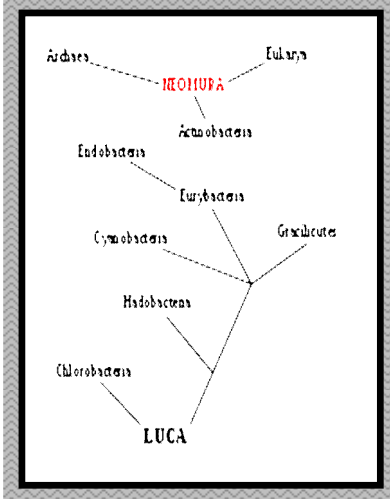

EMGEN Newsletter

Vol. 3, Issue 7, Dec-Jan, 2009-10

INSIDE THIS ISSUE:

Eastern Mediterranean Health Genomics and Biotechnology Network (EMHGBN) was created in 2004 with collaboration of representatives of selected centre 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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Molecular Analysis of Human Influenza Virus in Tehran, Iran

The article entitled " Molecular Analysis of Human Influenza Virus in Tehran, Iran" reports isolation and characterization of circulating influenza viruses in a sample of patients in Tehran. The study was done by Z. Soltani, M. Hosseini M. Shahidi, M. Hedayati, M.T. Kheiri. Corresponding author of this paper, Dr. MT. Kheiri is Assistant Professor of Virology Department in Pasteur Institute of Iran, Member of Board of Directorate of Iranian Association for Virology and Member of Iranian National Influenza Committee. The paper was published in Intervirology. 2009;52(2):63-7

Dr. Masoumeh Tavassoti Kheiri, Ph.D.

Human influenza viruses continually circulate and cause yearly epidemics. Novel strains emerge sporadically as pandemic viruses [1, 2]. The surface hemagglutinin (HA) glycoprotein of influenza viruses is the major target for neutralizing antibodies, and point mutations in the potential antigenic domains of this protein are thought to allow viruses to evade established immune antibodies in the human population. Analyses of epidemic influenza virus isolates, therefore, have chiefly focused on antigenic characterization of the HA glycoprotein in order to detect new variants of each epidemic strain for the recommendation of vaccine strains in each season [3, 4]. Annual epidemics are caused by the rapid evolution of the viral genome. Such changes can be monitored through antigenetic analysis and gene sequencing, particularly the gene that codes for viral HA. There are a few reports of human influenza viruses from Iran, a seroepidemiological description published in 2004 [5] and a more recent molecular and phylogenetic analysis in Shiraz [6]. Here, we collected a sample of human influenza viruses in Tehran during the 2006–2007 influenza seasons. We used molecular techniques to determine the typing and subtyping of human influenza virus on these samples. The data obtained were then compared to the vaccine strains that were recommended by the WHO for the same period.

We collected 57 nasopharyngeal swabs from individuals suspected of having influenza. The samples were collected in a clinic and at the influenza unit of the Pasteur Institute in Tehran, Iran, between October 2005 and January 2007. The MDCK continuous cell line was used to isolate influenza viruses in cell culture. Cells were seeded at a concentration of 5x10 *6 cells/ml. After 1 day, 200 µl of each sample was inoculated into wells containing MDCK cells. The culture medium was then examined for hemagglutinin activity using a 0.5% suspension of chicken erythrocytes.

Viral RNA was extracted from 300 µl of each sample using a commercial RNX-Plus TM solution (CinnaGen, Tehran, Iran) and immediately frozen at –70 ° C . The cDNA synthesis was performed using SuperScript TM III first strand synthesis kit (Invitrogen, Carlsbad, California, USA) according to the manufacturer's instructions. Amplification of each RNA segment was carried out by RTPCR, as described previously [6]. The isolates were selected for molecular characterization using bi-directional sequencing. The H1 (543 bp) and H3 (292 bp) fragments from influenza A virus and NS (334 bp) segment from influenza B were used for sequencing and phylogenetic analysis. The PCR products were sequenced in both directions by a CEQ TM 2000 dye terminator cycle sequencing kit (Beckman Coulter, Fullerton, Calif., USA) using an automated CEQ 2000XL microcapillary DNA analysis sequencing apparatus (Beckman Coulter). Alignment was performed using Clustal X software, version 1.81 [7]. GenBank accession numbers for sequences determined in this work are EU311401–EU311412. Phylogenetic trees were constructed using the neighbor-joining method [8]. Bootstrap analysis (n = 1,000) was performed to determine the best fitting tree for each gene [9]. Genetic distance was estimated by the Kimura 2-parameter matrix [10]. Molecular Evolution Genetic Analysis (MEGA) computer software, version 2.1 [11], was utilized in this study for phylogenetic and molecular evolutionary analysis and nucleotide differences within and between the isolate sequences.

A total of 12 of 57 samples were found to be positive for human influenza virus (21%). Molecular typing by RT-PCR and subtyping of the positive samples showed 7 as influenza A/H3N2 (58%), 3 as influenza A/H1N1 (25%) and 2 as influenza B (17%). The nucleotide and amino acid sequences of the HA1 (for type A) and NS (for type B) of the Iran-Tehran isolates were compared with other sequences in GenBank, and with the vaccine strains, during the 2005–2007 influenza seasons. Among Tehran H1N1 isolates, maximum similarity (99%) was observed with the A/Philipin/67/2004 strain and 95–98% with the A/New Caledonia/20/99 strain. These isolates contained 1–3 amino acid differences compared with A/New Caledonia/20/99 (Table 1). In Tehran H3N2 isolates, maximum similarity (99%) was observed with the A/Panama/2007/1999. The 2005-H3N2 isolates showed 81–93% homology to A/California/7/2004 (H3N2) and 2006-H3N2 isolates showed 83% to 99% similarity to A/Wisconsin/67/2005 vaccine strains. Alignment of the amino acids of the HA protein demonstrated 10–13 amino acid changes in 2005-H3N2 isolates and 5–15 amino acid changes in 2006-H3N2 isolates, in comparison with candidate vaccine strains.

