that the electrospun nylon-6 nanofiber including drug displayed potential antibacterial activity against *Escherichia coli* and *Pseudomonas aeruginosa*, and antifungal activity against *Aspergillus niger* and *Aspergillus flavus.* Based on Scanning Electron Micrograph (SEM), the effect of the electrospun nylon-6 nanofiber including drug on *Aspergillus niger* and *Aspergillus flavus* caused definite deformation and visible shrinkage in fungal strains studied. The most important result was a great reduction of wrinkling and deformation of the fungal cells.

On the other hand, *Aspergillus niger* and *Aspergillus flavus* cells were studied in damaged pellets and slightly looked like *pseudohyphae* that were highly abnormal and aborted. Moreover, the *Escherichia coli*

and *Pseudomonas aeruginosa* cells inspected using SEM were completely deformed and presented severe destruction. The surfaces of the bacterial cells were damaged and had become harsh and swollen, but unlisted. In contrast, it was found that complete cells of *Aspergillus niger* and *Aspergillus flavus* had steady surfaces with comprehensive whole morphology. It was ascertained that the structure of the cell wall surface layer was wrinkled, and around pores were partially distorted showing that the cytoplasmic structures were flushed out of the cells. irregular cell division was discovered at high frequencies among cells that tried to divide in the presence of the polymer. Many cells were enlarged, lengthened empty ghosts, or disconnected consistent with the extremely low viability. The effect was explored and contrasted with the control cells. This malformation in bacterial and fungal cells may be due to inhibition of cell wall synthesis, repression of protein synthesis, inhibition of nucleic acid synthesis, inhibition of metabolic pathways, and intervention with cell membrane morality (Tenover 2006, Hart et al. 2010). These consequences clearly indicate that the anti-bacterial and antifungal pursuit of the electrospun nylon-6 nanofiber including drug changes with the species of the organisms used. In fact, the appearance in recent years, of strains of microorganisms that are immune to commonly used antibiotics has stirred a search for new naturally happening bacterial agents who may have clinical utility. There is a lot of exploit to try to use antimicrobial peptides for therapeutics. This is be-cause bacterial resistance to traditional antibiotics has become a major problem worldwide due to their broad use. Thus, the study clarifies the value of the used of the electrospun nylon-6 nanofiber including drug, which could be of great interest to the development of new antimicrobial materials. in conclusion the author elongates his appreciation to Prof. Dr. Salem Al-Deyab, Supervisor of Petrochemical Research Chair, for giv-ing the services to carry out this work and his precious contribution as well as the nanofibers research team, Prof. Kenawy and Dr. Abdel-Megeed, at Petrochemical Research Chair. Furthermore, the authors develop their admiration to the Deanship of Scientific Research at King Saud University, for funding the work through the investigation group project No RGP-VPP-021.

Reference:

Mohamed H.El.Newehy, Salem S.AL-Devab, El-Refaie Kenawy and Ahmad Abdel-Megeed, (2011), Nanospider Technology for the Production of Nylon-6 Nanofibers for Biomedical Applications, *Journal of nanomaterial*, *ID 626589.*

Biomolecular Molecular Dynamics (MD) simulations

In the past, compared to our scientific knowledge of how natural biosystems function, we had practically no knowledge of how to engineer biosystems, i.e., how to plan, build, repair, maintain, operate, and change them in a logical and knowledgeable manner. Thus, various efforts such as the EcoCyborg research project began with the basic intent of making a contribution to the science and engineering of biosystems. Nowadays, researchers in bioinformatics and systems biology are increasingly using computer models and simulation to understand complex inter- and intra-cellular processes. They investigate Biological systems and Biotic communities by using different models and simulation methods. Also these kinds of methods are very practical for investigating the efficacy of drug in human body, diagnosing the reasons of diseases and finding the treatment of them. Molecular dynamic simulation is a famous computer simulation method.

