EMGEN Newsletter

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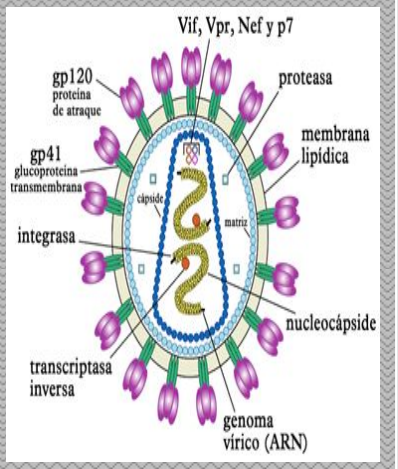
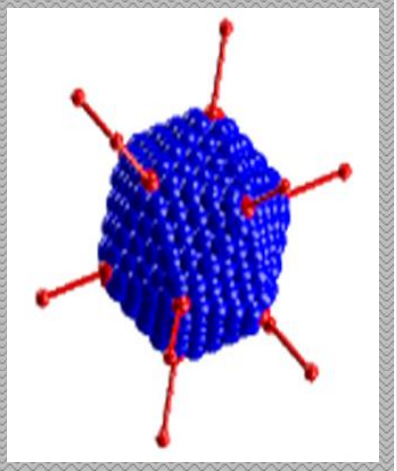
IN THIS ISSUE:





Eastern Mediterranean Health Genomics and Biotechnology Network (EMGEN) was created in 2004 with collaboration of representatives of selected centers 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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Generation of the First Structure-Based Pharmacophore Model Containing a Selective "Zinc Binding Group" Feature to Identify Potential Glyoxalase-1 Inhibitors

*The paper entitled: "Generation of the First Structure-Based Pharmacophore Model Containing a Selective "Zinc Binding Group" Feature to Identify Potential Glyoxalase-1 Inhibitors" which is published in Molecules (*2012, *17* (12), 13740-13758*) describes the role of the* Glyoxalase-1 (Glo-1) enzyme in any cell and especially cancerous cells to detoxify the harmful *by-products of metabolism, which is a very active process in cancer cells as they are non-stopping ones. The study was carried out by Dr. Qosay Al-Balas from the Medicinal Chemistry and Pharmacognosy Department of Jordan University of Science and Technology.*

Dr. Qosay Al-Balas

Cancer is considered one of the main causes of death worldwide according to WHO statistics with 8 million deaths annually. High prevalence of causalities is found in developing countries which suggesting that both its governments and scientists should collaborate to find new drug entities to battle this insidious diseases. The key point of challenging this disease is to find certain targets that are crucial for its survival. Glyoxalase-1 (Glo-1) enzyme is described to have this property; it is essential for any cell and especially cancerous cells to detoxify the harmful byproducts of metabolism, which is a very active process in cancer cells as they are non-stopping ones.

Glo-1 enzyme has been crystalized and deposited in the Protein Data Bank (PDB) under 1QIN code. Structurally, Glo1 is a metallo-enzyme, i.e., it has zinc metal as an essential cofactor through the active site that plays a structural and catalytic role in the isomerization of the reactive and toxic aldehydes. Furthermore, it is composed of two identical polypeptide chains forming a homodimer, where each chain contains of 183 amino acids with a molecular weight of 43 kDa. The active site of Glo1 is located in the jointing of the two polypeptide chains and when the zinc atom has a square pyramidal coordination with the adjacent amino acids. Within this study, our group has employed a structure-based drug design technique utilizing the well-equipped molecular modeling facility available at Jordan University of Science and Technology (JUST) to

unravel the essential features in designing potential and novel inhibitors of Glo-1. The presence of a zinc atom at the active site of this enzyme was the core of designing potential inhibitors. As a result, this is the first structure-based pharmacophore model [figure below] containing a "zinc binding feature" ever described for Glo-1 enzyme or any other metallo-enzyme. Therefore, it is suggested that this work will be a starting point for any future work for designing structure-based or ligand based inhibitors for metallo-enzymes.