Tehran B isolates were very close to Florida/02/2006, with 100% homology. As the HA gene was used in vaccine strains, we could not compare Tehran B isolates with vaccine strains. The 12 positive isolates were selected for phylogenetic analysis. In the H1N1 phylogenetic tree, Tehran isolates were clustered only in the recently discovered isolates of 2000–2006. However, in H3N2 phylogenetic tree, some Tehran isolates were clustered with the 1980–1999 strains while others were clustered with the 2000–2006 lineages. Phylogenetic analysis of Tehran H1N1 isolates confirmed that H1N1 isolates were branched in a unique cluster close to A/New Caledonia-like vaccine virus, with a 77% bootstrap value. The phylogeny of the H3N2 HA nucleotide sequence indicated that Tehran isolates were from the Wisconsin/67/2005 and A/California/7/2004 strains. They were branched in a cluster close to A/Panama/2007/1999- and A/Moscow/10/99-like vaccine strains.

The importance of predicting the emergence of new circulating influenza strains for subsequent annual vaccine development cannot be underestimated [12] . On the basis of WHO reports, during the 2005–2006 influenza seasons A/New Caledonia/20/99- (H1N1) and A/California/7/04-like (H3N2) were dominant [13] . Tehran H3N2 and H1N1 nucleotide sequence isolates were compared to the HA1 of other H3N2 and H1N1 reference virus isolates from GenBank. This analysis revealed that Tehran H1N1isolates were related to the A/New Caledonia/20/99 vaccine strain and clustered in a unique branch. The H3N2 phylogenetic analysis showed that some Tehran H3N2 isolates were closely linked with the Iranian isolates from previous years and some were related to A/Moscow/10/99 and A/Panama/2007/1999 strains. Amino acid comparison further supported the result of the sequence phylogenetic analysis. Between 1 and 3 amino acid differences in the HA1 protein were observed between Tehran H1N1 isolates and A/New Caledonia/20/99.

In 2005-H3N2 isolates 10–13 amino acid changes and in 2006-H3N2 isolates 5–15 amino acid differences were observed when compared with the candidate vaccine strains. The HA1 subunit of the influenza A protein consists of the globular head and contains 5 major antibody binding sites (A–E). Further analysis will be necessary to better understand the evolution of the mutational changes observed [14] .

Wilson and Cox [15] proposed that an epidemiologically important drift variant usually contains 4 or more amino acid substitutions located in 2 or more antigenic sites on HA1 protein. Amino acid substitutions in Tehran H1N1 isolates were not located in these major antigenetic sites. However, the amino acid substitutions in the H3N2 isolates were located in the antigenic sites B and D. It was also confirmed that Tehran H3N2 isolates were generated from the previous vaccine strains. In conclusion, human influenza AH3N2, A/

A/H3N2, A/H1N1 and B were dominant in a sample of patients in Tehran during the 2006–2007 influenza seasons. In addition, phylogenetic analysis on H1 showed some genetic drift among these samples from vaccine strains, but the phylogeny of H3 demonstrated that these isolates were from the previous vaccine strains generation. This study was supported by grant no. 295 from the Iranian Molecular Medicine Network, Pasteur Institute of Iran.

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Announcement

World Congress on Industrial Biotechnology and Bioprocessing

The World Congress on Industrial Biotechnology and Bioprocessing will bring together scientists, industry and government leaders, and academia from around the globe to exchange ideas about the growing biotechnology industry. Attendees will enjoy presentations various topics including biotechnology for climate change, cellulosic biofuels, renewable chemical platforms, energy from algae, specialty chemicals, food ingredients and more.

This unique conference will feature dynamic plenary sessions, international networking opportunities, and business partnering meetings. Sponsorship and exhibition opportunities are available;

please contact worldcongress@bio.org or 1-202-962-6630.

Date: 27-30 June 2010, Washington (DC), USA, North America

Second Conference of the Middle East and North Africa: Newborn screening infrastructure and research opportunities

The second conference of the Middle East and North Africa (MENA) about new born screening was held in Cairo, Egypt on April 11 to 13, 2008. Enhancement of public health importance of genetic condition and congenital disorders is growing throughout the world as well as in the Middle East and North Africa. Development of genetic science and technology has resulted in growing notice to more effective detection and treatment of congenital and genetic disorders. Considerable reduction in child and infant mortality is followed by strengthening newborn screening (NBS) that is performed in the Middle East and North Africa successfully. One of those risk factors contributing to increased potentially damaging conditions in Children is due to consanguineous marriages. The role of NBS is undeniable regarding that Physical disability, Mental retardation, neurologic damages and other possible harms are well controllable by NBS. The conference was held to evaluate the status of NBS in this area. In this conference the representatives from 18 countries in the region and a number from Asia, North America and Europe had attended. NBS program was confirmed by Marrakech declaration as priority for the public health in the region and every country was recommended to implement screen for at least one condition. These recommendations are followed by regional steering committee and would be proposed for the next meeting. Steering committee identified congenital hypothyroidism (CH) as one of those priorities in countries that have not started the NBS program. CH is a good model because of its high prevalence, accessibility of screening methods and being cost effective. Therefore a working group was formed to expand educational materials for policy makers, researchers and healthcare professionals.

