Volume 7, Issue 8 August 2014

Bioinformatics up to Date

(Bioinformatics Infrastructure Facility, Biotechnology Division)
North-East Institute of Science & Technology
Jorhat - 785 006, Assam

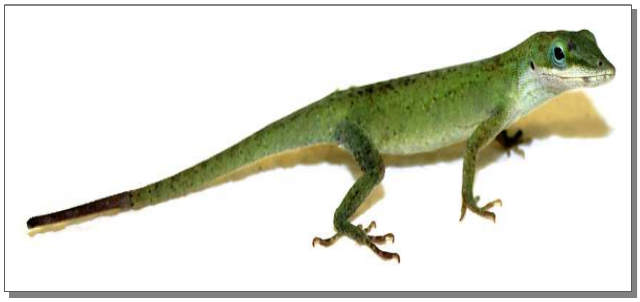
Inside…..

Protein Data Bank

As of Saturday August 31, 2014 at 5 PM PDT there are 102849 Structures

How Lizards Regenerate Their Tails: Researchers Discover Genetic 'Recipe'

By understanding the secret of how lizards regenerate their tails, researchers may be able to develop ways to stimulate the regeneration of limbs in humans. A team of researchers



from Arizona State University is one step closer to solving that mystery. The scientists have discovered the genetic "recipe" for lizard tail regeneration, which may come down to using genetic ingredients in just the right mixture and amounts.

An interdisciplinary team of scientists used next-generation molecular and computer analysis tools to examine the genes turned on in tail regeneration. The team studied the regenerating tail of the green anole lizard (Anolis carolinensis), which when caught by a predator, can lose its tail and then grow it back. "We have identified one type of cell that is important for tissue regeneration," said Jeanne Wilson-Rawls, co-author and associate professor with ASU's School of Life Sciences. "Just like in mice and humans, lizards have satellite cells that can grow and develop into skeletal muscle and other tissues."

"Using next-generation technologies to sequence all the genes expressed during regeneration, we have unlocked the mystery of what genes are needed to regrow the lizard tail," said Kusumi. "By following the genetic recipe for regeneration that is found in lizards, and then harnessing those same genes in human cells, it may be possible to regrow new cartilage, muscle or even spinal cord in the future."

Bioinfo Carrier.

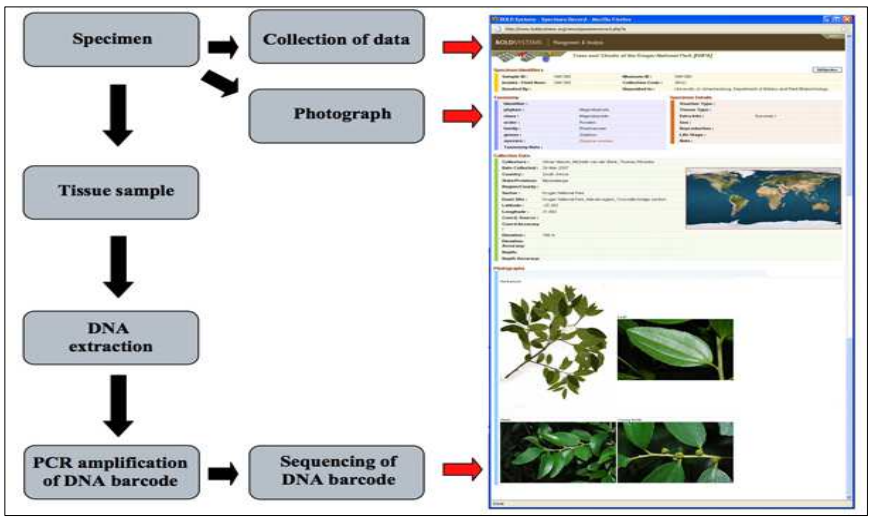
1. Walk-in-Interview for Research Associate/Senior Project Fellows/ Project Fellows/ Project Assistant, Research Interns on 15 & 16th September, 2014 CSIR-Institute of Microbial Technology, Sector-39/A, Chandigarh;

2. PhD program in Bioinformatics @ Swiss Institute of Bioinformatics / University of Geneva Medical School. [http://www.unige.ch/medecine/phdprogram/phdprograms.html]

3. 4 Computational Biologists (f/m) @ Max Planck Institute of Immunbiology and Epigenetics, Freiburg. [http://www.ie-freiburg.mpg.de/4476158/job_full_offer_8375367]