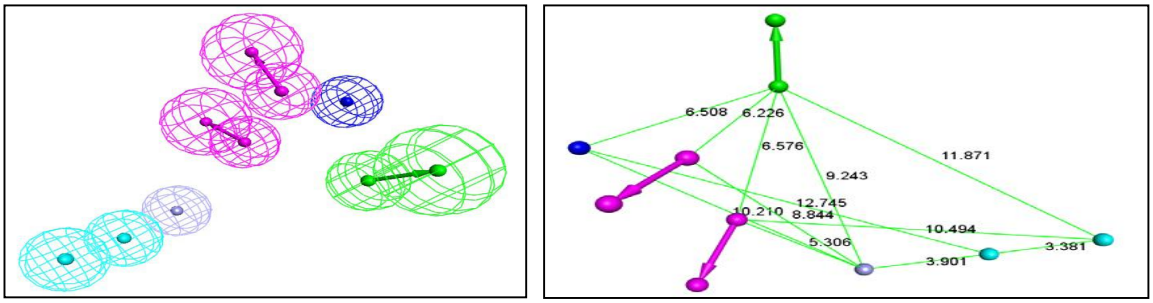
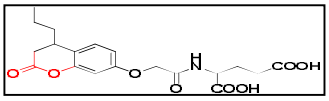
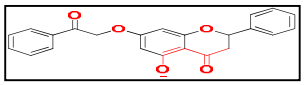
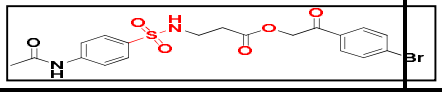


Figure: Structure-based pharmacophore of the active site of Glo-1 enzyme.

The strategy used in finding new and novel inhibitors *in silico* was to employ 2D similarity combined with 3D pharmacophore design. Firstly, a known inhibitor of this enzyme, i.e. curcumin was used as a reference ligand to screen a 10 million compound library to find similar molecules with three well recognized similarity protocols (Tanimoto, Dice, Cosine); secondly, the resulting ones will be mapped on the generated structure-based pharmacophore shown above. Thirdly, the resulting compounds will be docked using advanced and specialized docking programs such as CDOCKER, GOLD, and Libdock to predict the correct binding mode within the active site and always focusing on the essential feature "zinc binding group" to fit really well inside the active site. The final selection criteria were based on choosing inhibitors containing a "zinc binding feature" with the highest consensus score in docking [table below].

Table: Structure, consensus scoring and zinc binding groups of candidate compounds as Glo-1 inhibitors.

Name	Structure	Consensus score	ZB group
Zinc02120846		492.4	2H-pyran-2-one
Zinc05528245		486.9	4-oxo-4H-chromen-5-olate
Zinc13100715		485.8	Sulfonamide

Interview

In this issue, we present the following interesting interview with ***Dr. Ammar Almaaytah*** *from* Jordan University of Science and Technology (Any views or opinions expressed are solely those of the author and do not necessarily represent those of EMGEN Newsletter).

Please introduce yourself and explain your scientific discipline.

My name is Ammar Almaaytah, I'm currently an Assistant Professor in the Faculty of Pharmacy from Jordan University of Science and Technology. I'm also the assistant dean at the faculty. I received my bachelor degree in Pharmacy from Jordan University (2006) and I hold a Ph.D. degree in Pharmaceutical Biotechnology from Queen's University, Belfast, UK (2010).

Could you please tell us what your main research area is?

My research interests lie in the discovery and characterization of novel biologically active peptides in nature, specifically from venoms and through the application of molecular cloning and high analytical separation techniques. Our research efforts are also focused on using these natural peptides as platforms for the rational design of modified synthetic replicates of such peptides with improved activities and biological outcomes. Recently, we managed to identify novel peptides with potent selective cytotoxic activities against prostate cancer cell lines and also managed to design anticancer peptides with selective activity against highly metastatic tumors and specifically those tumors that are highly expressive of a group of enzymes called Matrix Metalloproteinase.

Why did you choose this field of research?

Since my years as an undergraduate student, I have always dreamt of being involved in the research and science of discovering new therapeutic agents that could benefit humans worldwide. I choose the field of Pharmaceutical Biotechnology because in my opinion, this field represents the future for drug discovery and could prove to be of great benefit to humans and the treatment of diseases.

Do you use any biotechnology or genomics tools in your research?

Most of our work is focused on identifying novel peptides using a technique called "Shotgun cloning" which is based on identifying lead peptides by designing random primers with high sequence homology to other peptides identified from other animal species and generating hit peptides from the cDNA library of the venom itself. So basically our work is a fusion of molecular cloning, bioinformatics as well as translational biology.

Are biotech scientists trained in your own country or abroad?

Our Biotech Scientists are mainly trained abroad, and mainly from the US or UK based organizations, although we have our own centers that train our students and technicians on techniques in the field of Biotechnology.

What about quality of knowledge they gain? Which one is better?

In my opinion, the quality of training at our centers is of the same caliber as abroad although scientists trained abroad have the advantage of acquiring the latest and cutting edge techniques in Biotechnology that are used worldwide and that is why our academic institutions focus on sending scientists abroad.

Are there significant biotechnology centers in your country?