Here is an example that used MD simulation in medical approach:

TAR is the first 59 nucleotide (nt) of the budding pre-mRNA transcript of human immunodeficiency virus (HIV). The standard of viral gene expression in HIV needs highly specific RNA-protein interaction. As a result, the RNA-protein (peptides) interactions have been greatly studied as a potential target for anti-HIV involvement. Recently, a TAR-binding tripeptide (L-Lys-D-Lys L Asn) was found to show the repression of Tat (a protein to actuate viral gene transcription by interacting with TAR)-mediated transcriptional activation in tissue culture. The attractive issue is that the NMR tests on this delimited TAR did not produce TAR NMR spectra characteristic of the arginine-induced configuration change. In order to find the special binding mode of this tripeptide with TAR, docking tactics and subsequent MD simulation methods have been utilized. A small furrow T type binding is found shown below.

Why Molecular Dynamic?

The stationary view of a biomolecule, as acquired from e.g. X-ray while radically useful, only supplies an average, frozen view of complex systems. Thus inadequate for understanding a wide range of biological pursuit MD imitations in many respects are very similar to actual experiments. We should select and set up a model system and balance then perform MD for a period of time and measure one or various noticeable which can be expressed as a role of the positions and moment of the particles.

History of biomolecular MD simulations:

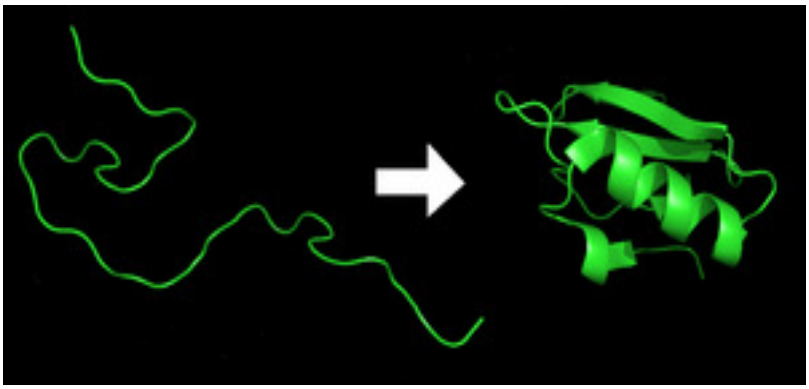
It is more than 30 years since the first MD simulation of a protein was presented, describing the dynamics of a folded non-filamentous protein consisting of 58 amino acids in vacuum for 8.8 ps. Since then advances in computing technology have enabled MD simulations to become considerably larger in size and cover significantly longer timescales. Nowadays, microsecond all-atom MD simulations are feasible. Furthermore, biological systems are now modeled more realistically by the inclusion of the surroundings, including aqueous solvent and counter ions in solution. Future work is likely to address *in vivo* conditions, where proteins experience a significantly different 'crowded' environment. Another major development in the past several years: Usage of PBC to ensure that the system does not have an abrupt border with a vacuum and to calculate electrostatic interactions using particle-mesh Ewald (PME) summation methods. Only PME methods enabled stable trajectories to be routinely obtained. In the mid 1990s it was, for instance, not possible to perform structurally stable MD simulations of DNA.

Initialization

Before the MD simulations can be started one has to perform below steps:

1. select an initial structure, e.g., an NMR or crystal structure
2. solvate this structure and add ions thereby neutralizing the system:
   - *-Water coordinates are taken from pure water simulations.*
   - *-Ion-placement algorithms are usually available in MD software that place positive ions in electronegative pockets and negative ions in positively-charged cavities.*
   - *-Removal of overlapping atoms.*
3. minimize the solvated system (energy relaxation)
4. equilibrate the system, i.e., a short MD simulation during which the system is equilibrated

Assignment of initial velocities is based on the equilibration of partition theorem. The total kinetic energy of a system, E-kin, is shared equally amongst all energetically accessible degrees of freedom of a system. It further states that each quadratic degree of freedom will, on average, possess an energy (1/2)kBT. A 'quadratic degree of freedom' is one for which the energy depends on the square of some property.