DNA Barcoding : New Perspective of Taxonomy

The DNA barcoding, a recent development of DNA-based method for species identification, required to acquire the final knowledge regarding the species using their morphological characteristics. DNA barcoding proposed



by Paul Habert, researcher at the University of Guelphin Ontario, Canada in 2003. The Consortium for the Barcode of Life (CBOL) is an international initiative devoted to developing DNA barcoding as a global standard for the identification of biological species was established in 2004. It involves a very short DNA segment (called gene) of the entire genome in a broad range of species which can be obtained reasonably quickly and cheaply. The mitochondrial cytochrome *c* oxidase I gene ("COI"), which is a 648 base paired region been proving highly effective in identifying birds, butterflies, fishes, flies and many other animals. But, in case of plant spp. Identification of this COI is no effective as it evolves too slowly. In that case two other gene regions in the chloroplast, *viz*. *matK* and *rbcL*, have been approved as the barcode regions for land plants. In 2013, Tripathy *et al.* had repoprted that, in large-scale biodiversity inventorization, particularly for tropicaltree species, considering the standard success rate of plant DNA barcode program reported so far, ITS, and *trnH-psbA* are can be considered as supplementary loci for identifying the tropical plants.

(Animesh Gogoi, Biotechnology, CSIR-NEIST)

Aberrant mTOR Signalling Impairs Whole Body Physiology

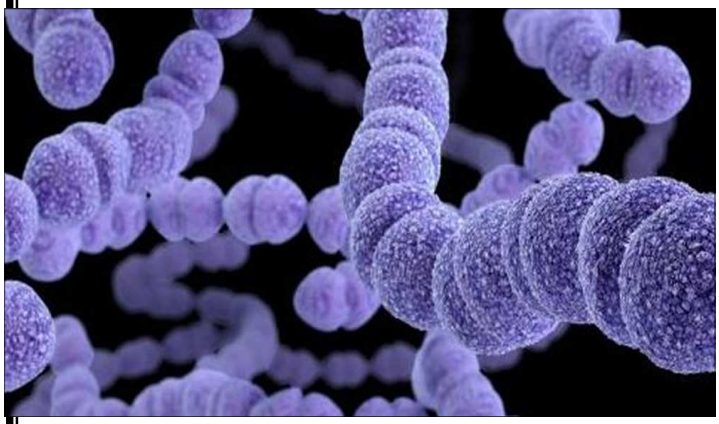
The protein mTOR is a central controller of growth and metabolism. Deregulation of mTOR signalling increases the risk of developing metabolic diseases such as diabetes, obesity and cancer. In the current issue of the journal Proceedings of the National Academy of Sciences, researchers from the Biozentrum of the University of Basel describe how aberrant mTOR signalling in the liver not only affects hepatic metabolism but also whole body physiology.

The protein mTOR regulates cell growth and metabolism and thus plays a key role in the development of human disorders. In the cell, this regulatory protein is found in two structurally and functionally distinct protein complexes called mTORC1 and mTORC2. In a recent study, the research group of Prof. Michael Hall from the Biozentrum of the University of Basel has shed light on the role of hepatic mTORC1 in whole body physiology and the relevance for human liver cancers.

[*Hepatic mTORC1 controls locomotor activity, body temperature, and lipid metabolism through FGF21* ; http://dx.doi.org/10.1073/pnas.1412047111]

Finding the Genetic Culprits that Drive Antibiotic Resistance

Researchers have developed a powerful new tool to identify genetic changes in disease-causing bacteria that are responsible for antibiotic resistance. The results from this technique could be used in clinics within the next decade to decide on the most effective treatments for diseases such as pneumonia and meningitis.

