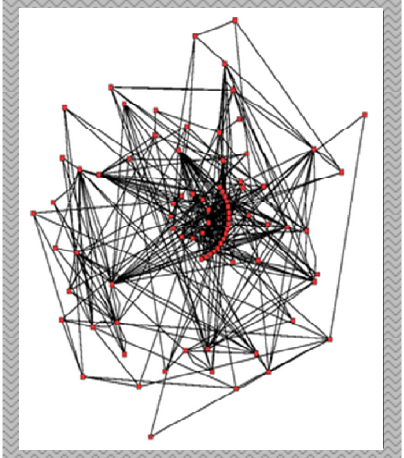

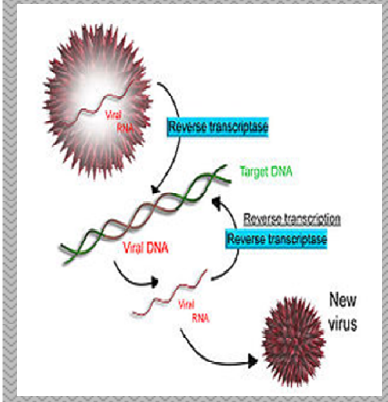

EMGEN Newsletter

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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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Isolation, recombinant expression and characterization of *the dprA* gene product in *Streptomyces rimosus* NRRL 2455

An article entitled "Isolation, recombinant expression and characterization of the dprA gene product in Streptomyces rimosus NRRL 2455" aims to identification of dihydrodipicolinate synthase of the order streptomycetes. The study was carried out by ***Khaled Mohamed Anwar Aboshanab****; he is working in Microbiology and Immunology department, Faculty of Pharmacy, Ain Shams University, Abbassia, Cairo, Egypt; and the paper was published in African Journal of Microbiology Research Vol. 4 (10), pp. 915-922, 18 May, 2010*

Dr. Khaled Mohamed Anwar Aboshanab

The biosynthesis of the amino acid lysine from L-aspartate and pyruvate occurs in most plants, bacteria and in some fungi (Voss et al. 2009). The lysine biosynthetic pathway was firstly investigated by Gilvarg (1960) where several biosynthetic steps are involved. Dihydrodipicolinate synthase (DHDPS) catalyzes the formation of dihydrodipicolinate from pyruvate and L-aspartate β-semialdehyde (ASA), the first enzymatic step unique to lysine biosynthesis via the diaminopimelate pathway (Bukhari and Taylor 1970; Girish et al. 2008). DHDPS (EC 4.2.1.52) has been isolated and its activity was determined in various plant tissues and as well as in several bacteria species (Wallsgrove and Mazelis 1980; Kumpaisal et al. 1987; Ghislain et al. 1990: Frisch et al. 1991; Dereppe et al. 1992). The activity of DHDP was found to be feedback inhibited by micromolar concentration of L-lysine (Frisch et al. 1991; Ghislain et al. 1990; Kumpaisal et al. 1987; Wallsgrove and Mazelis 1980).

Furthermore, the diaminopimelate pathway in bacteria acts as a branch-point for both lysine and cell wall components biosynthesis. This pathway involves also further enzymatic reactions with the generations of various intermediates such as *meso*-2,6-diaminopimelate, a key component in bacterial peptidoglycan.

Moreover, dipicolinic acid is an essential component of bacterial endspores which is mainly responsible for the spore resistance toward head and oxidizing agents (Prescott 1993). Therefore, this enzyme would

play a crucial role in keeping the integrity of bacterial cells as well as their ability to form spores. Several investigators had determined the crystal structure of DHDPS from different sources including *Nicotina sylvestris*, *Escherichia coli*, *Thermotoga maritima*, *Bacillus anthracis*, *Mycobacterium tuberculosis* and *Staphylococcus aureus* (Mirwaldt et al. 1995; Blickling et al. 1997; Pearce et al. 2006; Girish et al. 2008; Kefala et al. 2008) exploring the different catalytic sites where both pyruvate and ASA bind. The amino acid sequences of some putative DHDPS homologous proteins are now available in the proteins bank database from different bacterial species. These include enzymes from related *Streptomyces* (*S.*) species such as *S. coelicolor* (accesion codes: NP 626178.1), *S. avermitilis* (accesion code: BAC74054.1), *S. sviceus* (accession code: YP 00220875, *S. griseus* (accession code: 001827119) and *S. pristinaespiralis* (accession code: YP 002197764.1). However, the biochemical activities of the respective putative proteins have not been analysed.