Yes, the largest and most equipped Biotechnology Center in Jordan is the Princess Haya Biotechnology Center, which is located at Jordan University of Science and Technology. The center provides robust and excellent scientific infrastructure for faculty members, graduate students, and regional organizations to support crucial experimental research in biotechnology, specially in the fields of genomics and proteomics.

What kinds of difficulties do you face, in research and commercialization of medical Biotechnology in your country?

Our pharmaceutical industry is quite prominent in the region, but still has not ventured into producing biotechnological or biological products due to lack of clear international regulations regarding biosimilar and due to the lack of technical expertise in the industrial aspects of pharmaceutical biotechnology.

Do you have any governmental support for biotechnology in your country? And, at what level?

We have several organizations that provide financial support for research activities in Biotechnology in Jordan; the major ones include the Jordan Scientific Research Fund (SRSF) which is a financially and administratively independent government institute, responsible for encouraging and supporting scientific research in the kingdom. It is administered by a Board of Directors headed by the Minster of Higher Education and Scientific Research. Another organization which supports biotechnological research in Jordan is the National Center for Research and Development (NCRD) which is affiliated with the Higher Council for Science and Technology.

What about public perception of biotechnology in your country?

I think the significance and importance of biotechnology and their perception by the public in Jordan is still below the desired level which places big responsibilities on both the governmental and academic institutions to promote the importance of biotechnology in benefiting humans at the medical as well as the agricultural level.

Are there any biotechnology products that have been made in your country? (I.e. your native researchers involved in the project)

To my knowledge I don't know any biological product that has been commercialized in Jordan, but we have several startup companies which aim to produce biotech products in the future such as MONOJO, which is a company focused on producing highly specialized biopharmaceutical compounds such as monoclonal antibodies. The company was established as joint venture between the private sector and public academic institutions in Jordan to promote the biotechnology industry in Jordan.

Is there any journal that is published in your country and deals with biotech issues?

Yes. The Jordanian Journal of Pharmaceutical Sciences and Jordanian Journal of Biological Sciences publish articles related to biotechnology.

What is your opinion about the development of biotechnology and genomics in your place?

I think great efforts are needed by both the public and the private sector in order to establish a strong biotechnology industry in Jordan and this requires extensive collaboration and planning to generate a national agenda that focuses on joint ventures between our organizations and their international counterparts to ensure technological transfer between those countries in order to achieve our goals.

Would you tell us about the differences of biotechnology and its applications between developed and developing countries? What should we do in this regard?

The main difference between developed countries and the developing ones with regard to biotechnology is that the developing countries are still at the level of basic research with no market applicable discoveries generated so far. Most of the work in biotechnology is done by academic institutions with an outspoken absence of the private sector which should be able to outline market opportunities in the region that could be exploited to generate financial returns.

Are you familiar with EMRO countries and EMGEN (Eastern Mediterranean Health Genomics and Biotechnology Network)? Would you please tell us how you know the EMGEN?

Yes, I'm familiar with both and that is through some colleagues of mine and through the internet although I haven't attended any conference or a meeting regarding both personally.

What are your suggestions for the EMGEN development?

I think more regional meetings and conferences should be organized between the EMGEN and EMRO countries in order to promote collaboration and joint projects between its members and I believe a strong database of all the research centers and their specialties including the scientists involved, could prove to be of great benefit to all the scientists working in this field in our region.

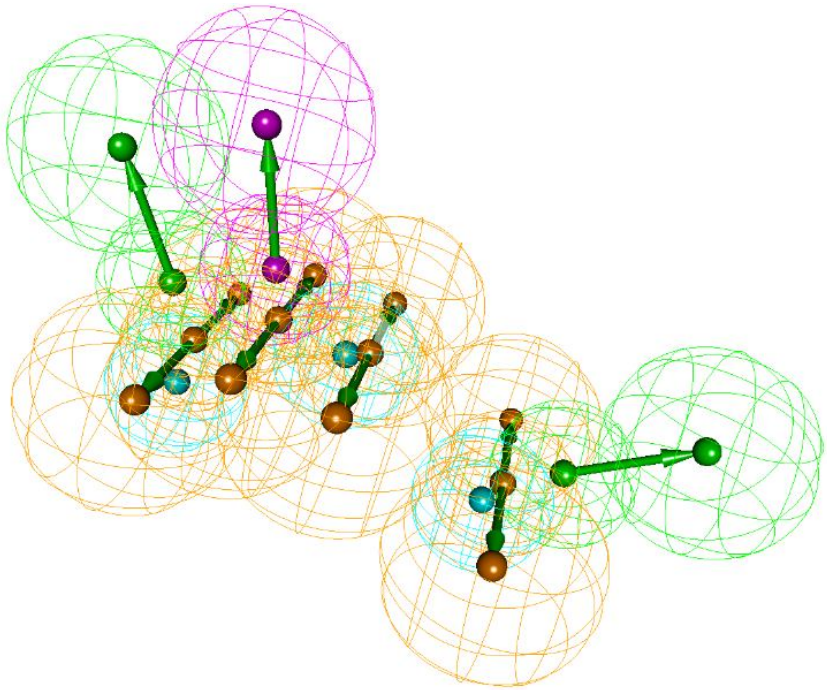
At the end of the interview is there anything special you want to mention?