This conference was divided by two groups:

The first group provided guidance of building national NBS systems and developments

The second group provided technical information and practical application

What were the presentations focusing on?

1-Overview of NBS system including the following aspects:

Infrastructure

Education

Legislation

Ethics

Law

Culture

2-The importance of integrating research into NBS programs

3-The role of research teamwork in strengthening the identification and treatment of detected conditions

4-Usefulness of program outcomes

The MENA population is about 500 million people with just about 12 million births annually.

The MENA countries have experienced different NBS programs that can be seen clearly in the following results that are extracted from country situation analysis survey.

What are the barriers to implementation of national NBS programs according to survey analysis?

Infant mortality:
Generally ranges between 9 and 29 per thousand births
In Yemen and Pakistan the rate is more than 75 per thousand births

Home delivery:

Egypt 34%	Morocco 38%	Pakistan 81%	Persian Gulf Countries<1%

Consanguineous marriages:
Morocco and Bahrain (Between first and second cousins) 12%
Qatar (between first cousins) 54%
Other countries over 23%

Political support

Financial and human resources

Greater coordination within the region and with the international community

Improvement in technical resources

National plans

According to NBS program implementation the countries were divided in 3 groups:

1- Those countries had not yet started the program

The name of countries: Libya, Morocco, Syria, Yemen

The goal: implementation of a pilot NBS program: All the four countries organized to start screening with CH and may include PKU

Training: Plans were trained to countries including laboratory and follow up procedures

Barriers: shortage of trained professionals, financial and political support

2- The countries that have completed pilot studies for at least one condition

The name of countries**:** Jordan. Kuwait, Lebanon, Pakistan, Tunisia

3- The countries which have had screen for at least one condition, primary CH and most screen for two or more conditions

The name of countries**:** Bahrain, Egypt, the Palestinian authority, Oman, Saudi Arabia, United Arab Emirates

Special feature:

1. Tandem mass spectrometry is used by both Qatar and Saudi Arabia for a large panel of metabolic conditions

2. Expansion of partnership within and outside of the region in order to accelerate development of NBS program in some of the countries in this group. The following items outline some of theses partnerships:

- Qatar and it's partner (university of Heidelberg in Germany) which their activity is Establishment of tandem Mass spectrometry.
- Bahrain and it's partner (French institute de la santé et de la recherché medicale) which their activity is Developing an integrated system of NBS for hemoglobinopathies.
- Egypt and it's partner (US agency for international development partnership) which their activity is Piloting a national NBS program for CH.

Reference:

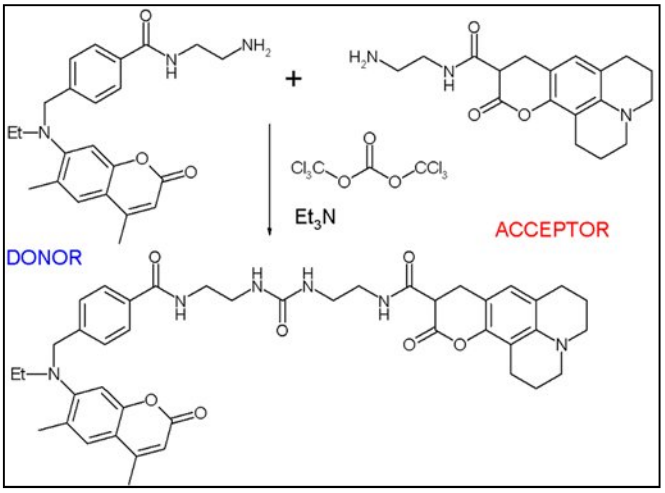
D. Krotoski et al., Conference report: Second conference of the Middle East and North Africa newborn screening initiative: Partnerships for sustainable newborn screening infrastructure and research opportunities. Genetic in Medicine (2009). Vol.11 (9).

FRET" AND "PCA" ASSAYS USED IN PROTEIN-PROTEIN INTERACTION

There are many methods for studying protein- protein interaction that among them we in this issue take a look at Fluorescence resonance energy transfer (FRET) which is an extensively exploited technique to study protein –protein interactions. This method is mainly on base of energy transfer between two chromophores.

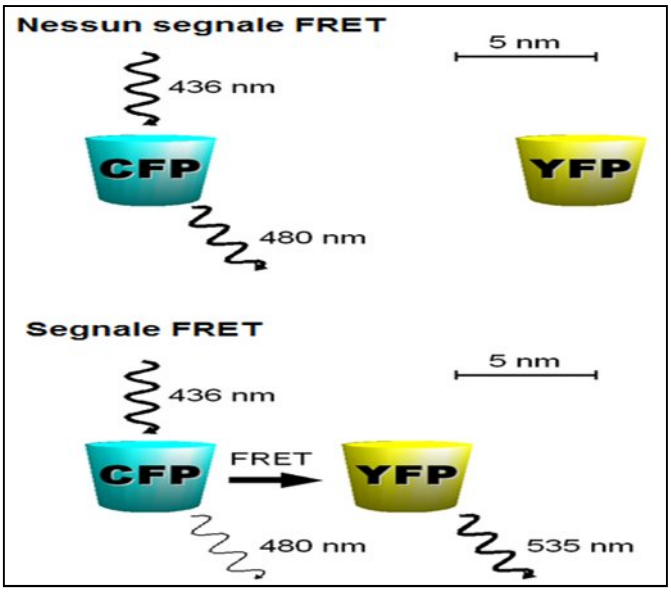
In this technique, the emission energy of one chromophore from donor molecule overlaps with the excitation energy of a second molecule (acceptor). Therefore, as excitation happens at specific fluorescence excitation wavelength of donor molecule, some of the excited energy is transferred to the second molecule.