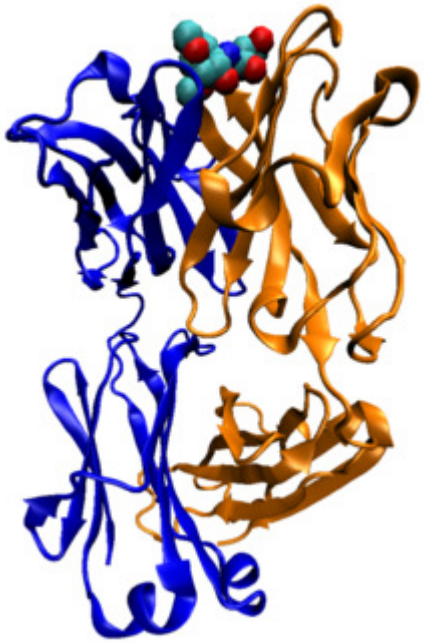
Protein before and after folding

Integrating the Equations of Motion

Firstly we should perform classical MD one has to solve Newton's equations of motion. Then we should numerically solve this initial value problem, a time step is chosen and the sampling point sequence considered. The task is to construct a sequence of points Rn that closely follow the points R(tn) on the trajectory of the exact solution. One of the simplest, but also usually the best algorithm is the Verlet algorithm. To derive the Verlet algorithm, we should start with the Taylor expansion of the coordinate of a particle, around time t. An energy-conserving trajectory gives results for a micro canonical (N,V,E) ensemble (i.e., fixed N, volume, and total energy). More typically, we are interested in a thermal ensemble for biosystem simulation, such as the canonical (N,V,T) ensemble (fixed N, volume, and temperature) and at last we should thermostat, barostats, time steps, total time of simulation and the radius of cut-off .

Using molecular dynamic simulation for investigating protein folding

Proteins consists of linear chains of amino acids, but they do not simply flop in your cells, instead, the regarding proteins "fold" up into a particular three-dimensional conformation in solution (tertiary structure), and this conformation helps the proteins to carry out the functions, which are responsible for. Understanding the protein folding is the next step in deciphering the genetic code. Protein folding mechanisms have been widely investigated over the past few decades through either experimental and computational means, although the long timescales required for simulation of the folding steps have meant that simulation of complete folding trajectories in the required solvent were not possible until very recently.



Ribbon diagram of a mouse antibody against cholera that binds a carbohydrateantigen

Instead, protein foldable simulations have widely made use of course models, implied solvent, or the use of very large entireties of shorter trajectories to obtain information on the physical folding pathway.

The close interaction between complicated experiments and specialized simulations has led to a general understanding of the mechanism of protein folding.

Recent advances, however, have made combined experimental and computational investigation of protein folding possible through the development and proteins that fold on the microsecond and even sub-microsecond timescale, and through advances in molecular dynamics (MD) simulations allowing simulation of multiple microsecond folding trajectories within a few months on new supercomputers. Through simulations of a variety of protein mutants with different folding rates, it is hope to gain a general understanding of factors driving protein folding.

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Genetically modified foods

Genetically modified foods (GM foods or GMO foods) are kinds of foods derived from genetically modified organisms (GMOs). They are most used to refer to crop plants created for human or animal consumption using the latest molecular biology techniques. Such plants are modified in the laboratory to improve desired traits, for example, increased resistance to herbicides or improved nutritional values. The creation or improvement of desired traits have traditionally been carried out through breeding, but ordinary plant breeding methods can be very time consuming and may not be successful. However, genetic engineering, can create plants with the desired trait very rapidly and with acceptable accuracy.

Genetic modification involves the insertion or deletion of genes. In the process of cisgenesis, genes are transferred between organisms that could be conventionally bred. In the process of transgenesis, genes from various species are inserted, which is a form of horizontal gene transfer. In nature this can occur when exogenous DNA penetrates the cell membrane for any reason.

To do this artificially, one may need transferring genes as part of an attenuated virus genome or physically inserting the extra DNA into the nucleus of the intended host using a microsyringe, or as a coating on gold nanoparticles fired from a gene gun. However, other methods exploit natural forms of gene transfer, such as the ability of *Agrobactrium* to transfer genetic material to plants, and the ability of lentiviruses to transfer genes to animal cells. For example, plant geneticists can isolate a gene responsible for drought tolerance and insert that gene into a different plants. The new genetically-modified plant will gain drought tolerance as good. Not only can genes be transferred from one plant to another, but genes from non-plant organisms also can be produced. Other techniques by which humans modify food organisms include selective breeding; animal breeding, and somaclonal variation. GM foods were first put on the market in the early 1990s. Typically, genetically modified foods are transgenic plants products: soybean, corn, canola, and cotton.

