ISSN: 2454-6968

BIOTECH EXPRESS

Rs. 475

RNI No. UPENG/2013/54102

Volume 6
Issue 62
September
2018

Events:
XVth BRSI Convention

Guest Article:
A BRIEF STUDY ON RADIO 12 TOLERANCE OF TARDIGRADE PROTEINS

Guest Article:
Whole Exome Sequencing: An Alternate way to WGS

Guest Article:
"Bioterrorism: Exploitation of Microorganisms"

Guest Article:
National Institutional Ranking Framework: An aspiration without essentials

News in Focus

Blueberry Therapeutics Completes £10m Series B Fund-raising

Pall Corporation and Aetos Biologics Partner to Deliver Integrated, Off-the-Shelf Biosimilar Manufacturing Solutions

FIRST HUB: Facilitation of Innovation and Regulation for Startups and Innovators

India bans 328 combination drugs

SpiceJet operates India's first biofuel- powered flight

Editorial:

PhD blues: Untold Story of every PhD student

CAN YOU BELIEVE WHAT YOU READ?

Biotech Express

Better. Belive it

With fake and misleading news leaving most Biotechnology people confused abbout even the basic facts, Biotech Express keeps it real. Whether in print or digital people trust it to be expertly researched written and fact checked.

Bring real matters. That's a fact.

Believe Biotech | Believe Biotech Express

BIOTECH EXPRESS
Only Biotech Nothing Else

Only Global Biotech Magazine | Less Advertisements | Study Guide | +Research News | Events | Policies | Notices | Career | Criticism | Fantasies | Reports | +Articles | Industry | Govt.

Explore Biote

India's Biggest Biotech Annual Event with pr

International Conference on
Innovation for Sus

XVth BRS

V Asia-Oceania Algae I

22-25 November,

Industry-Young Researchers Interactive Session
Scientists-Children Meet
BRSI- Skill Development Program
Bio-Entrepreneurs Conclave

The conference as part of CS
global networking amongst t
gether scientists, young rese
deliberate and showcase the

ech with BRSI

resence of most eminent scientific talent and Industry patrons

n Biotechnological Research and
tainable Development
&
I Convention
&
nnovation Summit (AOAIS)

2018, CSIR-IICT

IR-IICT platinum jubilee celebrations provides a vibrant platform for sharing knowledge and the biotechnology fraternity focusing on sustainable development. BioSD 2018 will bring to- archers, entrepreneurs, industrialists, policy makers, innovators and other global experts to current trends and future challenges of the underpinned biotechnology research domains.

CONTENTS

BEM

inside...

Volume 6 Issue 62 September 2018

EDITORIAL: PhD blues: Untold story of every PhD student

Chief Editor
Dr. Seema P. Upadhye
(Former Principal, Biochemist)

Managing Editor:
Kamal Pratap Singh

VOLUME 6 ISSUE 62
September 2018

Subscription and Article Submission

Annual Subscription
Please see Subscription Rate card inside.

Send your all entries at:
Biotech Express, V-31/4, Ext-1, Shalimar Garden, Sahibabad, Ghaziabad, U.P- 201005.

Article submission
All queries related to article submission can be sent to biotechexpressindia@gmail.com. For more information kindly visit website: www.kashbiotech.com

Publisher : Kamal Pratap Singh

Printed at : Monex offset, B-12 SD complex, near MMG hospital, Ghaziabad- 201005.

Individual rates available to subscribers paying by personal cheque or NEFT. Order for Students, PhDs, postdoc subscription must be accompanied by a copy of student ID.

The Biotech Express magazine publishes between 10th to 15th of every month.

News in Focus

Scientists at Institute of Life Sciences (ILS), Bhubaneswar discovers a drug target for neurodegenerative diseases and cancer

40

INDUSTRY & RESEARCH NEWS

Press Release: Blueberry Therapeutics Limited Completes £10m Series B Fundraising

Pall Corporation and Aetos Biologics Partner to Deliver Integrated, Off-the-Shelf Biosimilar Manufacturing Solutions