In protein- protein interaction study we try to link A tag to protein 1as the donor molecule and the Acceptor molecule (protein 2) is also tagged Considering as our test protein. If there is any Interaction between these two proteins, the Fluorescence emission from acceptor Protein is Detectable by fluorescent microscopy or flow-Cytometry. FRET is also used for studying, Protein-DNA interactions and protein Conformational changes. Green Fuorescent Protein (GFP) is one a component that is greatly used as an indicator for studying proteins especially inter-cellular ones.



For studying protein-protein interaction in live cells exploiting cyan fluorescent protein (CFP)-yellow fluorescent protein (YFP) pair is very common that both are derived from (GFP). Fluorescent protein BFP and enhanced green fluorescent proteins (eGFP) are other pairs of proteins but are used when fluorescent microscopy and flow cytometry are available; otherwise, are not usable because BFP possess weak fluorescence. Illumination from external source can create noise in the results from negatives. Therefore, to prevent such False –positive results, it is essential that the two proteins do not interact with each other.

In view of the fact that the emission spectrums of donor and acceptor overlap, a signal cross-talk be-tween the donor and acceptor flurophores take place; hence, two main points should be considered



to gain clear results from this method including:
1. Optimization of the genetic modifications of the fluorophores
2. Operation of the imaging acquisition (including proper tuning of the fluorescent microscope)

A summery about PCA (Protein Fragment Complementation Assay) technique

Advantages:

1. Easier to scale up
2. There is no requirement to optimize the protein expression levels for the two fragments to form an active 3D structure.
3. The dynamic range of a fluorescent signal is at highest because the base of PCA is dependent on the folding of the fluorescent protein structure
4. The technique is extremely functional in protein interactome assembly studies

Disadvantages:

1. Lack of distinction between direct or indirect protein–protein interactions
2. Other techniques should be undertaken to confirm the results obtained from protein– protein interactions by PCA.

References:

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2nd ANNUAL CONFERENCE ON RECENT ADVANCES IN CHEMICAL & ENVIRONMENTAL SCIENCES - 2010 (RACES 2010)

We welcome you at 2nd Annual Conference on Recent Advances in Chemical & Environmental Sciences - 2010 to be held from 22nd Jan 2010 to 23rd Jan 2010.

22 to 23 January 2010
Patiala, Punjab, India

Web site: http://modicollege.com/members/?L=blogs.blog&article=19

Cancer Vaccines

The first documented vaccine against smallpox was developed by Edward Jenner. All vaccines developed in past (except rabies vaccine), are considered as prophylactic vaccines while today the view has changed and more focus is on producing therapeutic vaccine. Most recently, vaccines are not only used for elicitation of immunity but also are applied potentially for induction of tolerance.

Challenges facing cancer vaccines:

Right antigen

The first step to develop vaccines is choosing the right antigens meaning that the best antigens are those which are not present natively on normal cells in body. Pathogen antigens are a good example since there are not similar ones in body and immune system can detect them efficiently and destroy them completely. Most of cancer antigens are mutated forms of normal antigens over expressed on tumor antigens and possess to some extent tolerance to immune response. One of the most significant challenges is to overcome such undesirable tolerance.

The "right" adjuvant

Adjutants have the capability to provoke antigen-presenting cells (APCs) to arouse a potent and strong cellular immune response (T cells). Natural killer cells along with other immune system cells are also produced to secret cytokines that are able to keep and promote survival of antigen-specific T cells.

There are only two adjuvants approved worldwide for clinical use:
Aluminium-based salts (alum)
Squalene–oil–water emulsion (MF56)

Many other molecules are being tested such as:
Cytokines, bacterial products (toll like receptor (TLR) agonists),
Heat-shock proteins
Microspheres virus-like particles
Immunostimulatory complexes (ISCOMs)

The "right" immune response

The body's defense system called the immune system comprises of a network of specialized cells and tissues that struggle infection and disease. Therapies that utilize the immune system to struggle or prevent cancer are called biological therapies. The cancer vaccines should be able to induce immune system efficiently in order to abolish tumor cells and prevent the recurrence of tumor formation. Therefore, it seems that the