Usage of GM foods

Pest resistance. Crop damages due to pest insects can be staggering, resulting in huge financial suffering for farmers and starvation in developing countries. Farmers usually use many tons of chemical pesticides annually. Consumers do not wish to eat food that has been treated with pesticides because of potential health dangers. By using GM foods such as B.t. corn we can eliminate the application of chemical pesticides for reducing the cost of bringing a crop to market.

Disease resistance. There are many viruses, fungi and bacteria that led to plant diseases. Plant biologists are working to produce plants with genetically-engineered resistance to these diseases.

Cold and drought tolerances. unanticipated frost can destroy sensitive seedlings. An antifreeze gene from cold water fish has been introduced into plants like tobacco and potato. With this antifreeze gene, these plants can tolerate cold temperatures that normally would kill unmodified seedlings. Also as the world population grows and more land is utilized for housing instead of food production, farmers will need to grow crops in locations previously unsuited for plant cultivation. Creating plants that can withstand long periods of drought or high salt content in soil and groundwater will help people to grow crops in formerly inhospitable places. As we said before the scientists try to insert drought tolerance gene into a different plant.

Pharmaceuticals. Medicines and vaccines often are costly to produce and sometimes require special storage conditions not readily available in third world countries. Researchers are working to develop edible vaccines in tomatoes and potatoes.

Nutrition. Malnutrition is common in third world countries where impoverished peoples rely on a single crop such as rice for the main staple of their diet. However, rice does not contain enough amounts of all necessary nutrients to prevent malnutrition. If rice could be genetically engineered to contain additional vitamins and minerals, nutrient deficiencies could be alleviated.

Herbicide tolerance. In some condition for some crops, it is not cost-effective to remove weeds by physical means such as tilling, so farmers will often spray large amounts of different herbicides needed **(**weed-killer) to destroy weeds.

Crop plants genetically-engineered to be resistant to one very powerful herbicide could help prevent environmental damage by decreasing the amount of herbicides.

What could be some possible dangers of GM foods?

- *New toxins and allergens in foods*
- *Other damaging effects on health caused by unnatural foods*
- *The creation of herbicide-resistant weeds*
- *The spread of diseases related traits across species barriers*
- *Loss of biodiversity in crops*
- *The disturbance of ecological balance*

Artificially induced characteristics and inevitable side-effects will be passed on to all subsequent generations and to other related organisms. Upon releasing such, they can never be recalled or contained. The consequences of this could be immeasurable.

How Genetic Engineering Can Create Hazardous Foods

Genetic engineering introduces into foods new proteins that can either directly or indirectly threaten health. Genetic engineering introduces new genes, that is equal to new genetic data, into the cells of a food producing living organism. Since a gene contains the information for a protein, that new genetic information causes the organism to produce one or more new proteins.

The food produced by that genetically engineered organism will include those new proteins. Therefore, genetic engineering introduces new components into the foods. The new proteins that genetic engineering introduces into foods can come from virtually any organism on earth, and most of these new proteins will never have before been present in significant amounts in human foods. Because people have never previously eaten these proteins, the effects that they might have on health will not be known.

These new proteins could, themselves, led to allergies or be toxic. They could alter the cellular metabolism of the food-producing organism in unintended and unanticipated ways, and in turn, these alterations in metabolism could cause allergens or toxins to be produced in the food. One more possibility is that, as a result of these changes in metabolism, the food-producing organism might fail to make some important vitamins or nutrients. Consequently, the genetically engineered food would lack important nutrients that are usually present in the corresponding, natural, non-genetically engineered food.

Genetic engineering can potentially provide dangerous foods by generating mutations in the DNA of the food-producing organism. Introducing a recombinant gene into the DNA of a food-producing organism can disrupt the natural sequence of genetic information within that DNA. Thus, the process of genetic engineering could lead to mutations to the food-producing organism. These mutations can be considered a second source of potential destroying effects of genetic engineering. It must be pointed out that the DNA of most food-producing organisms is very complicated. Part of this DNA is in the form of genes, but many parts of the DNA of these organisms do not contain genes. Now the functions of these other portions of the DNA are not fully understood by science. Genetic engineers usually assume that genetic manipulations will be harmless if are bound to the DNA of unknown function and avoid genes. However, this argument is really no better than saying that what you do not know cannot hurt you.