FIRST HUB: Facilitation of Innovation and Regulation for Startups and Innovators

India bans 328 combination drugs in setback for pharma companies

SpiceJet operates India's first biofuel-powered flight from Dehradun to Delhi

Enzyme in milk production identified as target for novel breast cancer drugs

First interactive model of human cell division

Genes are key to academic success, study suggests

Properties of stem cells that determine cell fate identified

Scientists develop new drug treatment for TB

44

Publisher retracts two papers, will correct five more for lab with high "level of disorganization"

Researcher who once tried to sue critics has another dozen papers retracted

UPCOMING EVENTS

34

SelectBio's Next Gen Crops for Sustainable Agriculture

BRSI's International Conference on Biotechnological Research and Innovation for Sustainable Development

From Desk of Editor

Dear Readers,

In this issue we have covered some interesting and diverse articles submitted by our associates and writers.

Article like PhD blues will discuss mindset and situation of PhD student who still think about career option even after this high rated degree.

The other article on Tardigrade proteins is innovative article on proteins pocessed by these tardigrade species. This article discusses history and future research on tardigrade proteins.

Though criticism, article on NIRF ranking discuss future prospects of ranking system of University by NIRF.

You are cordially invited to submit articles on various aspects of Biotechnology and for this you need not to pay any fee, so reach to largest audience of Biotechnology and convey your message/research easily and effectively.

All the best!

Dr. Seema P. Upadhye

Advisory Board

From the very first issue, Biotech Express team has been delivering what's best for Biosciences community. The audience of this magazine includes students, researchers, faculties and executivesof highly prestigious organizations of India. In year 2016, BEM has made new editorial Board combining experience of eminent Advisory Board Members who have been into Award winning Research and head prestigious Administrative positions.

Managing Editor
Kamal Pratap Singh

Assistant Editor
Piyush Kumar

Chief Editor
Seema Pavgi Upadhye, MSc, PhD

Advisory Board Members

Kaul Sunil

PhD, FGSI, FBRS, FIAN, FNASc
Chief Senior Research Scientist,
National Institute of Advanced Industrial Science & Technology (AIST), Japan

Mishra Kaushala Prasad

Ph.D., F.M.A.Sc., FNASc.
Former Head, Radiation Biology Dept., BARC, India
Former Vice-Chancellor, Nehru Gram Bharati University
Founder, Radiation Biology Society, Founder President, Society for Radiation Research , India(SRRI)
Mumbai, President, Asian Association for Radiation Research (AARR)2017-2021

Pandey Ashok

D.Phil., FRSB., FNASc., FBRS., FIOBB., FISEES., FAMI.
Distinguished Scientist, CSIR-IITR
Former Dy Director & Chief Scientist, Centre for Biotechnology & Biofuel Division, CSIR- National Institute for Interdisciplinary Science and Technology
Founder, Biotech Research Society of India.

Editorial Board

Editorial Board Members

Views

PhD blues: Untold story of every PhD student

by Haaris Ahsan Safdari, PhD student (Pre-Doctoral Fellow)
Indian Institute of Science, Bengaluru- 560012, India
Email: haariss@iisc.ac.in

"I will not be able to complete my graduate studies, I am very dumb", a sad and gloomy face of my lab mate popped up as I saw her rising across from her chair. "I even don't comprehend the fundamentals of my work and my "simple" experiments fail miserably" continued the explanation. There was sense of dejection as the fear of her PhD work rose over her. "You have lots of data and you are going good in PhD" my voice rose as I saw clear signs of despondency on her face. If this sounds usual to you, probably you are graduate student. Popularly known as "Impostor's syndrome", it grips many graduate students over the course of PhD life. Surprisingly, there is lot range of so called "graduate student life metrics" on which your colleagues and even professors will judge you, be it publications, travel grants, conference awards. The pressure to cope up with these metrics mostly puts the life of a graduate student at stake. One of the worst and fatal mistake that most often leaves students dwell into this is the comparison of these metrics with other people. This feeling is further substantiated in top notch institute where people may feel "inferior" to other colleagues and see people dropping out or lagging in the race of "self-obsessed" metrics.