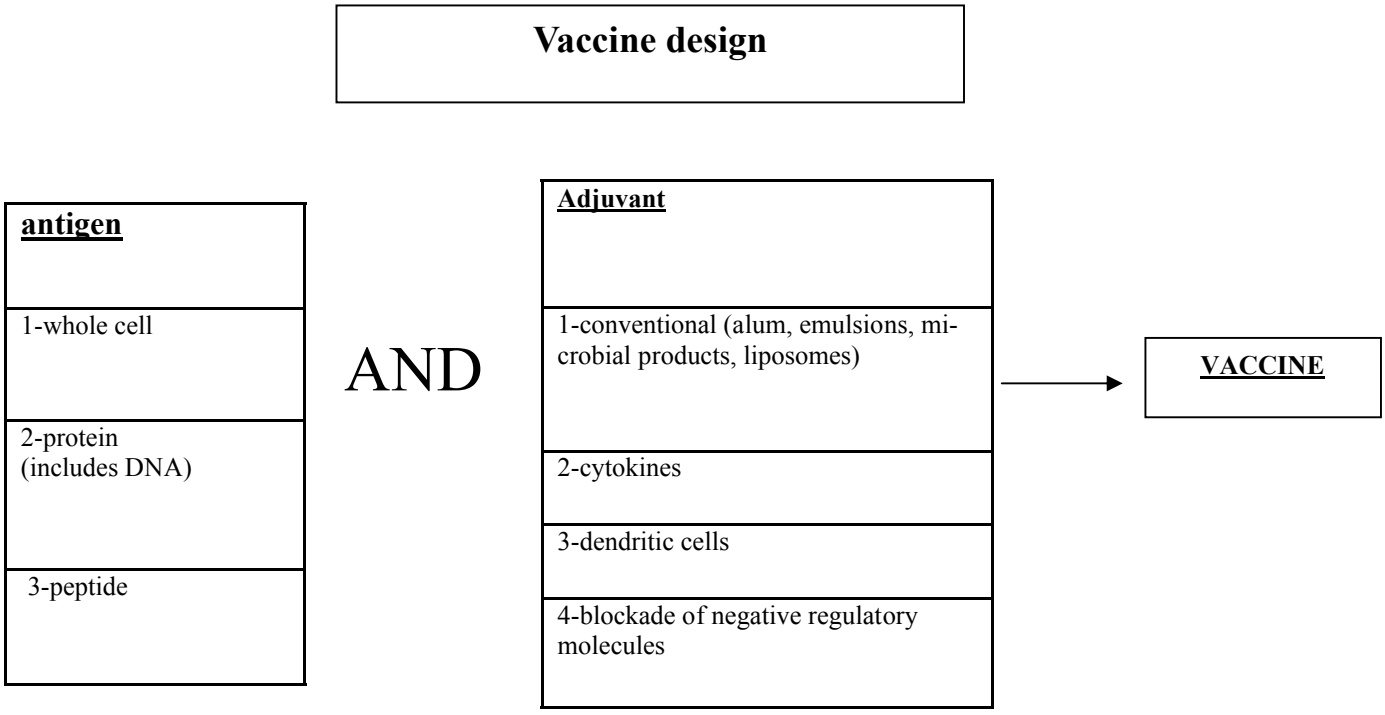
stimulated immune response should have the ability to provide a long term memory to prevent tumor relapse. On the other hand it is identified that a powerful provoked immune system in large great depends on cancer vaccine that can stimulate both the innate and the adaptive immune system.

Different types of immune responses include:

Systemic versus mucosal immunity,

T-helper 1 (Th1) versusT-helper2 (Th2)

Primarily antibodies versus primarily cytotoxic T lymphocyte (CTL)



The pioneering work of Boon and Rosenberg Leading to the isolation of the first Human melanoma antigens

Tumor antigens, candidates for cancer vaccines:

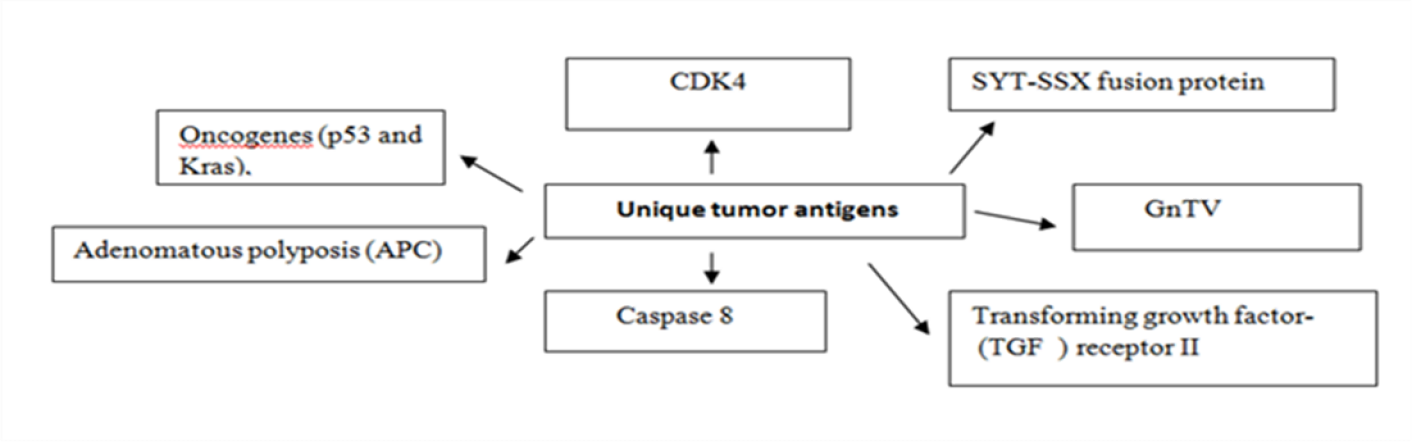
Tumor antigens can be broadly classified into two categories:

1- Shared tumor antigens: expressed by many tumors and either not on normal tissues or expressed by normal tissue in a quantitatively and qualitatively different form. Examples of such shared tumor antigens are the cancer testes antigens (MAGE, GAGE and NY-ESO1)