In the present study, the biochemical activity of the *dpr*A gene product, putatively involved in the biosynthesis of dihydrodipicolinate in *S. rimosus* NRRL 2455 was biochemically analyzed. *S. rimosus* NRRL 2455is a paromomycin producer, a 2 deoxystreptamine (2DOS)-containing aminocyclitol aminoglycoside antibiotic with broad spectrum activity against most of gram positive and gram negative bacteria. For accomplishing this work, two universal heterologous primers were designed and were able to amplify various homologous *dpr*A genes in related bacterial species. Also, the *dpr*A gene coded for DHDPS in *S. rimosus* was amplified via PCR, cloned, sequenced and heterologously expressed in *E. coli* BL21 (DE3). The biochemical activity of the expressed *dpr*A gene product was determined, characterized and the phenotypic changes occurred in the *dpr*A$^-$ knock out mutant were also studied

In this study, cloning and submission of 3639 bp from *S. rimosus* NRRL 2455 to the EMBL database under the accession code EU617017 were carried out. The entire *dpr*A gene has been cloned and heterologously expressed and the gene product was purified and analysed spectrophotometrically. A *dpr*A$^-$ knock-out mutant has been created and showed a reduction of mycelia growth and spore formation by about 43 and 37%, respectively, as compared to the wild strain. Fed with *meso*-diaminopimelic acid, the *dpr*A$^-$ mutant regained its capability of mycelial growth, however no significant effect on spore formation was observed confirming that *dpr*A gene product was involved in the biosynthesis of dihydrodipicolinate in *Streptomyces rimosus* NRRL 2455.

Interview

In this issue, we present an interview with ***Dr. Raida Wajih Khalil*** *from Biotechnology and Genetic Engineering Department Philadelphia University . She is the head of Biotechnology Division whom we had the following interesting interview with.*

1. Dear Dr. Wajih Khalil could you please briefly introduce yourself and explain your educational status?

I am Holding a PhD Degree in molecular biology, Institute of Medical Sciences, Aberdeen University-United Kingdom. BSc in Microbiology (Major) and Biochemistry (Minor), MSc (Biochemistry) both degrees obtained from Kuwait University-Kuwait.

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

Basically, the major Area is Molecular genetic and Diagnosis, Human Genetics and Cytogenetics and Gene Expression.

3. Why did you choose this field of research?

Actually, I have gained good experience either during practical work before doing PhD in Molecular Genetic and Cytogenetic as service for community and supported with Molecular Biology tools exposed to during my PhD. This field additionally is vastly growing and applicable

4. Do you apply any biotechnology or genomics tools in your researches and please explain how and where?

Yes.

5. What kinds of biotechnology facilities do you have in your laboratory?

PCR, Real TIME PCR, prepare all the prerequisites steps for sequencing analysis, PCR-RFLPs

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

Yes.

7. Are there any late stage biological products to be commercialized in your center? Could you please explain more?

NO.

8. Are there significant biotechnology centers in your country?

NO.

9. Are there any academic training courses in biotechnology in your country? If yes, to above question, in which level and how many students are trained annually?

Yes. Up to my knowledge nearly Average level. Regarding the number of Students , I do not have information about this issue

10. 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 am familiar with the EMRO countries and EMGEN via Email.

11. Do you have any suggestions for establishing/extending collaborations with EMRO countries?

Lunch the wider database and make it well known to researchers in EMRO countries

12. Are there any possibilities for young researchers from EMRO countries to participate in training courses in your biotech centers?

Sure.

13. What kinds of difficulties do you face, in research and commercialization of medical biotechnology in your country and the region?

Limited Funds!!

14. Do you have any training courses or workshops in your research centre?

Yes , but very limited.

15. What is your idea about genomics and its applications in improving public health?

It is crucial and should be applied widely in the field of environmental, health and other critical fields related to human daily life.

16. What is your idea about commercialization of researches in the field of bioscience?

Very important and should be focused and oriented most of the grants towards the investment of science and commercialization of the products.

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

Again should be paid attended similar to other disciplines and even more in term of Funds and support training in this field, recommend young undergraduate students towards Postgraduate in Biotechnology particularly speaking, Environment and Pollution, Water, Agriculture and improvement of crops in our countries in addition to health issues

18. Would you please tell us about the differences of genomics and its applications between developed and developing countries? What should we do in this regards?

Basically, we have excellent researchers with high skills in this field in our countries but need more collaboration to put ideas together and establish center of excellence, and before that raise up the funds which is given the priority

At the end of interview, do you want to mention anything special?

Thanks and wish all success for EMGEN

Thank you Dr. Wajih Khalil for sharing information and your opinion with us. Also we are grateful for your kind and useful cooperation.

Epigenetic and its effect on brain function

By: Akram Zamani

The idea that genes remain balanced during our life and that our chance of what had been written by our genes is non-reversible has changed recently. The reality is that, our circumstance is rapidly changing and there must be a layer of information that tells the genome how to purpose in the changing conditions. The body accommodate to these changes by the use of epigenetic.

The word was first coined by Conrad Waddington in 1942 and is allude to the second code of DNA. The code that unlike the first code (DNA sequence), can change during the lifetime. The science of non-genetic factors that can change the gene's expression without changing the DNA sequence is Epigenetic. It changes the expression of genes much sooner than mutation that wants the change in DNA sequence. The epigenetic code adds up to DNA methylation arrangements that are not totally inherited and histone modifications such as acetylation, phosphorylation and methylation of the proteins. The methyl group is added toCpG sites, convinces cytosine to 5-methylcytosine. DNA methylation and histone adaption mechanisms cause the gene silencing or gene expression respectively and changes in the cell in response to different signals.