I want to thank you for giving me the opportunity to share my modest experience with the readers and for your interest in this important field of science.

Thank you *Dr. Ammar Almaaytah* for sharing information and your opinion with us. Also, we are grateful for your kind and useful cooperation

Tree-dimensional pharmacophore models generation

The concept of a pharmacophore is one of the most fundamental concepts in drug design in those cases where the X-ray structure of the target is not available. However, this discipline is sometimes given the wrong name as 'ligand-based design', but a better name would be 'pharmacophore- based design'. Moreover, pharmacophores are useful even in such cases when their X-ray structures are available. Pharmacophore discovery is the process of taking a structure–activity relationship (SAR) and distilling it down to a pharmacophore.



A pharmacophore example

Based on the International Union of Pure and Applied Chemistry's definition, a pharmacophore "is the ensemble of steric and electronic aspects that are essential to ensure the optimal supramolecular interactions with a defined biological target structure in such a way to trigger or to block its biological response.

A pharmacophore does not represent a real molecule or the real association of functional groups, but a purely abstract concept that accounts for the most common molecular interaction capacities of a group of compounds toward the target structure. The pharmacophore can be assumed as the largest common denominator shared by a set of active molecules. The concept of pharmacophore discovery is referring to the process of distilling a SAR into a pharmacophore, which was introduced by Kier in 1968 and it was further developed in the context of its use as a search query in three-dimensional (3D) database searching. The first commercial software that was pharmacophore centric was Catalyst, which was released in April 1992 by Bio-CAD.

1. Pharmacophore discovery is trying to solve the problems below

1.1. Virtual screening of 3D databases

Discovery of a pharmacophore is finding a pattern of features common to all active molecules (SAR), which could be used as a search query to a 3D database (virtual screening). For instant, the final result of the method is a pharmacophore of which the validation is found experimentally through biological testing of the hits emerging from that database search.

1.2. Calculation of a model of activity

It is used to calculate a model of activity, based on spatial relationships of molecule features in a SAR. The result is a regression equation, correlating various 3D properties to a real number for biological activity, and the experimental validation is the ability of the model to predict the activity of molecules outside the original SAR.

1.3. Calculation of an overlay in 3D space of a set of conformations

From such an overlay, the final result is a set of molecules oriented in a specific way, indicating how pharmacophores may be inferred 'by inspection' of that overlay. The experimental validation, which is reported for such methods is normally a comparison with ligands in X-ray cocrystal structures, based on a 3D alignment of the protein.

2. The process of pharmacophore discovery

This is the common path for most of the softwares that have been used for pharmacophore discovery.

2.1. Assembling the SAR

Although this may sound simple, there are a number of aspects one must be aware. One of the crucial aspects in this respect is to ensure mechanistically that the biological data are mediated by a common receptor, *i.e.* they are mechanistically homogeneous. Another one is to be sure that the SAR contains pairs of molecules which allow the program an opportunity to discover the right trends. However, the use of structure–activity landscapes is sometimes helpful, but there are no definitive ways to make these assessments.

2.2. Identifying features on the molecules

This is the next step in the pharmacophore discovery process. This is the point at which representation comes to the fore and it typically involves performing substructural pattern matching.

2.3. Conformational analysis

Conformational analysis is an important step in a distinct set of methodologies. It is important, since typically, all conformations are included whose energies are within some delta of the lowest conformation, a parameter sometimes called τ. The methods for conformational analysis that have been reported in the pharmacophore discovery literature are:

- Genetic algorithms (BALLOON)
- Torsion-driving algorithms coupled to energy minimization (Catalyst FAST, and OMEGA)
- Ruled-based methods (CONCORD and CORINA)
- Molecular-mechanics-based methods (MCMM)

2.4. Finding candidate pharmacophores

In this step, the program tries to specify one possible pharmacophore consistent with the SAR

by the rules or constraints between the features. In most of the cases, more than one pharmacophore is consistent with the SAR; this happens especially when the molecules are flexible, or not very potent. This is an important step and if the method does not acknowledge explicitly that multiple solutions may arise, it is incomplete.