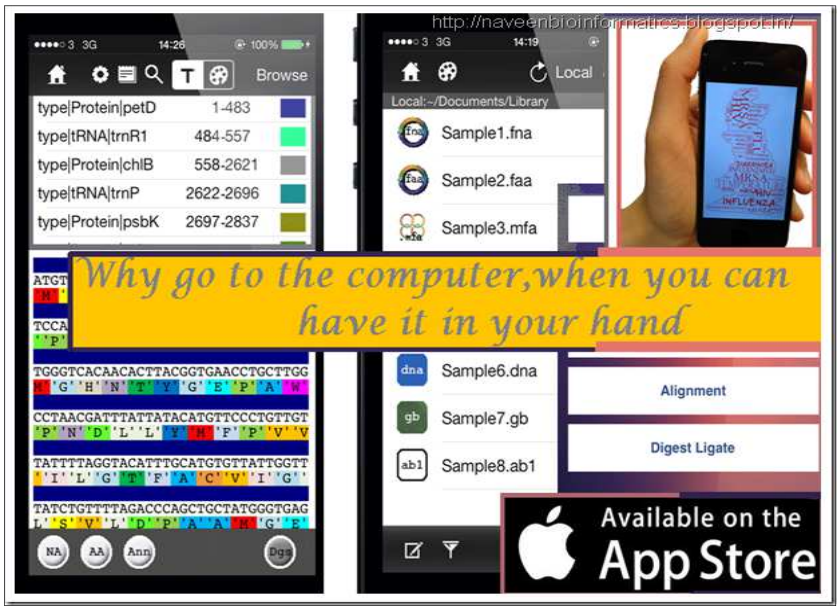


"The results of this research are very interesting," says Claire Chewapreecha, first author from the Wellcome Trust Sanger Institute. "For the first time, we are able to see, at large scale, causative variants that allow bacteria such as Streptococcus pneumoniae to resist our efforts to treat and control it. "We can begin to see how this might help us to develop more effective treatment strategies in the near future."

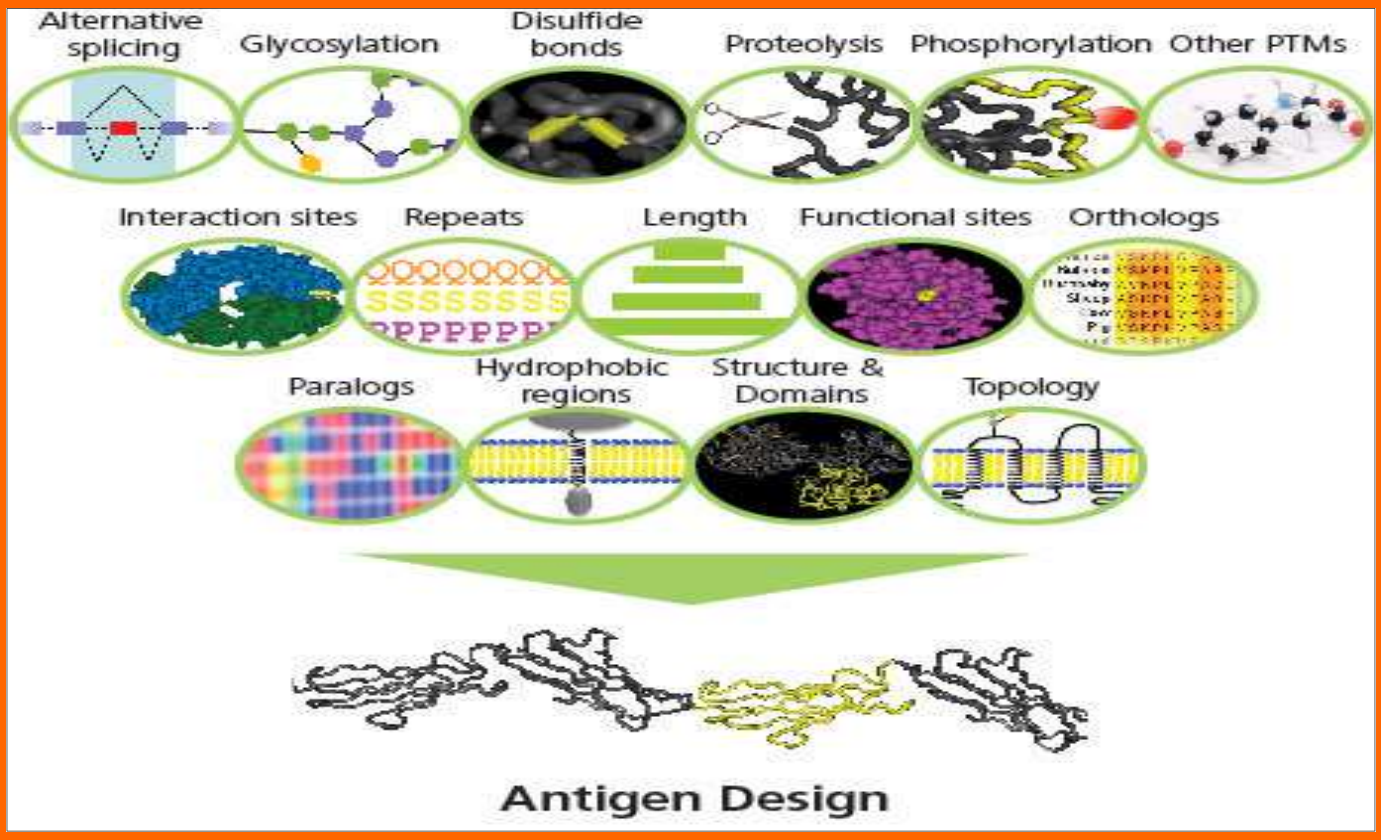
GWAS (genome-wide association study) studies search through the genome for locations where single DNA changes are associated with properties of the organism, like antibiotic resistance. "In this study we've shown that this powerful genetic tool, which has transformed our understanding of human genetics, can be applied to bacteria," says Professor Stephen Bentley, a senior author from the Sanger Institute. "This opens up new avenues of research into antibiotic resistance, transmission and virulence that were previously thought impossible in bacterial genomics."