It is imperative that one should assess their "weakness" in starting years of a graduate life, rather than being scooped up later. It should be realized that PhD life is more about failures rather than success and failures are key to generating ideas in the project. Perfectionism often leads to high expectations and goals which are often not achieved. One cannot be sure of results in research and one cannot be sure to get 100% result every time. You generally don't try new things unless you know that your previous hypothesis failed miserably. There will be times in the research life when thing don't work as expected, everything goes haywire and you

don't know what to do next! In these moments, relax and never let depression overtake you. Remember, Rome was not built in a day; PhD thesis is a compilation of your efforts to unleash the ideas of your research domain and it takes time. Work slowly in those days but be steady. You will see your progress at the end of the day. Meanwhile, learn to reward yourself for small achievements in the work. Many a times this really helps to ward off the anxiety and depression that has built over time. I usually had a sumptuous dinner with my friends when I achieved something worthwhile in lab, be it abstract getting selected in a conference and that really helped me to forget the negative results of another lab work.

The aim of a PhD student should be to learn to answer question, design experiments and observe and interpret results meticulously. I heard Prof. P. Balaram who is well known Indian biochemist and former director of IISc Bengaluru saying that "PhD is obtained with the efflux of time". The temperament, attitude and zeal for understanding nature starts to build up gradually during course of time. One of the habits that need to be developed over time is the habit of reading published papers related to the research. Being up to date with latest developments in the field through published articles is pivotal to generating new ideas and working towards it.

Interestingly, PhD is quite different from regular MS degree or bachelor's degree where you must frame questions and solve them rather than just read about the solved problems. It poses unique challenges which just cannot be solved by "brain power". There are countless examples where so called mediocre student judged by grades of a MS program went on to perform excellent in research and vice versa. The attributes of a great PhD student encompass passion, perseverance and most importantly meticulousness. It brings me to one of the quotes which many of you might have heard, "when the going gets tough, the tough gets going". When the challenges of the problem are not trivial, we tend to strive harder. It is at this stage that love for the work develops and failure then is not an option. At this stage, it is imperative that patience and focus should not be lost.

One of the factors commonly not paid so much importance is the attitude in the PhD life. A person should accept "constructive criticism", be it from supervisor or lab colleagues and try to improve upon the criticism rather than falling in pit of "it's not my cup of tea". Simultaneously, one should learn not to get dwelled by external factors of praise or criticism by anyone-be it your supervisor. Cherish your capabilities and move ahead! Being ready to learn is one of the asset which goes long way in success of an individual. I remember my graduate mentor saying to me one day, that he wanted to learn basics of circular dichroism experiments from us!!

It should be realized at this stage that your supervisor is your guide, counsellor, motivator but not teacher. It is injudicious to consider your supervisor as your teacher. Always remember that the relation between you and your supervisor is because of your work. The harder you work to help yourself and your supervisor, he will always be standing in your difficult times. The duty of supervisor is to share ideas, show the path and not to dictate it. In fact, at the end of graduate program, a PhD student should be able to get a vivid knowledge of his area of research much better than his supervisor. More importantly, PhD is not an end of a journey but a start of new outlook of life where you look for unanswered questions of nature and you enjoy solving problems. This change should be the sole metric of "success" in a PhD program and requires self-introspection at every stage of PhD program.

Guest Article

A BRIEF STUDY ON RADIO TOLERANCE OF TARDIGRADE PROTEINS

by Ramachandra Dilip, Sri Shakti institute of engineering and technology, Tamil Nadu

ABSTRACT

Tardigrade also known as water bear are one of the extremophiles which are said to have survived five mass extinction events. This tardigrades species are so stress tolerant that it can survive the vacuum of space, high and low temperatures, and strong doses of ionizing radiations. Ramazzotius varieornatus is one of tardigrade species, which have the genome size of 75 to 800 mbp of DNA, revealed to have about 19000 proteins.The genome is protected by a protein called DSUP, is one kind of a protein found in tardigrades that tend to bind around the DNA helping it to withstand radiation. DSUP protein allows these species to protect its DNA from harmful radiation and it was able to save a human cell line with less than 40% damage. The protein could with stand median lethal dose of 5000 Gy(gammarays), 6200Gy(heavyion) while hydrated animals were able to tolerate only5-10Gy.

In this article we will discuss the types of extremophiles and give a surface brush of its adaptation manual and highlight about the tardigrades and their protein which gives the man immense tolerance. In addition it emphasizes the need to conduct a thorough study on the peculiarity of this proteins to withstand such high doses of radiation, which might help humanity to adopt such are source.