In human somatic cells, m^5C accounts for 1% of total DNA bases and consequently affects 70-80% of all CpG dinucleotides in the genome. In the early expansion stages this amount contract to 30% and the De novo methylation restores it to a normal level. This shows that the methylation patterns are not totally inherited and then it can be changed due to the changes during development. The methyl backers for the de novo methylation mechanism during development really depend on diet. Nutritional Methionine and choline are the main foundation for mammalian methyl groups and Folic acid and vitamin B12 are cofactors for the mechanism. This supports new studies that have announced the importance of prenatal and early post natal nutrition on vulnerability to chronic diseases such as cardiovascular diseases, type 2 diabetes, cancer and brain development disorders later in life.

In addition to diet, different signals that our cells receive can influence the methylation procedure . Studies have shown that motherly behavior in the early days of birth can influence the epigenome of the progeny. In rats, Offspringsreceiving more thrashing and grooming in the first week of birth have revealed

higher levels of NGFI-A (Transcription factor Nerve Growth Factor- Inducible Protein A) that can be upturned by cross development. This is what happens, the increase in thrashing and grooming (motherly care), increases the levels of serotonin in offsprings, high levels of serotonin increases the activation of cAMP that next activates cAMP dependent Protein kinase A that leads to the increase in NGFI-A activation. On the other hand studies have shown that licking and grooming is linked with unmethylation of CpG sequences of NGFI-A response constituent on exon 1_7 GR promoters and as a result NGFI-A has a better chance of binding to the promoter. Increased Glucocorticoid receptor expression is resulted in offspringsand they show better responses to stress in their maturity and are much more relaxed compared to offsprings that had low motherly care.

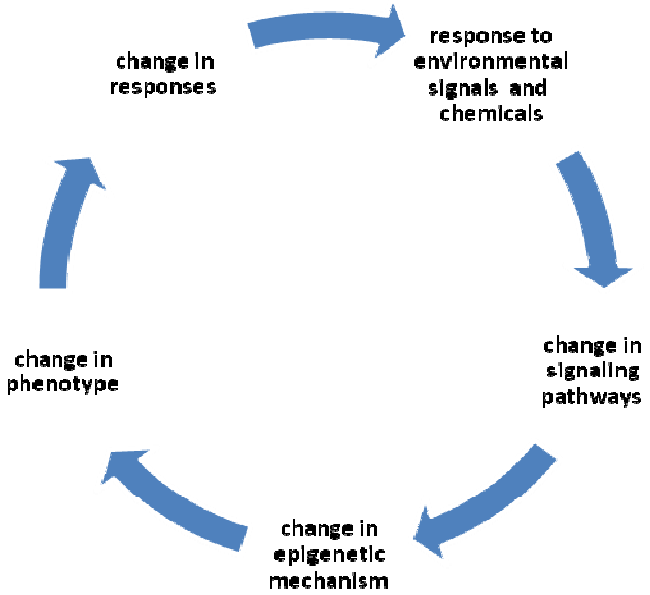
The result of motherly care on epigenetic does not stop there; studies disclose the association of postnatal mistreatment and Brain resulting Neurotropic Factor (BDNF) methylation. In rats, poor motherly care causes increase of the methylation of the exon 4 of *bdnf* promoter and reduce in BDNF mRNA in the prefrontal cortex. BDNF is a protein that as a neurotropic factor,acts on certain neurons of the central nervous system and the peripheral nervous system, helping to support the survival of existing neurons and support the growth of the new neurons and synapses.

Even as the result of signals in childhood can make changes of *bdnf*promotor, different factors in maturity have also been shown to change DNA methylation of *bdnf*promotor that is triggered by changes in the activity of DNMT (DNA methyl transferase) in exact regions of the adult brain. In addition to DNA methylation, post translation modifications of histones that as mentioned earlier can be acetylation, phosphorylation or methylation can also make changes in *bdnf* genes expression. These epigenetic changes of *bdnf* gene have been shown in new studies that have effect on learning and memory functions in the brain. Its consequence on Long term memory (LTM) has been proved by different studies.

Other proteins have shown to be effectual for the control of synaptic purpose. MeCP2 (methyl CpG binding protein) arises to be essential for normal nerve function. It binds to methylated DNA, and by making connections with different proteins it can turn the gene off. Current studies have shown that it can have result even on gene expression in addition to silencing genes, and is said it has double roles in gene expression. Any injury in MeCP pathways can lead to several neurodevelopmental abnormalities such as Rett syndrome, childish autism, mental retardation and schizophrenia (Moretti and Zoghbi, 2006).

In the recent years the rate of autism has augmented radically, this can be an alarm that the effects of the environment on nerve development has to be in more focus and more information on diet and healthy existence has to be given.

What has to be renowned, is that, the epigenic procedure is not a linear pathway, it acts in a circle that can lead to stronger result and responses. we get signals from the environment that activates convinced signaling pathways in cells, these signals have an effect on the epigenome and change DNA methylation or the histone congregation on the DNA, changes of the epigenic patterns changes our phenotype and the type of response to each signal and again makes changes in signaling pathways and so on.