2.5. Screening among the candidate pharmacophores

The final step involves screening through the candidate pharmacophores that are identified through Finding candidate pharmacophores. The goal of this step is identifying one or more high-quality pharmacophores among others. At this stage, the underlying principles and equations come to the fore.

3. computer software packages for pharmacophore design

At the end I would like to introduce the following computer software packages that enable the user to generate the pharmacophore model:

Discovery Studio,

Phase,

MOE,

LigandScout,

ICM-Chemist,

ZINCPharmer.

Reference:

1. John. H, Generation of three-dimensional pharmacophore models, *WIREs Comput Mol Sci 2012*, 1129.
2. Schuster. D, 3D pharmacophores as tools for activity profiling, *Drug Discovery Today: Technologies 2010*, 7(4), 205-211.
3. http://en.wikipedia.org/wiki/Pharmacophore

Cancer Vaccines

1. Vaccine

Science of immunology was begun by Edward Jenner's work in 1798 that describing a vaccine against small pox. Immunology has since then made many contributions to scientific investment and to various scientific disciplines, but the most important one is the development of vaccines (Figure 1: of *Avian flu* vaccine development by reverse genetics techniques).

At present, around 26 infectious diseases could be prevented through vaccination. In spite of two century efforts for vaccine development, some bacterial, parasitic and viral disease, such as Chagas, tuberculosis, malaria and hepatitis C have not been protected through vaccination. The previous successes and increasing level in our understanding of the immune mechanism as well as the ability to manipulate them, would predict future success.

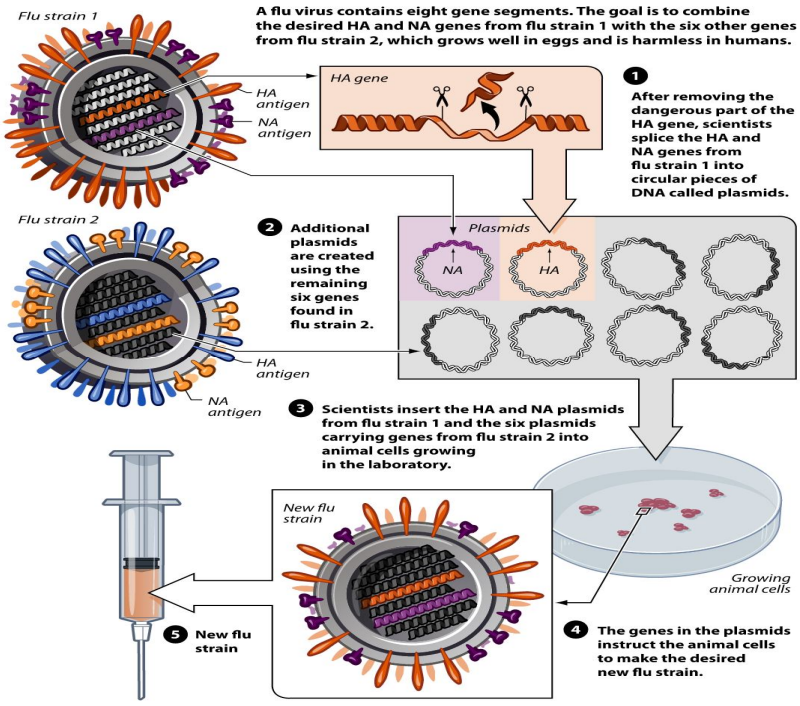


Figure 1: *Avian flu* vaccine development by reverse genetics techniques.

2. Cancer vaccines

Cancer vaccines are the kind of medicines that belong to a class of substances defined as biological response modifiers. They work by restoring or stimulating the immune system's ability to fight against infections and diseases. There are two main broad types of cancer vaccines: Preventive or prophylactic vaccines that are predestinate to prevent cancer from developing in healthy people; and treatment or therapeutic vaccines that are destined to treat an existing cancer by strengthening the body's natural defenses against the cancer. Both types of cancer preventive vaccines are available in the United States, and recently one cancer treatment vaccine has become available.

3. Vaccine's challenges

In addition to picking up the challenge to design suitable vaccines for infectious diseases, immunologists endeavor to explore the possibility of using vaccines for diseases involved in the immune system. A most noticeable effort is directed toward development vaccines for autoimmune disease and cancer. All vaccines are faced with certain common challenges that are summarized below.

3.1. Challenges for all vaccines

3.1.1. Choosing the right antigen

Traditionally, successful vaccines have been developed from live feeble pathogens. However, vaccines effective at the population level, they have some negative effects such as a significant risk of activation or harmful side-effects. The first cancer vaccines were included of tumor cells that were inactivated or irradiated previously. In the experiments, this immunization strategy could produce tumor-specific immune responses and rejection of a tumor challenge, indicating success of this strategy. Moreover, immunologists discovered that native T cells required an additional co-stimulatory signal. Whole tumor cell vaccines are associated with significant health risks as well as pathogenic based vaccines of which autoimmunity is the major side effect.