2-Unique tumor antigens

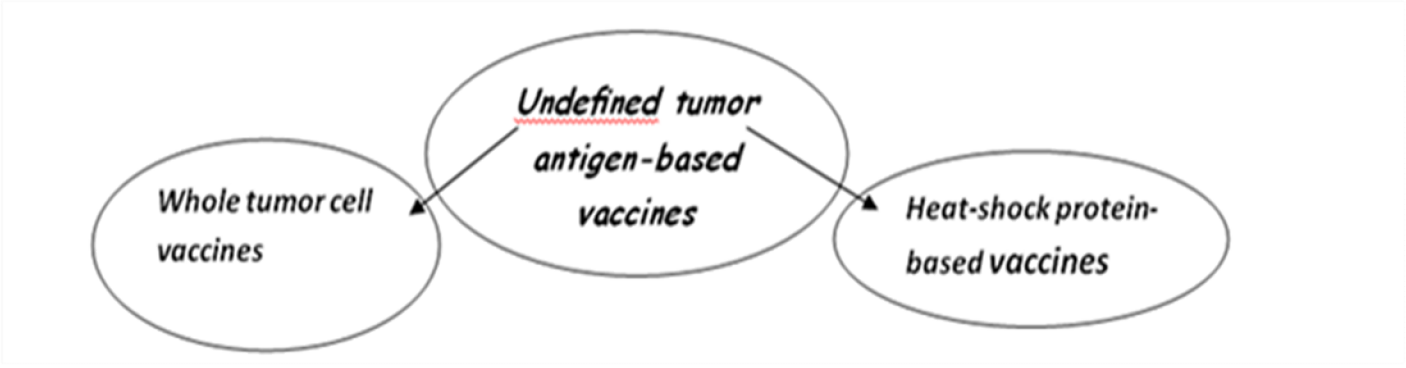
These are products of random mutations induced by physical or chemical carcinogens, and expressed uniquely by individual tumors

Some of the unique tumor antigens are shown in the following schematic diagram



Undefined tumor antigen-based vaccines:

Among cancers functional proteins including transcription, adhesion and invasion in breast and colon cancers are most affected and mutated (on average 11 mutations). So one strategy is to confront body with all the candidate antigens and the body itself can identify better antigens and desired immunity response be produced. However, tolerance to normal antigens might be Brocken down and autoimmunity begins to start.



1-Whole tumor cell vaccines:

Another strategy for cancer vaccine is to use whole tumor cells. In this way, major histocompatibility complex (MHC) restriction and the need for specific epitope identification for individual patients would be eliminated.

In this approach, the tumor antigens can be genetically modifies to secret cytokines such as granulocyte macrophage-colony stimulating factor (GM-CSF), then, immune system is more stimulated and more dendretic cells and macrophages are recruited.

Whole tumor cell vaccines are currently being developed to treat aggressive cancers such as Acute Myeloid Leukemia (AML)

2- Heat-shock protein-based vaccines:

The heat-shock proteins themselves are conserved proteins but the tumor peptides bound to them are derived from both shared and unique tumor antigens. Some of their features are including:

1. Ubiquitous, intracellular molecular chaperons
2. Their expression increases under conditions of elevated temperatures and increased stress.
3. Heat-shock proteins carrying multiple undefined tumor antigens can be purified from a patient's tumor cells
4. Used as a polyvalent autologous cancer-vaccine preparation
5. Serve as adjuvants and stimulate antigen-presenting cells

Mechanism of action:

Upon engagement of this receptor by a heat-shock protein, Dendretic Cell (DC) undergoes a maturation process that enables them to become potent antigen-presenting cells. *In vivo*, heat-shock proteins (Hsp) released by necrotic tumor cells act as endogenous "danger signals" that mature DCs for efficient presentation of tumor antigens.

How Heat-shock protein work (Mechanism of action):

When DCs faces to a heat-shock protein, under maturation process it would be able to turn into powerful antigen-presenting cells. *In vivo,* necrotic tumor cells produce heat-shock proteins (HSP) as endogenous "hazard signals" make DCs efficient for proficient presentation of tumor antigens.

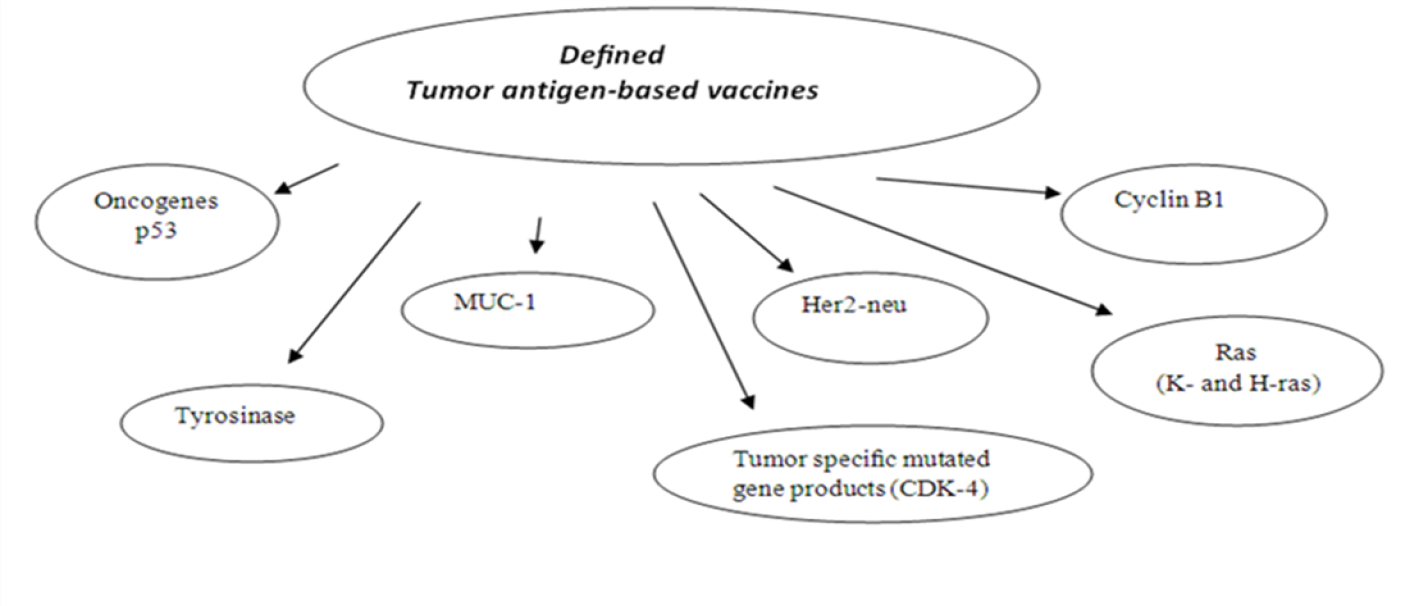
Defined tumor antigen-based vaccines

Features:

1. The type of tumor antigens is defined
2. Extract a very specific effector and memory cell response with greatly diminished risk of autoimmunity
3. Immunity will develop to other antigens on tumor cells not incorporated in vaccine formulation.

Disadvantages:

Immune response is directed to a single molecule or an epitope and thus could be evaded by a tumor antigen loss variant.



Why do search about cancer vaccine can be interesting?

Vaccination against microbes is efficacious and saves lives

Activation of the innate immune system can provide clinical benefit for select cancers Identification of tumor antigens

New vaccination strategies.

There are many strategies for vaccine delivery to body that most important ones are outlined in the following:

Vaccination strategies and approaches:

Anti-idiotypic antibody-based vaccine

Dendretic Cell-based vaccines

DNA and RNA vaccines

Viral-vector based vaccines

Particle-based vaccine

The aim of cancer vaccine development is to provoke a robust immune response in body that not only eradicate tumors but also produce and maintain a strong memory response that never permit tumor relapse.

One of the great advantages of cancer vaccines is that they can target both surface and intercellular antigens involved in cancer progression as well as stimulating immune response for a long-lasting time that need for

multiple administration of vaccination is abolished. Many giant biopharmaceutical companies are working on such therapeutic vaccines and basic and translational immunology would help to this research filed considerably.

Up to know the vaccines have been approved by FDA that can prevent cancer. One of these vaccines prevents infection with the human papillomavirus (HPV), which is the reason of almost all cervical cancers. The other vaccine prevents infection with the hepatitis B virus, causing liver cancer. Other vaccines that may prevent or reduce the risk of cancer are also being tested in ongoing clinical trials like cancer vaccines for melanoma, breast cancer and etc…

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3- http://www.cancer.gov/clinicaltrials/learning/cancervaccines

Announcement
The Peptide Conference 2010

The conference features leading researchers and experts from the various fields of peptide therapeutics development presenting the latest scientific and technological knowledge in these rapidly advancing areas of life sciences. The applications of peptide chemistry from synthesis through purification and analytics, to bioactivity testing in biotechnology, biomedical and other applications from analytical to industrial scales are presented.

Date: 30-31, March 2010, Cambridge, United Kingdom, Europe

Contact: mark@avakado.eu (Mark Harrington)

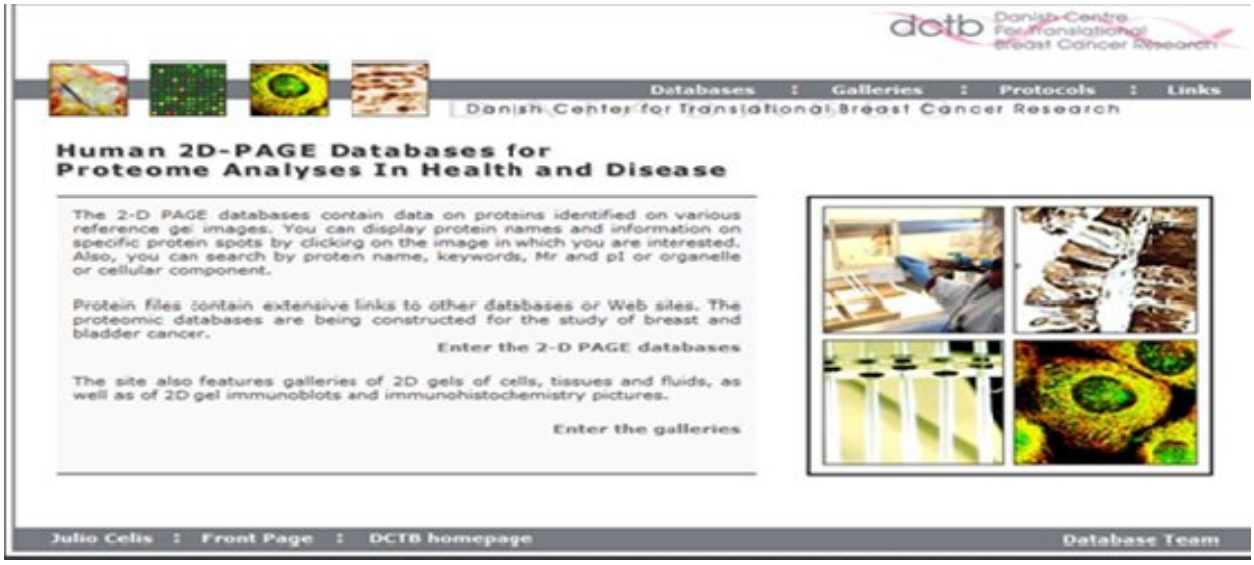
Website: http://www.avakado.eu/dev/node/264

Announcement

In Collaboration with the WSEAS IWG (International Working Group) on Oncology, the WSEAS IWG on Biology and Chemistry, the WSEAS IWG on Physiology, the WSEAS IWG on Histology and Embryology, the WSEAS IWG on Psychiatric, the WSEAS IWG on Pharmacology .These conferences are going to be held in the University of Cambridge, UK, February 23-25, 2010.