INTRODUCTION

A peculiar property of life is to resist entropy, and life is known to be very good at it" In the modern era, it seems to be impossible to move away from technology such as smart phones, computers, signal towers and even some synthetic clothes are an indirect source for ionizing radiations. Ionizing Radiation is known to be the cause of cancer in many cases. It's a common misconception that all type of radiations are lethal, those radiation which is able to cause damage to the DNA are lethal and are called Ionizing radiation. These radiations are high frequency radiation which are able to remove an electron from the atom easily, thus making the atom unstable.

Namely there are three major types of radiations, alpha, beta, and gamma. These are electromagnetic radiation which comes from decaying atomic nucleus. From this alpha is a helium nucleus, beta is an electron, and gamma is a photon. According to Max Planck, photons are packets of energy, and the energy in proportional to the frequency. Gamma rays possess the highest frequency and thus have more energy. Not only gamma radiations, but several type of infrared, UV, and radio waves are also relative to this.

Nature has given them specific adaptive feature to some species which makes them stress tolerant. All though these stresses are known to be harmful for us, some organisms are known to outlive these types of harmful radiations; these are a class called as 'extremophiles'.

Psychrophiles are organisms to survive temperatures up to -4F and it produces antifreeze proteins, which gives them an ability to withstand freezing. The other organisms that are able to survive high temperature like 140F thermophiles. Some adaptation algae are known to be rich in content of protein (50-55%) and has small amount of polysaccharides. A 13 amino acid cell wall gives them a tolerance towards a wide range of temperatures. Radio resistant microbes are known to survive huge doses of radiation. The gram positive Deinococcus is a phylum of bacteria that are highly resistant to radiation hazards.

Tardigrade

Tardigrades, first discovered in 1773 by a German zoologist Johan August, stands top in the extremophile profile. They are found in almost in all corners of the world including your backyard. We know that species only show tolerance towards a particular stress. But all of these characteristics were shown by the tardigrade. The tardigrade body is covered with a flexible cuticle, which is smooth or covered with gibbosities, spines or plates.Tardigrade survive the conditions that are known lethal to other life forms. They have a barrel shaped body and stubby legs and the cuticle contain chitin and protein. The eggs were also tolerant to lethal doses of radiation up to 4000Gy and still gave live young ones. It has a true coelum found near the gonad and use stylets to pierce plant cells to feed.

Tardigrade genome has size of 75 to 800 mbp of DNA and they range from a length of 0.3mm to 0.5mm. The brain is developed in a bilaterally symmetric pattern. It includes multi lobes and three bilaterally clustered neurons. Many species possess a pair of rhabdomeric pigmented eyes. Tardigrade also possesses a buccopharyngeal apparatus which along with claws is used to differentiate among species. These species may look like small bugs and was first expected to be on the phylum arthropods, but later it was combined with the phylum crustaceans. Later their stumpy legs made them to be in the phylum Onychophora. It's a class of worm like species.

Tardigrade species are known to have the ability to suspend their metabolic activity. Many species have been known to survive without water for five years. Depending upon the circumstances they may hibernate, enter cryoptobiosis, osmobiosis. Their metabolic state in such circumstances will only drop by 0.01%. It is noted that

they have high level of non-reducing sugars which give them this ability. Their DNA is protected from radiations by a protein called DSUP. It was also note that the tardigrade possesses 5 HOX genes that are similar to Nematoda.

A team of researchers at the University of Edinburg has sequence of the tardigrade DNA, and has found that most of the gene code for genomic repairing and the rest for oxidation sheilding. This remarkable discovery led scientists to think that these proteins could be used for preservation. Although several researches were conducted as to how they manage to survive such huge doses of radiation was still adsorb. Mostly they are found feeding on lichens and plant. This was proved from the outcome of a project done at and near James River Power Plant. The sample was taken from tress which are exposed to up winds and down winds. They undertook the research further and has found nematodes along with tarigrades. The species diversity is high on the up wind (Candelaria and pertusaria were found on the up wind). The density of tardigrade increased as we moved away from the plant.

Thermophiles ; organisms that are able to survive temperatures ranging from 140F or even higher. An example for these species is cynadium, an algae found in the hot water springs of Yellow Stone National Park.