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Immunoproteomics

Immunoproteomics is an expression used to explain the study of large sets of proteins (proteomics) concerned in the immune response. Proteomics is a rapid advance to analyze large number of proteins using 2D-E and mass spectrometry. Information created from proteomics has amplified a kind of biological regulatory networks and has opened different scientific avenues such as “Structural proteomics”.

There are some examples of common applications of immunoproteomics:

- the separation and mass spectrometric recognition of MHC (major histocompatibility complex) binding peptides.
- purification and recognition of protein antigens compulsory specific antibodies (or other similarity reagents).
- identification of proteins and pathways modulated by an exact infectious organism, disease or toxin.

Proteomics also usually indicate that mass spectrometry is the final method used for protein identification. Challenges related with resolving and sequencing individual peptides from the multifaceted mixture of MHC-bound material is not only one to immunoproteomics. This type of experiment is similar to the shotgun proteomics-type approaches that make complex mixtures of tryptic (or other proteolytic) remains derived from a subset of the cellular proteome. Because MHC-bound peptides normally have different termini and the proteolytic specificities that make them are fairly diverse, positive assignment of the peptide series can be difficult. Similarly, it is unusual to detect peptides resulting from the same protein unless analyze is related to infection, for example, where target antigen sequences are recognized or supposed. These properties of MHC-bound peptides decrease assurance in their sequence assignments by MS/MS methods and dictate the obligation for extra screening algorithms in epitope recognition strategies. For example, if the compulsory motif for the given allele is known, this frequently can act as a original filter for transmission fragmentation spectra resulting from immunoaffinity- purified class I MHC molecules. As proteomics instrumentation becomes more available to a more varied array of researchers, so to do the stress for robust methods

for protein and epitope recognition. One limitation in study of MHC-bound peptides is operator partiality in selecting peptides from enormously complex mixtures for MS/MS. Newer technologies, such as the MALDI-TOF- TOF-MS/MS instruments will agree to much-higher throughput analyses in an automated form. This will allow many more peptide fractions to be analyzed without operator partiality and make it possible to use higher-resolution collection of HPLC fractions for study. The condensed peptide repertoires of narrower fractions will improve the potential to distinguish many more peptides due to the condensed possibility of the coincidences of masses of peptides in wide-fraction cuts and a lowered propensity for containment of ionization of peptides. The suppleness of numerous MS/MS modes of other recently developed MS analyzers connecting linear ion trap should also facilitate other aspects of immunoproteomics.

The specificity and compassion of the immune response is unmatched in biology, and the use of antibodies, for example, as analytic and research tools have been ordinary for many years. Proteomic study of the peptides and antigens concerned in immune responses to pathogens and to irregular or even usual tissues presents exciting and difficult challenges to the researcher. Fundamental all these analysis is the power of the immunological reagents and practical readouts that offer delicate sensitivity unrivalled by the analytical methods we have at hand. The use of these reagents as show tools or as a fractionation method will drive immunoproteomics study in the future. The use of antibodies and recombinant reagents such as MHC-tetramers and other markers of immune effecter cells give opportunities to get large numbers of homogeneous cells from tissues and fluids using fractionation or separation methods such as flow cytometry and cell categorization and laser capture microscopy. When used in mixture with more characteristic fractionation methods such as subcellular fractionation and affinity chromatography, the degree to which declaration of specific cells can be remote and analyzed is improved dramatically. What are the challenges that lie ahead in immunoproteomics?

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DNA nanotechnology

One of the branches of nanotechnology is **DNA nanotechnology** which uses the molecular detection properties of DNA and other nucleic acids to make intended synthetic structures out of DNA for technological ambitions. In this field, DNA is used as a structural material rather than as a bearer of genetic information, making it an example of bionanotechnology. DNA nanotechnology has applications in molecular self-assembly and in DNA ascertaining. Although in the context of molecular biology DNA is usually cogitated as the transporter of genetic information in living cells, DNA nanotechnology considers DNA exclusively as a chemical and as a material, and is usually followed outside of any biological context. DNA nanotechnology makes use of the information that, outstanding to the specificity of Watson-Crick base pairing, only allocations of the strands which are matching to each other will attach to each other to form duplex DNA. DNA nanotechnology assaults to rationally design sets of DNA strands so that preferred portions of each strand will collect in the correct positions to for some desired target structure.

Although DNA nanotechnology values apply equally well to other nucleic acids such as RNA and PNA, and structures combining these have been made. For this reason the field is infrequently referred to as **nucleic acid nanotechnology**.

Fundamental concepts

Nucleic acid double helices will only appearance between two strands of compatible sequences, where the bases are coordinated into only A-T or G-C pairs.

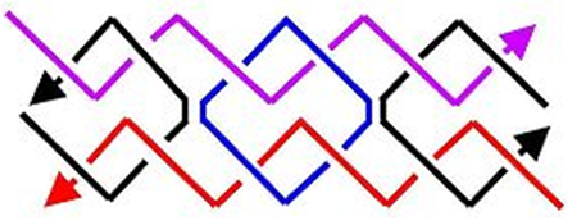
DNA nanotechnology creates multifaceted structures out of nucleic acids by creation use of the specificity of base pairing in nucleic acid molecules. The structure of a nucleic acid molecule involved a sequence of nucleotides, illustrious by which nucleobase they have. The four bases in DNA, used are adenine (A), cytosine (C), guanine (G), and thymine (T). Nucleic acids have the possessions that two molecules will join to each other to form a double helix only if the two sequences are complementary, sense that they form matching sequences of base pairs, with A's only binding to T's, and C's only to G's.