An example of a class of genetically engineered foods that are of definite concern are those that have been modified to produce biological control agents, such as the family of insecticidal Bt toxins. Each of the Bt toxins is specific for a certain class of insects. The Btk toxin, which has been used in organic farming for years, has not been reported to cause toxic reactions in consumers when used in this way.

However, it would not be astonishing if a compound, such as Btk toxin, that has powerful biological activity in one class of organisms might also have some biological activity even in a distant phylum such as the vertebrates. Such activity might become apparent if the toxin is consumed in larger quantities, as will occur in transgenic foods derived from organisms engineered to express this toxin constitutively at high levels. Some of the potential biological properties of genetically engineered proteins or their metabolites can be assessed by various *in vitro* tests.

However others maynot, and by the very diversity of possible effects and the complexity of the physiology, it is improbable to carry out laboratory experiments that will exhaustively, thoroughly, and conclusively establish that a genetically engineered food is free of adverse biologic effects, and therefore safe.

In many cases, a finite probability could remain that some toxin or other biologically active molecule has been produced in the recombinant food for which no adequate test is available. Therefore, it seems crucial that each transgenic food be tested for toxicity in human volunteers.

Without these experiments, there will always be an appreciable probability that the toxic qualities of some genetically engineered foods will not become apparent until that food is placed on the market and the health of consumers is measured in a post marketing surveillance, which can be seen as unethical by some.

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Knockout of Protein Prevents Colon Tumor Formation in Mice

A protein that regulates cell differentiation in normal tissue may have a divers role in colon and breast cancer, activating proliferation of damaged cells.

The protein, called PTK6, is found in normal skin and gut cells and also in cancerous, but not normal, breast tissue. The research and proof have concentrate on the normal function of this protein in the gut, where it regulates growth and differentiation. Epithelial cells turn over quickly. To change them, new cells must be continuously produced that become specialized, or differentiated, to perform specific functions. The researchers developed a mouse that laced the PTK6 gene.

Based on their investigation of increased growth in the intestine, mice lacking PTK6 would be more susceptible to cancer. Researchers induced colon tumors resembling human sporadic colon cancer in mice lacking the PTK6 gene and in normal mice by using carcingon. Mice lacking PTK6 were highly resistant to the carcinogen and developed fewer tumors.

They understood that PTK6 was activating a protein responsible for turning genes on and off called STAT3 that it plays an important role in many epithelial cancers, including skin cancer and colon cancer.

Reference:

Jessica Gierut, Yu Zheng, Wenjun Bie, Robert E. Carroll, Susan Ball-Kell, Andrea Haegebarth, Angela L. Tyner, (2011)., Disruption of the Mouse Protein Tyrosine Kinase 6 Gene Prevents STAT3 Activation and Confers Resistance to Azoxymethane. *Gastroenterology*; DOI: 10.1053/j.gastro.2011.06.071

Septin proteins take bacterial prisoners

This cellular defence system could help researchers to create therapies for dysentery and other diseases, the researchers think that This is a new way for cells to control an infection. Pascale Cossart, a cell

biologist at the Pasteur Institute in Paris presented the findings in a poster session at the annual meeting of the American Society for Cell Biology in Denver, Colorado.

Cellular proteins called septins might have an important role in the human body's ability to fight off bacterial infections, according to a study. Septins are found in many organisms, and are best known for building scaring. Folding to provide structural support during cell division and to rope off parts of the cell. However, most studies of septins, or guanosine-5-triphosphate (GTP) binding proteins, have been confined to yeast cells.

The latest research in human cells suggests that septins build 'cages' around bacterial pathogens, immobilizing the harmful and dangerous microbes and preventing them from invading other healthy cells. The researchers found the caging behaviour with *Shigella*, a bacterium that causes sometimes lethal diarrhoea in humans and other primates.