For more information please refer to: www.wseas.org

Human 2D-PAGE Databases for Proteome Analyses in Health and Disease



The site http://proteomics.cancer.dk/ is titled" Human 2D-PAGE Databases for Proteome Analyses in Health and Disease" A look into this website revealed significant promise. It is Danish site that is a collection of invaluable information about protein 2D gel electrophoresis. The 2-D organization and image collection was some of the best that could be found on the web. It is surly worth visiting.

The features:

It is somewhat hierarchically organized with sections on breast cancer, bladder cancer, and other types of cancer.

Another section with a different hierarchy led to many images from numerous cell lines.

Images at each place are only a click away.

Categories of proteins (e.g., chaperonins) could be straightforwardly marked on the image at the user's direction.

Other attributes on the site comprising an image of the First 2D PAGE, miscellany, and a link to the human protein atlas.

Source: http://proteomics.cancer.dk/

Healthcare and Biotechnology in the Middle East

Demanding for modern medicine is growing throughout the world as well as Middle East (ME) and it counts a good opportunity for large companies to find their markets in this area. The population of the region is getting up to 280 million. Major companies have found this area for large investment associated with governments of Middle East that would like to develop biotechnology as their first priorities in healthcare policies.

Why Middle East could be a golden opportunity for modern medicine market?

It is the fastest growing regions in the world with about 280million population.

Countries are confronted with about 2% raised cost for the healthcare of their aging population.

The growth of communicable and non-communicable diseases

The share of ME market is less than 2% of global pharmaceutical trades but is on the rise quickly:

It is estimated that the total pharmaceutical market in ME be US$10.6 billion.

It is predicted that ME market will go beyond US$15 billion by 2014.

Egypt has largest market (accounting for 20% of regional worth);

Palestine and Iran are the next ones (each 17-18% of regional worth); and then Saudi Arabia (16% of regional worth).

The countries would have the largest market growth in the Middle Eastern are:

Saudi Arabia, Bahrain, Kuwait, Oman, Qatar and the UAE.

The market value is close to US$4 billion in above countries that Saudi Arabian pharmaceutical market would have the most portions meaning that getting to US$2 billion in value by 2012.

Which companies in which countries?

The large companies have recognized the potential market in this region and are investing in Middle East as the following are several examples:

The UAE:

Pfizer, Amgen and Genzyme are establishing their regional headquarters at Dubai Biotechnology and Research Park (DuBiotech).

Dubai Health Care City is a place that AstraZeneca and Wyeth Pharmaceuticals have their regional headquarters. Ranbaxy (Indian company) already has 160 drug approvals in the region and is the market leader in UAE.

Saudi Arabia

GSK possess 10% market share in Saudi Arabia, Pfizer has just over 6% of market

In Egypt

GlaxoSmithKline has a 9% market share and lately obtained the Egyptian mature products business of BMS.

It was a summery look to one of interesting books about development of biotechnology in Middle East. This fantastic book is written by Dr. Faiz Kermani on April 2009. The publisher oh this book is Bioplan Associates. Inc which ISBN number is 9781934106082. The main aim of this book is to give readers a fresh look to be more familiar with the Middle East and its potential opportunities for production and investment. If you would like to read the whole book you need to order to www.bioplanassociates.com

Cover Picture

Title: Phylogenetic tree
Description: showing how Eukaryota and Archaea are more closely related to each other than to Bacteria In biology, phylogenetics is defines as the study of evolutionary relatedness among diverse groups of organisms which is discovered via molecular sequencing data and morphological data matrices even though Phylogenetic relationships in the past were reconstructed by looking at phenotypes, regularly anatomical characteristics. Phylogenetic can help taxonomy to classify, identify and naming of organisms. Evolution is considered as a branching process, by which populations are changed over time and may speciate into separate branches, hybridize together, or terminate by extinction. These findings can be seen in a phylogenetic tree
Source: en.wikipedia.org/wiki/Phylogenetic_tree

Title: Protein mass spectrometry
Description: It is a technique that strongly characterizes and identifies protein attributes which is exploited in a great deal in protein study. In the first approach Electrospray ionization (ESI) and matrix-assisted laser desorption/ionization (MALDI are two main methods to prepare samples by ionization and then the proteins are introduced to mass analyzer. This approach is referred to as "top-down" strategy of protein analysis. In the second approach, a protease like trypsin is used to digest proteins into smaller peptides .next, these peptides are introduced into the mass spectrometer and identified by peptide mass fingerprinting or tandem mass spectrometry
Source: en.wikipedia.org/wiki/Protein_mass_spectrometry

Title: Algae
Description: Algae are a large and diverse group of simple, typically autotrophic organisms, ranging from unicellular to multicellular forms. They are categorized in cyanobacteria that are included to eukaryote organisms. Nearly all algae have photosynthetic machinery ultimately derived from the Cyanobacteria. Today Algae are used by humans in many ways; for example, as fertilizers, soil conditioners and livestock feed A microalga is a subgroup of algae that holds a great promise in biotechnology. They possess the ability to be genetically engineered to produce recombinant proteins although research in this field is in primary stages. Furthermore algae are good candidates for production of biofuels, directly related to the potential to produce more biomass per unit area in a year than any other form of biomass.
Source: en.wikipedia.org/wiki/Alga