3.1.2. Choosing the right adjuvant

The crucial component of all cancer vaccines are adjuvants whether they are composed of defined proteins, whole cells or peptides. However, there are only two worldwide approved adjuvants for clinical use at present (Alum and MF59). Many other substances that can increase the immunogenicity of vaccines have been tested in animal models and humans and there are indication that they could be successful. The new adjuvants are from molecules whose function is known, therefore, their mechanisms of action are understood better. Adjuvants of cancer vaccines can simulate T cells, natural killer cells or other cells from the innate immune system more effectively by activated antigen-presenting cells.

3.1.3. Generation of the right type of immune response

More attention is paid to antigens, adjuvants and the role of administration of vaccines that can stimulate mucosal response effectively as well as systemic immunity, because many tumors originate at mucosal sites and are encountered by the mucosal immune system. To understanding immune responses to against mucosal tumors, a comprehensive understanding of the immune effector mechanisms is required, because they are responsible for protecting the mucosa. Keeping the balance between a swift reaction against pathogens and no-response to environmental antigens such as food and non-pathogenic bacteria flora is the mucosal immune system's function. The mucosal vaccines need to maintain this balance alongside the protective response at the same time.

3.1.4. Elicitation of long-term memory

Immune memory is a crucial mechanism that the majority of vaccines cannot elicit. The main problem in this field is the relative paucity of specific markers that could differentiate memory T cells from other forms of T cells. For example, chemokine receptors have been used successfully to differentiate functional subset of T cells from others. These markers will help to understand the role of tumor antigens as well as adjuvants and routes of injection with regard to the intensity, complexity and the type of memory response.

3.2. Additional challenges for cancer vaccines

3.2.1. Aging immune system

Patients with cancer in whom vaccines are being tested are between 65 and 80 years old (without exception). Hence, the generation of an effector-cell population in response to a vaccine depends on the recognition of the vaccine antigen by memory T-cells. In a mouse model, experiments have shown that young mice have a stronger primary response in comparison with old mice owning to age-associated changes in the function of immune system components. Reports show an age-related increase in susceptibility to cancer on account of changing T-cells subset's patterns and induction of effective antitumor immune responses. Therefore, more attention should be paid to designing vaccines with a capacity to overcome age-related problems.

3.2.2. Tumor-induced immunosuppression and immune evasion

Tumor cells may grow slowly without much destruction of the surrounding normal tissue. It is, therefore, that the immune system may not detect them. Over time, tumor cells acquire further mutations, some of which facilitate invasion and growth. Tumor growth induces tumor cells begin to cause tissue destruction and the adaptive immune system is alerted to activate the DCs so that these cells pick up tissue debris and tumor cells presentation into the lymph nodes to T cells. Cancer patients by presenting of tumor-specific cellular and humoral responses indicate that the immune system has recognized the tumor. The Immune system is tries to get rid of tumors which in the loss of various tumor antigens or MHC molecules expression. Progressive tumor growth indicates that tumor cells have tried to evade immune defenses. Cancer immunoediting is the process of trying to change a tumor so that the result will not be complete tumor rejection.

4. Therapeutic cancer vaccines

Most primary tumors can be removed and mostly there is a long period of time before recurrence of the tumor at metastatic sites. Cancer vaccines have been introduced as therapy; they are designed to cause or elicit antitumor immunity with minimal residual diseases in patients, consequently preventing recurrence

or prolonging the time till recurrence. Phase I and II have been studied as well as late stage disease and in the presence of a large tumor burden after the failure of standard therapies. The success of therapeutic vaccines would depend on the ability of the immune system to overcome tumor-induced, or age-induced, or therapy-induced immunosuppression. Outgrowth of tumor cells could be the additional factor for evasion of the immune response.

5. The future of cancer vaccines

After developing the cancer vaccines one option will be testing the vaccines in cancer patients in phase I and II of trials with different forms of individual antigens, in different vaccine formulations, different adjuvants, taking advantage of new technological developments and hoping for improvements in efficacy. The other option is to decide whether cancer vaccines that have shown efficacy and safety in preclinical studies are relevant for the prevention of cancer and begin to test them as such.