To propagate from cell to cell, *Shigella* bacteria develop actin-polymer 'tails', which propel the microbes around and allow them to force their way into neighboring host cells. To counterattack, human cells produce a cell-signaling protein called TNF-α. The scientists found that when TNF-α is present, thick bundles of septin filaments encircle the microbes. This, in turn, interferes with tail formation and stops *Shigella* in its tracks. Microbes that become trapped in septin cages are broken down in a stage of the cell's life cycle called autophagy. Autophagy is more efficient because of the septin cage, and the septin cage does not occur if you do not have the autophagy. The work implies that septins are more dynamic than before thought.

Until now, the function of septins in helping yeast cells to divide was well known, but no one could relate that to mammalian cell physiology. Septin's role is pretty mysterious. The cool thing to me is that pathogenic bacteria have been so instrumental in figuring out how actin works, and this is the first sign that they will help to figure out how septins work. The scientists discovered the caging behavior with *Shigella*, a bacterium that causes sometimes lethal diarrhea in humans and other primates.

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Autophagy is more important because of the septin cage, and the septin cage does not occur if you do not have the autophagy. The scientists are now working to better understand the link between septins and autophagy, and to determine how useful septins are in humans *in vivo*.

Recent studies have suggested that disruptions in septins and mutations in the genes that code for them could be involved in causing leukaemia, colon cancer and neurodegenerative conditions such as Parkinson's disease and Alzheimer's disease.

Potential therapies for these, as well as for bacterial conditions such as dysentery caused by *Shigella*, might bolster the body's immune system with drugs that mimic the behaviour of TNF-α and allow the septin cages to proliferate, says Cossart. If we have a way to increase the number of cages, we have a new way to fight against infection,.The method is still at a very early stage of testing. In that way they can fit the nanotubes to the different folate receptors present on cancer cells.

a useful property of carbon nanotubes is that they absorb near-infrared radiation. This causes them to heat up very fast. Once the nanotube is attached to the cancer cells, Dai uses a near-infrared laser beam to heat the nanotubes until they kill the cancer cells.

Reference:

Mostowy, S. & Cossart, P., (2011), Autophagy and the cytoskeleton, New links revealed by intracellular pathogens, *Autophagy* 7(7): 780–782.

Biocompatible Nanomaterials:

Synthesis, Characterization and Applications

This book (**ISBN: *978-1-61209-070-2***), aims to distribute the most current investigate in applied biotechnology science and provides new research and developments about the biocompatible nanomaterials conducted by the scientists who are currently working on Nanoscience. Importantly, the biocompatible nanomaterials are used to replace or applied instead of natural materials to function or contact with the living systems. Biocompatible Nanomaterials would keep growing in the field of Nanoscience and Nanotechnology. Researchers are spending much effort on the design, preparation and applications of diffeent biocompatible nanomaterials, due to their potential applications in biomedical science, biosensors, bio-chip designing, drug delivery, etc.

This volume offers an appealing information of biochemical Perspective, new role for nanomedicine, synthesis, characterization and application of biocompatible magnetic nanoparticle, immunogenicity and adjuvant properties of novel biocompatible nanoparticles, preparation and biomedical application of ferrite nanobeads, lipid-Based nanoparticles for enhancing oral bioavailability of drugs, application of nanobiosensors in immunoassay field and etc in a collection of 19 chapters written by leading experts in the field, who afford critical insights into numerous topics, review current research and discuss future directions to stimulate further deliberations. It was published in 2010 by Nova Science.