Nucleic acid strands are predictable in most cases to bind to each other in the conformation that

maximizes the number of properly paired bases because the arrangement of correctly matched base pairs is energetically favorable. This property, that the sequence determines the outline of binding and the overall structure, is used by the field of DNA nanotechnology in that sequences are rationally designed so that a preferred structure is preferential to form.

Almost all structures in DNA nanotechnology create use of branched DNA structures containing junctions, as opposite to most biological DNA which exists in a linear double helix form. Four-arm junction which can be made using four different DNA strands which are interdependent to each other in the correct pattern is one of the simplest branched structures, and the first made. Unlike in normal Holliday junctions, in the artificial motionless four-arm junction shown below, the base sequence of each arm is different, meaning that the junction point is set in a certain position.

Junctions can be used in more complex molecules. The "double-crossover" or DX motif is one of the more widely-used of these. A DX molecule can be consideration of as two DNA duplexes located parallel to each other, with two crossover points where strands cross from one duplex into the other. Each junction point is itself topologically a four-arm junction. This molecule has the benefit that the junction points are now forced to a single orientation as opposed to being flexible as in the four-arm junction. This makes the DX motif appropriate as a structural building block for larger DNA complexes.



These four strands connect into a DNA four-arm connection because this structure maximizes the number of correct base pairs, with A's matched to T's and C's matched to G's. A double-crossover (DX) molecule. This molecule adds up to five DNA single strands which form two double-helical domains, on the left and the right in this image. There are two crossover points where the strands aggravated from one area into the other.

Design

Because of DNA nanostructures must be intended they will gather into the preferred structures. This adds in both the design of secondary structure, deciding which parts of which nucleic acid molecules should connect to each other, and primary structure, the specification of the uniqueness of each individual base.

Structural design

The first step in a scheming a nucleic acid nanostructure is to decide how a given structure should be represented by a precise arrangement of nucleic acid strands. Therefore this design step determines the secondary structure of the nucleic acid complex which will assemble into the preferred shape. There are several approaches which have been confirmed:

- **Sequence regularity minimization.** The target structure is a thermodynamic minimum because of most design in DNA nanotechnology focuses on designing sequences, and miss-assembled structures have higher energies and are thus broke.
- **Folding structures.** An option to the tile-based approach, two-dimensional DNA structures can be made from a single, long DNA strand of random sequence which is folded into the preferred shape by using shorter, "staple" strands. This allows the creation of two-dimensional shapes at the nanoscale using DNA. Confirmed designs have incorporated the smiley face and a crude map of North America.
- **Kinetic assembly.** Recently, there has been interest in scheming to the kinetics of DNA self-assembly, so that fleeting dynamics can also be programmed into the assembly. Such a method also has the advantage of happening isothermally and thus not requiring a thermal annealing step required by exclusively thermodynamic approaches.

Sequence design

A real sequence of nucleotides must be devised which will form into the preferred structure after any of the above approaches are used to design the secondary structure of a target molecule. Nucleic acid design is the procedure of generating a set of nucleic acid base sequences that will connect into a desired conformation. Nucleic acid design is focal to the field of DNA nanotechnology.

Nucleic acid design has analogous aims to protein design: in both, the sequence of monomers is designed to favor the preferred folded or related structure and to disfavor exchange structures. However, nucleic acid structures are less adaptable than proteins in their functionality.

Types of structures

Application

There are many synthesized and characterized structures made from DNA:

Periodic lattices

Constructing nanostructures out of smaller discrete units is the earliest method for creating DNA. This method has the benefit of being able to theoretically separate the stronger connections which form each tile from the assembly of the larger complete structure. It is often used to make intermittent lattices, but can also be used to apply algorithmic self-assembly, making them one stage for DNA computing.

In order to combine into a two-dimensional periodic lattice, DX, or Double Crossover molecules can be equipped with sticky ends. Each DX molecule has four termini, one at each end of the two double-helical domains, and these can be accurate with sticky ends that program them to combine into an exact outline. More than one type of DX can be used which can be made to place in rows or any other tessellated pattern. They thus form extended flat sheets which are fundamentally two-dimensional crystals of DNA.

Two-dimensional arrays have been made out of other designs as well, including the Holliday junction rhombus array as well as a variety of DX-based arrays in the shapes of triangles and hexagons.

Nanotubes

In addition to flat sheets, DX arrays have been made to form empty nanotubes of 4-20 nm diameters. These DNA nanotubes are rather similar in size and shape to carbon nanotubes, but the carbon nanotubes are stronger and better conductors, while the DNA nanotubes are more easily customized and linked to other structures.