References:

1. Finn. OJ, Cancer vaccines: between the idea and the reality, *Nat Rev Immunol 2003*, 3(8):630-641.
2. Paul. H. et al, Peptide Based Vaccine Approaches for Cancer—A Novel Approach Using a WT-1 Synthetic Long Peptide and the IRX-2 Immunomodulatory Regimen, *Cancers 2011*, 3, 3991-4009.
3. http://en.wikipedia.org/wiki/Cancer_vaccine
4. http://en.wikipedia.org/wiki/Vaccine
5. http://www.cancer.gov/cancertopics/factsheet/Therapy/cancer-vaccines
6. http://www.ctvnews.ca/health/canadian-made-therapeutic-cancer-vaccine-showing-promise-1.1145166

Bioelectric Signals Can Be Used to Detect Early Cancer

Bioelectric signals underline a significant series of control mechanisms that regulate how cells grow and multiply, and electric incidents tell the cells what they should do. The voltage changes are not just a sign of cancer, they control and direct whether the cancer occurs or not. Researchers examined the bio-electric attributes of cells that expand into tumors in *Xenopus laevis* frog embryos. In this study, the re-searchers assumed that cancer may occur when bioelectric signaling networks are disturbed and cells stop the patterning that orchestrates their normal development. By using a membrane voltage-sensitive dye and fluorescence microscopy, they concluded that tumor cells exhibit a bioelectric effect, and chang-ing this electrical potential will reduce occurrence of tumors. Furthermore, they induced tumor growth by injecting the mRNAs, encoding well-recognized human oncogenes Gli1, KrasG12D, and Xrel3 in the frog embryos. The embryos developed tumor-like growths that are related to human cancers such as mela-noma, leukemia, lung cancer, and rhabdomyo sarcoma (a soft tissue cancer that most often affects chil-dren). According to the research, transport of butyrate, a known tumor suppressor was responsible for hyperpolarization activity to inhibit tumor formation.

Reference:

Chernet. B. T. et al, Transmembrane voltage potential is an essential cellular parameter for the detection and control of tumor development in a Xenopus model. *Disease Models & Mechanisms 2013,* 6, 595-607.

Engineered Oncolytic Herpes Virus Inhibits Ovarian and Breast Cancer Metastases

Although novel methods such as surgery, chemo- and radio-therapy, or combinations during the past decade showed good results for the treatment of cancer cases, some of these methods are not good enough, since many treatments prolong life for a short time only, or are associated with a poor quality of life. In this study, researchers by using unarmed reprogrammed *oncolytic herpes* virus, no longer pathogenic but with the capacity to act as a distinctive weapon against tumor cells that express the HER-2 oncogene, were able to inhibit ovarian and breast cancer metastases.

Reference:

Patrizia. N. et al, Preclinical Therapy of Disseminated HER-2 Ovarian and Breast Carcinomas with a HER-2-Retargeted Oncolytic Herpesvirus. *PLoS Pathogens 2013,* 9 (1),e1003155.

Gene Finding May Lead to Treatments Effective Against All MRSA Strains

MRSA or Multidrug-Resistant *Staphylococcus aureus* (or Methicillin-Resistant *Staphylococcus aureus*) is a bacterium responsible for several difficult-to-treat infections in humans. During the last decade a new strain of MRSA has appeared that can spread in the environment and put everyone at risk of contracting the dangerous bacterial infection. This special strain of MRSA (known as USA300) possesses a slice of genes not assigned by any other strains, although it is unknown how this matchless genetic material enables the bacteria to survive and remain in the community. A slice gene containing 34 genes named the Arginine Catabolic Mobile Element (ACME) results in a new strain. Its resistance to peculiar compounds on the skin i.e. polyamines that are toxic to other forms of the bacteria, allow it to survive longer than other strains on the skin, and allow it to be passed in the community more easily. Polyamines are anti-inflammatory and promote tissue regeneration. Researchers after evaluating this gene fragment one-by-one detected a gene (SpeG), its presence allowing USA300 to remain longer on the skin, from a day to a week, giving the infection time to expand to the next

Reference:

Lance. R. et al, Functional Modularity of the Arginine Catabolic Mobile Element Contributes to the Success of USA300 Methicillin-Resistant Staphylococcus aureus. *Cell Host & Microbe 2013,* 13 (1), 100-107.

Nanoparticles That Look and Act Like Cells

Nanoparticles are suitable carriers to transport drugs and chemicals in the body such as anti cancer drugs, but their most important weakness is that, immediately after injection of these nanoparticles into the body, the immune system will recognize them as alien and invasive and will destroy them. Therefore, somehow they must not be recognized by the immune system. Researchers by coating these nanoparticles with a layer of normal cell membrane (white blood cells) could adapt these to the body so that the immune system will not react to them and it is, therefore, that this method prevents the binding of Opsonins, signaling proteins that activate the immune system, to the Nanoparticles.