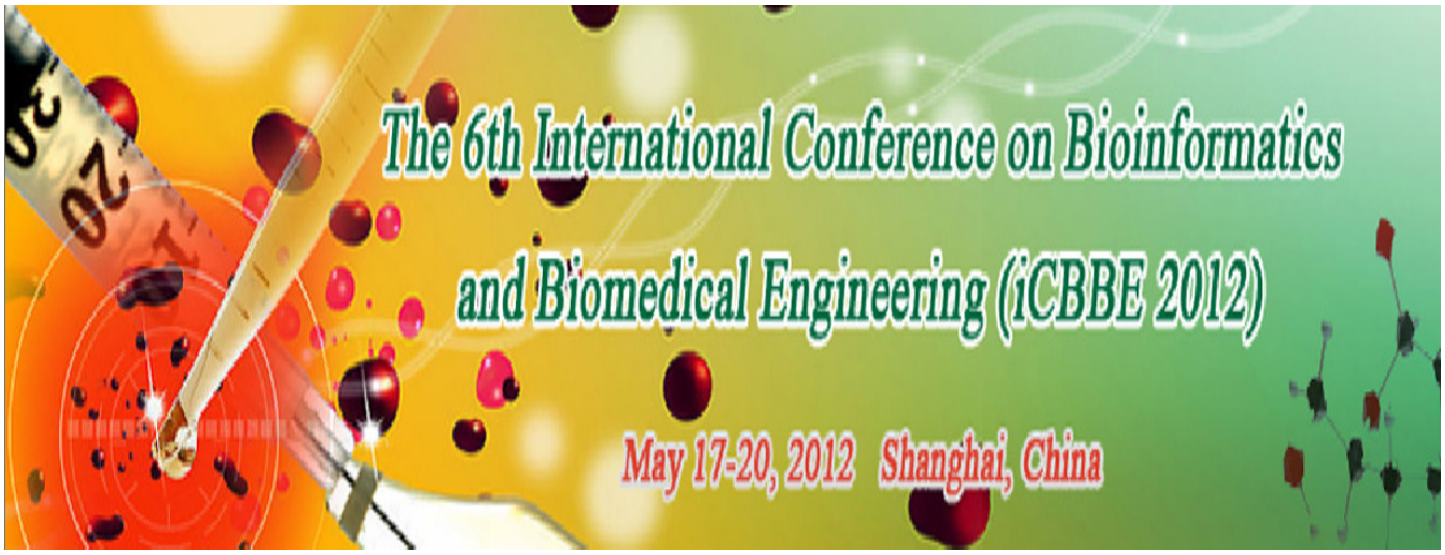
Editors: S. Ashok Kumar, Soundappan Thiagarajan and Sea-Fue Wang (National Taipei University of Technology, Taipei, Taiwan)

Readership: Anotechnology Science and Technology

Announcement

http://www.ifbls-dvta2012.com

http://www.icbbe.org/2012



Announcement

http://www.vaccines-congress.com/

http://www.keystonesymposia.org/12X6

Cover Picture

Title: Killer T cells

Killer T cells are a sub-group of T cells that kill cells that are infected with viruses (and other pathogens), or are otherwise damaged or dysfunctional. As with B cells, each type of T cell recognizes a various antigen. Killer T cells are activated when their T cell receptor (TCR) binds to this definite antigen in a complex with the MHC Class I receptor of another cell. Recognition of this MHC: antigen complex is aided by a co- receptor on the T cell, called CD8. The T cell then travels throughout the body in search of cells where the MHC I receptors bear this antigen. When an activated T cell contacts these cells, it releases cytotoxins, such as perforin, which form pores in the target cell's plasma membrane, allowing ions, water and toxins to enter.

Reference: http://www.wikipedia.org/wiki/Immune_system

Title: Mechanism of Gene Therapy

Gene therapy is the insertion, change, or removal of genes within an individual's cells and biological tissues to treat disease. It is a technique for correcting defective genes that have responsibility for disease development. The most normal form of gene therapy involves the insertion of functional genes into an unspecified genomic location in order to replace a mutated gene, but other forms involve directly correcting the mutation or modifying normal gene that enables a viral infection. Although the technology is still in its infancy, it has been used with some success.

Reference: http://www.wikipedia.org/wiki/Gene_Therapy

Title: Genetic recombination

A DNA helix usually does not interact with other segments of DNA, and in human cells the various chromosomes even occupy separate parts in the nucleus called "chromosome territories". This physical separation of different chromosomes is important for the ability of DNA to function as a stable repository for information, as one of the few times chromosomes interact is during chromosomal crossover when they recombine. Chromosomal crossover is when two DNA helices break, swap a part and then rejoin. Recombination allows chromosomes to change genetic information and produces new combinations of genes, which increases the efficiency of natural selection and can be important in the rapid evolution of new proteins.

Reference: http://en.wikipedia.org/wiki/Genetic_recombination