A model of a DNA tetrahedron described in Goodman, 2005. Each border of the tetrahedron is a 20 base pair DNA duplex, and each apex is a three-arm junction.

Arbitary shapes

DNA structures with solid faces have also been assembled, using the DNA origami technique. These can be programmed to open and discharge their load in response to a incentive, making them potentially useful as programmable molecular cages.

Functional nucleic acid nanostructures

DNA nanotechnology focuses on generating molecules with intended functionalities as well as structures. Many classes of useful systems have been verified.

Nanoarchitecture

The attitude of using DNA arrays to template the conclave of other functional molecules was first recommended by Nadrian Seeman in 1987, but only recently has development been made in plummeting these kinds of schemes to do. In 2006, researchers covalently linked gold nanoparticles to a DX-based cover and showed that self-assembly of the DNA structures also assembled the nanoparticles hosted on them. A non-covalent hosting scheme was shown in 2007, using Dervan polyamides on a DX array to assemble streptavidin proteins on specific kinds of tiles on the DNA array. There has also been interest in using DNA nanotechnology to collect molecular electronics devices.

DNA nanomechanical devices

DNA complexes have been made which modify their conformation upon some incentive. These are planned to have applications in nanorobotics. "Molecular tweezers," is one of the first such devices that changes from an open to a closed state based upon the presence of control strands. DNA machinery has also been made which show a parody movement. One of these makes use of the change between the B-DNA and Z-DNA forms to react to a change in buffer conditions.

The fascinating potential of DNA nanotechnology

DNA, the main building block of our genetic makeup, has become an intense nanotechnology study field. DNA molecules can serve as exactly convenient and programmable scaffolds for organizing useful nanomaterials in the design, fabrication, and description of nanometer scale electronic devices and sensors.

The reason why DNA could be useful in nanotechnology for the design of electric circuits is the fact that it really is the best nanowire in life – it self-assembles, it self-replicates and it can adopt a variety of states and conformations. Then of course there is a rich body of work on DNA use in nanorobotics.

Conclusion

Many of these self-assembly procedures are computational based and programmable and it seems probable that interdisciplinary methods will be essential to other emerging subfields of nanoscience and bio-molecular totaling.

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Oxytocin Promises Hope in Prader-Willi Syndrome

Prader-Willi syndrome is an unusual genetic disorder which affects one child in 25,000. Children born with this syndrome have a variety of compound neurological and developmental problems which carry on into adult life. These can obvious as cognitive and behavioral difficulties, weight gain, problems in controlling their anger and assistant difficulties in socialization. New research published in open access journal Orphanet Journal of Rare Diseases, confirms that the oxytocin hormone is able to absolutely affect patients by improving trust, mood, and plummeting troublesome behavior.

A key hormone in social structure interactions and empathy is oxytocin. It has been shown that taking oxytocin can recover the aptitude of both healthy and autistic people to read faces and distinguish feeling in others. Since Prader-Willi syndrome shares some individuality with autism, and is also linked with decreasing in the number of oxytocin producing neurons, researchers from France enrolled people at a devoted centre on a trial testing the use of the hormone.

Patients involved in the test often stayed at the centre for one month visits where they took part in daily professional and physical activities. They also received medical care and psychological support if it was needed. During one of their customary visits the patients received a single dose of either oxytocin, or gesture, and their eating and behavior monitored for two days prior to the treatment, and two days after.

Professor Tauber from Centre de Référence du Syndrome de Prader-Willi, France, said, "Two days after direction of oxytocin, we noticed that our patients had augmented trust, decreased sadness and showed less disruptive behavior. In spite of the small size of our test, a single dose of oxytocin had an important, late acting, effect on our patients. This is really hopeful news for the sustained management of people with Prader-Willi syndrome."

Reference:

1- Maithé Tauber, Carine Mantoulan, Pierre Copet, Joseba Jauregui, Genevieve Demeer, Gwenaëlle Diene, Bernadette Rogé, Virginie Laurier, Virginie Ehlinger, Catherine Arnaud, Catherine Molinas, Denise Thuilleaux. Oxytocin may be useful to increase trust in others and decrease disruptive behaviours in patients with Prader-Willi syndrome: a randomised placebo-controlled trial in 24 patients. *Orphanet Journal of Rare Diseases*, 2011; 6: 47

First Genetic Mutation related to Heart Failure in Pregnant Women

Researchers at the Intermountain Medical Center Heart Institute have recognized the first genetic mutation ever linked with a mysterious and potentially shocking form of heart disease that affects women in the final weeks of pregnancy or the first few months after delivery .

The disease, peripartum cardiomyopathy (PPCM), debilitates a woman's heart so that it no longer pumps blood professionally. The disease is comparatively unusual, affecting about one in 3,000 to 4,000 previously healthy American women. Most PPCM patients are treated with medicine, but about 10 percent need a heart remove or mechanical heart-assist device to live. The reason of PPCM has been mysterious.