Reference:

Alessandro. P. et al, Synthetic nanoparticles functionalized with biomimetic leukocyte membranes possess cell-like functions. *Nature Nanotechnology 2012,* 8 (1), 61.

Book Alert

Biotechnology for Medicinal Plants

Editors: Suman Chandra; Hemant Lata; Ajit Varma **ISBN:** 978-3-642-29974-2

As we know plants play important roles in plant-based medicines in those countries specially using traditional medicines in the eastern world. In this book the latest progress in the enhancement of medicinal drugs, like plant tissue cultures, secondary metabolite production, metabolomics, metabolic engineering, bioinformatics and further biotechnological directions for the use of plants to produce novel drugs, is explained.

Reference: http://link.springer.com/content/pdf/bfm:978-3-642-29974-2/1.pdf

Applied Computational Genomics

Editor: Yin Yao Shugart ISBN: 978-94-007-5558-1

"Applied Computational Genomics" focuses on statistical enhancement and usage in the field of human genomics including candidate gene mapping, linkage analysis, population-based, genome-wide association, exon sequencing and whole genome sequencing analysis. This book is valuable to human geneticists, medical doctors, health educators, diplomacy investors, and graduate students majoring in biology, biostatistics, biotechnology, and bioinformatics.

Reference: http://www.springer.com/biomed/human+genetics/book/978-94-007-5557-4

Structural Biology

Editor: Quincy Teng ISBN: 978-1-4614-3964-6

This book is an updated version of the 2005 first edition, describing the use of NMR as applied for the first time to solve problems in structural biology; containing new data and figures that will be valuable to researchers in the field of biochemistry, chemistry, structural biology and biophysics. To understand the basics of NMR spectroscopy, the book starts with an introduction to basic NMR principles. Moreover, NMR instrumentation is discussed starting with hardware components. Subjects include probe circuits, magnetic field homogeneity and constancy, signal generation and detection, frigorific probe, analog-to-digital conversion, and test tooling.

Reference: http://www.springer.com/biomed/molecular/book/978-1-4614-3963-9

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Reference:

http://www.acgssr.org/files/bio_inst.pdf/

Announcement

http://www.biologicalproduction.com/?mc=EL/

http://www.icebb.org/

The First International Aizu Conference on Biomedical Informatics and Technology

ACBIT'2013, 16-17 September 2013, Aizu-Wakamatsu, Japan

http://web-ext.u-aizu.ac.jp/conference/acbit/

Announcement

http://www.icmbs.org/

http://www.icbfe.org/

http://www.lsbe.org/index.asp/

Cover Pictures

Green fluorescent protein

The Green Fluorescent Protein (GFP) is a protein containing 238 amino acid residues with a weight of 26.9 kDa, for the first time isolated from the jellyfish, *Aequorea Victoria,* which displays green fluorescence when exposed to light in the ultraviolet range. In cell and molecular biology, the GFP gene is mostly used as a marker/reporter of gene expression. In changed forms it has been used to engender biosensors, and a lot of animals have been obtained that transformed by GFP as a proof-of-concept showed that a gene can be expressed all over an organism. The GFP gene can be injected into organisms and preserved in their genome via breeding, injection with a viral vector, or cell transformation.

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

Human immunodeficiency virus (HIV)

Human Immunodeficiency Virus (HIV) is a slowly replicating *retrovirus* of the *lenti virus* family that causes acquired immunodeficiency syndrome (AIDS). AIDS is an infectious disease in which progressive destruction of the human immune system leads to life-threatening opportunistic infections and cancer. HIV infects biotic cells in the human immune system such as T cells, macrophages and dendritic cells. HIV infection decreases the level of CD4+ T cells via three main mechanisms: First, direct killing of infected cells; second, increasing the rate of apoptosis in infected cells; and third, killing of infected CD4+ T cells by CD8 cytotoxic lymphocytes that recognize infected cells. When the numbers of CD4+ T cell degrade below a critical level, cell-mediated immunity is lost, and the body becomes gradually more susceptible to opportunistic infections.

Reference: http://en.wikipedia.org/wiki/HIV/AIDS

Adenovirus structure

Adenoviruses belong to the *Adenoviridae* family that can infect various species of vertebrates, including humans. These viruses are medium-sized, without envelope (absence of a bilayer outer membrane). They are icosahedral viruses composed of a nucleocapsid and a double-stranded linear DNA genome. There are about 60 described serotypes which are responsible for about 10 percent of upper respiratory infections in humans especially in children. *Adenoviruses* were first isolated in 1953 from human adenoids.

Reference: http://en.wikipedia.org/wiki/File:Adenovirus_structure.png