Morph Bioinformatics: Cloning on Your Smartphone

Morph Bioinformatics Limited is a UK Biotech company offering automated lab and IT solutions for bioinformaticians and bioscientists. Its incorporation in April 2013 has evolved from the Synthetic Biology competition iGEM 2012. The main aim is to provide a platform to develop tools and services to increase the efficiency and productivity of R&D processes within the field of biotechnology. Therefore apply bioprocess engineering principles with expertise in genetic engineering to develop a robotic laboratory platform which decouples the scientist from the physical aspects of experimentation Main ethos is to integrate molecular biology, bioprocess engineering and artificial intelligence to allow research to be done in a new way - quickly, cheaply, reproducibly, in massive parallel and fully automated.



Bioinfo. Animation



Patent News

Method for performing bioinformatics analysis program and bioinformatics analysis platform

US 7647290 B2

Inventors: Tateo Nagai, Daniel Reda,

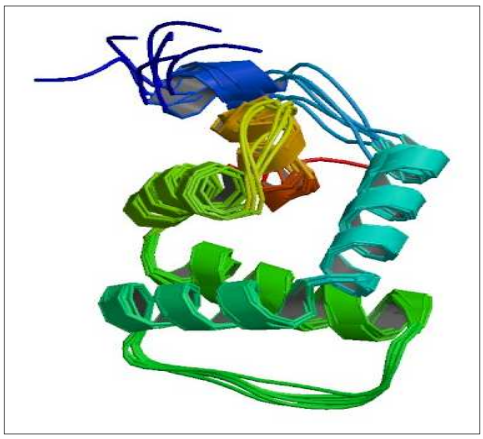
Takahiko Kasuga,

Yasuyuki Nozaki

ABSTRACT

A system in which researchers can freely and effectively use worldwide bioinformatics analysis programs available on the Internet is provided. When a bioinformatics analysis program available on the Internet is used by a user computer, a broker program is used. The broker program has a function of absorbing differences in input/output format between analysis programs, and each analysis program is provided with the broker program. A broker program-providing server stores various broker programs provided by users and makes them available to the public. When the user uses bioinformatics analysis programs available on the Internet, the user can use broker programs that are made available by the broker program-providing server and that are created by other users.

Solution NMR structure of the NLRC5 Caspase Recruitment Domain



The cytosolic nucleotide-binding domain and leucine rich repea containing receptors (NLRs) are key sensors for bacterial and viral invaders andendogenous stress signals. NLRs contain a varying Nterminal effector domain that regulates the downstream signaling events upon its activation anddetermines the subclass to which a NLR member belongs. NLRC5 contains an unclassified N-terminal effector domain that has been reported to interactdownstream with the tandem caspase recruitment domain (CARD) of retinoic acid-inducible gene I (RIG-I). Here we report the solution structure of the Nterminal effector domain of NLRC5 and in vitro interaction experiments with the tandem CARD of RIG-I. The N-terminal effector domain of NLRC5 adopts asix α-helix bundle with a general death fold, though it displays specific structural features that are strikingly different from the CARD. Notably, α-helix 3 isreplaced by an ordered loop, and α-helix 1 is devoid of the characteristic interruption. Detailed structural alignments between the N-terminal effectordomains of NLRC5 with a represe- ntative of each death-fold subfamily showed that NLRC5 fits best to the CARD subfamily and can be called an atypicalCARD. Due the specific structural features, the atypical CARD also displays a different electrostatic surface. Because the shape and charge of thesurface is crucial for the establishment of a homotypic CARD-CARD interaction, these specific structural features seem to have a significant effect on theinteraction between the atypical CARD of NLRC5 and the tandem RIG-I CARD.

Upcoming Events

International Conference on

"Stem Cell Research, Cancer Biology, Biomedical Sciences, Bioinformatics and Applied Biotechnology"

1st and 2nd November, 2014
Venue: Jawaharlal Nehru University, New Delhi

National Seminar on

"Recent Advances in Biotechnological Research in North East India: Challenges and Prospects"

November 27-29, 2014
Department of Molecular Biology and Biotechnology (MBBT)
Tezpur University, Napaam , Tezpur

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