The research team gathered DNA samples at Intermountain Medical Center from 41 women in their 20s and 30s who had hurt from PPCM. They also took samples from 49 women who were over age 75 and had never experienced cardiac problems. The samples were sent for testing to a lab in Iceland, which used a particular credit-card size tool enclosed with 550,000 tiny dots of protein that, when mixed with human DNA, can separate genetic mutations. To the group's surprise, the testing found that about two-thirds of the women with PPCM communal a genetic mutation on chromosome 12. So they performed a second round of testing in a diverse set of patients- again, one group of women with PPCM and a control group of older women who had never experienced heart problems. This time, a second control group of younger women was also evaluated. The results of the second round mirrored the first. So they did it again with a third healthy set of women. In the end, all three sets of tests established their first finding: Women with PPCM in the study were about two-and-a-half times more likely than healthy women to carry the genetic mutation. the mutation on chromosome 12 is located near a gene that is a good candidate for pregnancy-related cardiomyopathy and has been shown to be involved in regulating blood pressure and muscle contraction in the uterus and the heart."The research group from Intermountain Medical Center is already moving forward with new studies that aim to construct on this finding and help women who develop this disturbing condition.

Reference:

1- B. D. Horne, K. D. Rasmusson, R. Alharethi, D. Budge, K. D. Brunisholz, T. Metz, J. F. Carlquist, J. J. Connolly, T. F. Porter, D. L. Lappe, J. B. Muhlestein, R. Silver, J. Stehlik, J. J. Park, H. T. May, T. L. Bair, J. L. Anderson, D. G. Renlund, A. G. Kfoury. Genome-wide Significance and Replication of the Chromosome 12p11.22 Locus Near the PTHLH Gene for Peripartum Cardiomyopathy. *Circulation: Cardiovascular Genetics*, 2011; DOI: 10.1161/CIRCGENETICS.110.959205

Journal Alert

Jordanian Journal of Pharmaceutical Sciences

The Jordan Journal of Pharmaceutical Sciences (JJPS) (http://journals.ju.edu.jo/JJPS) is scientific, bi-annual, peer-reviewed publications that will clarity on existing topics of attention to the pharmaceutical community at large.

Though the JJPS is planned to be of interest to pharmaceutical scientists, other healthy workers, and developed professionals will also discover it most interesting and educational. Papers will cover basic pharmaceutical and functional research, scientific commentaries, as well as views, reviews.

Topics on products will include developed procedure, excellence control, pharmaceutical engineering, pharmaceutical technology, and philosophies on all aspects of pharmaceutical sciences. The editorial optional board would like to place an importance on new and innovative methods, technologies, and techniques for the pharmaceutical industry. The reader will find a wide range of important topics in its issues.

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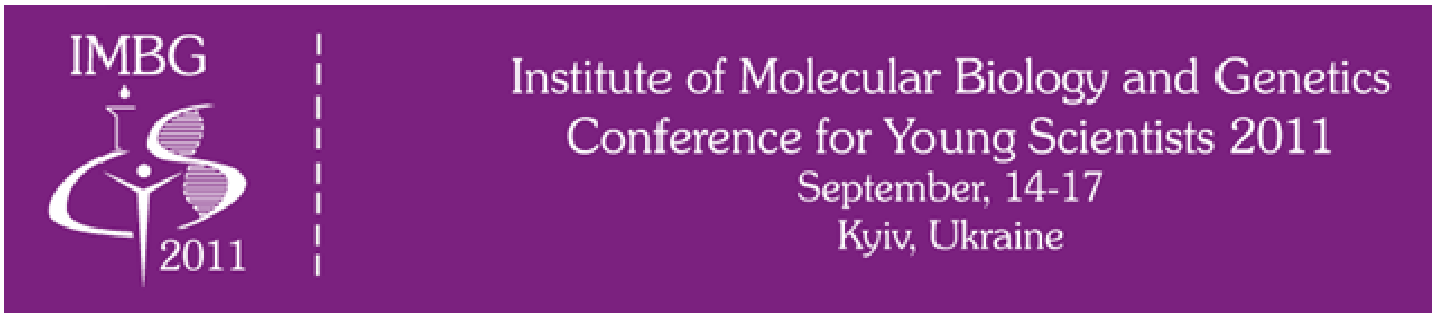
Announcement

http://www.phacilitate.co.uk/pages/singapore_vax/index.html

http://cys2011.imbg.org.ua/index.php/en/



http://www.icbem.org/

http://www.omicsonline.org/biomarkers2011/index.php

Announcement

http://www.upcp.org

UPCP 2012
Up Close and Personalized

Welcome

The first Up Close and Personalized, International Congress on Personalized Medicine will take place February 2-5, 2012 in Florence, Italy.

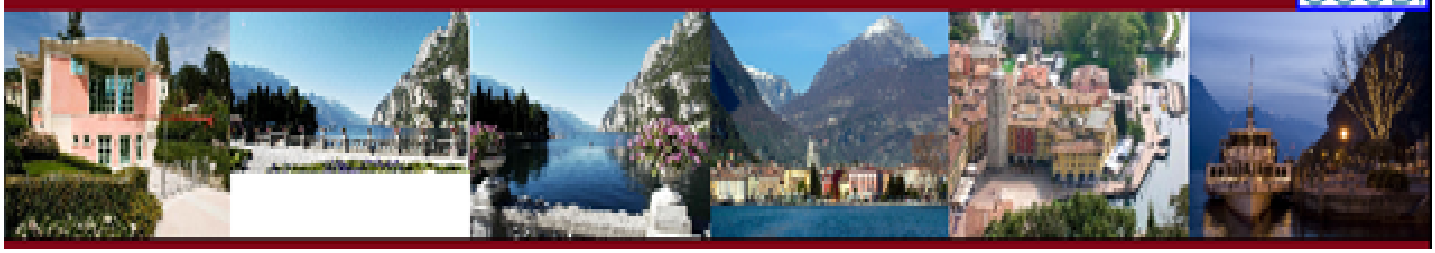
The main focus of the Up Close and Personalized Congress is to examine the essential clinical, genomic, proteomic, metabolomic, pharmacogenomic and biomarker data necessary to predict, prevent and treat major medical conditions concerning metabolism (diabetes and obesity), cardiovascular complications and cancer. In addressing the need and challenge for narrowing the gap between knowledge and clinical practice, one of the key themes will be to explore bio-informatic tools, algorithms, artificial intelligence techniques, decision support systems and other new platforms for predicting clinical outcome and better tailoring treatment modeling to the individual patient.

http://www.nrcbioinformatics.ca/acmsac2012

ACM-SAC BIO 2012

ACM-SAC 2012 CONFERENCE TRACK ON BIOINFORMATICS AND COMPUTATIONAL SYSTEMS BIOLOGY (BIO) - RIVA DEL GARDA CONGRESS CENTER, ITALY, MARCH 2012

COSBI



Centers for Disease Control and Prevention

In this issue, we would like to introduce The Centers for Disease Control and Prevention (CDC) Web-site (http://www.cdc.gov/genomics), which was established the Office of Public Health Genomics (OPHG) in 1997. This website is a very useful portal, which consist of seven different information sections:

- *Impact Update*
- *Genomics and Health*
- *Podcasts*
- *Genomic Resources*
- *Family Health History*
- *Genetic Testing*
- *Training Professional*

Weblink

Impact Update contains interesting information about Genetic and Health impact updates, The Office of Public Health Genomics (OPHG) affords updated and believable information on how genomic information and family health history can increase health and ascendancy policy and practice.

The next section is "***Genomics and Health***", gives the information about affiliation between genes, environment, and behaviors, and is divided into five groups;

- *Diseases, Genetics and Family History*
- *Genetic Testing*
- *Family Health History*
- *Frequently Asked Questions*
- *Genomic Resources*

Podcast section provides videos about particular diseases, genetics, and family history, and will be updated on a normal basis.

The next part is "***Genomic Resources"*** Contains an A - Z list of Web links to selected genomic resources.

You can read all about evidences of the diseases and health situation present in your family in **Family Health History**.

Despite the many scientific improvement in genetics, researchers have only recognized a small fraction of the genetic constituent of most diseases. So, genetic tests for many diseases are developed on the basis of restricted scientific information and may not yet prepare valid or practical results to individuals who are tested. CDC has provided professional information about genetic test in ***Genetic testing*** section.

One of the most useful link in this site is ***Training for Professionals*** section, this section has specialized information for students, educators and health professionals.

Cover Picture

Title: *Metabolic network of the Arabidopsis thaliana*

Classically, metabolism is studied by a reductionist approach that focuses on a single metabolic pathway. it is now possible to use this genomic data to reconstruct complete networks of biochemical reactions and produce more holistic mathematical models that may explain and predict their behavior. These models are especially powerful when used to integrate the pathway and metabolite data obtained through classical methods with data on gene expression from proteomic and DNA microarray studies. Using these techniques, a model of human metabolism has now been produced, which will guide future drug discovery and biochemical research. These models are now being used in network analysis, to classify human diseases into groups that share common proteins or metabolites

Source: *http://www.wikipedia.org/wiki/Metabolic_network_modelling*

Title: *Ribbon diagram showing human carbonic anhydrase II*

The carbonic anhydrases (or carbonate dehydratases) form a family of enzymes that catalyze the rapid interconversion of carbon dioxide and water to bicarbonate and protons (or vice-versa), a reversible reaction that occurs rather slowly in the absence of a catalyst.

Source: *http://www.wikipedia.org/wiki/Enzyme*

Title: *Scheme of reverse transcription*

Some viruses (such as HIV, the cause of AIDS), have the ability to transcribe RNA into DNA. HIV has an RNA genome that is duplicated into DNA. The resulting DNA can be merged with the DNA genome of the host cell. The main enzyme responsible for synthesis of DNA from an RNA template is called reverse transcriptase. In the case of HIV, reverse transcriptase is responsible for synthesizing a complementary DNA strand (cDNA) to the viral RNA genome. An associated enzyme, ribonuclease H, digests the RNA strand, and reverse transcriptase synthesises a complementary strand of DNA to form a double helix DNA structure. This cDNA is integrated into the host cell's genome via another enzyme (integrase) causing the host cell to generate viral proteins that reassemble into new viral particles.

Source: *http://www.wikipedia.org/wiki/Transcription_(genetics)*