Radio resistant microbes are known to survive huge doses of radiation, which are lethal to mankind. Deinococcus radiodurans are known not just radio for its tolerance but its ability to convert theses radiation as food!! It has been listed in the Guinness Books of World Record as "the toughest bacterium, another type of fungi was found in the remains of Chermobyl nuclear reactor, in 1986.

Deinococcus is a phylum of bacteria that are highly resistant to radiation hazards. They are gram positive means only their cell wall can be stained, but researches has shown that they have a second layer which makes them partially gram negative. Another peculiar characteristic of deinococcus is that they don't retreat from gamma radiation zone, or change their cellular structur. It is still unclear st to how they are tolerating high doses of gamma , UV radiations.

ADAPTATION
It has been noted that these algae are known to be rich in content of protein (50-55%) and has small amount of polysaccharides. A 13 amino acid cell wall gives them a tolerance towards a wide range of temperatures.

Tardigrades in space mission and space research

In 1964,in the article "Actions différentielles des rayons x et ultraviolets sur le tardigrade Macrobiotus areolatus" it was suggested that tardigrades can be a model for space missions and researches. 37 years later Bertolani suggested in his article," Tardigrades as a potential model organism in space research" that tardigrade can be used in space missions. Later on many journals regarding this was published. At that time, cryptobiosis related studies were being conducted on the tardigrade. In 2007 it was revealed that, tardigrades can survive the vacuum of space. A paper published on 2010 by Rebecchu et al also explained and emphasized the complex body nature of tardigrade that also fueled the need for space research on tardigrads, the extraordinary character of these species to survive in extreme conditions made it a best model for space missions. In 2008, Horikawa et al, also suggested the same idea in his article. It also emphasized on breeding *R.varieornatus*. Also in the same year it

was proved that tardigrades could travel through space in a meteorite confirming the theory of panspermia.

After a brief research on the published journals, the research committee decided to assign a team of researchers associated with TARSE(The Tardigrade Resistance to Space Effects). This project was first involved with FOTON-m3. Its aim was to analyse the impact of environmental stress on anhydrobioptic tardigrades. They exposed the tardigrades to intense radiation and micro gravity. The survival rate was high with response to antioxidant response.

The next project was FOTON-M3 with TARDIS (Tardigrade in Space). The main aim was to find out whether Milnesium tardigradum Doyère, and Richtersius were able to survive the space. But high ionizing radiation from the sun reduced their survival rate. Then the third mission regarding the initial surviving capability was examined on terrestrial tardigrades. But the result was never issued.

Then came was TARDKISS in 2011. The objective of this was to examine the level of DNA damage done by flight and micro gravity on the DNA. Initial results didn't show significant damage but however significant activity of ROS scavenging enzymes was shown and total glutathione and the fatty acid content was compromised. This significantly led to another failure on the research team. Then the last research was Phobos Life Project. This was done with an agenda of proving the panspermia theory, by studying space flight conditions for normal metabolism. This was done on different taxa and of all strains. This includes tardigrades: M. tardigradum, R. coronifer and Echiniscus testudo. But the experiment was unfortunate and crashed on to the pacific on Jan 2012. There after no researches based on tardifrade as space model was never done…

The species of Ramazzotius is around 20-25. The noted species is as follows:

- Ramazzottius affinis Bertolani, Guidetti and Rebecchi, 1993
- Ramazzottius andreevi Biserov, 1998
- Ramazzottius anomalus Ramazzotti, 1962)
- Ramazzottius baumanni Ramazzotti, 1962)
- Ramazzottius bunikowskae Kaczmarek, Michalczyk and Diduszko, 2006
- Ramazzottius cataphractus Maucci, 1974)
- Ramazzottius caucasicus Biserov, 1998
- Ramazzottius edmondabouti Séméria, 1993
- Ramazzottius horningi Binda and Pilato, 1995
- Ramazzottius ljudmilae Biserov, 1998
- Ramazzottius montivagus Dastych, 1983)
- Ramazzottius novemcinctus Marcus, 1936)
- Ramazzottius oberhaeuseri Doyère, 1840)
- Ramazzottius rupeus Biserov, 1999
- Ramazzottius saltensis Claps and Rossi, 1984)
- Ramazzottius semisculptus Pilato and Rebecchi, 1992

- Ramazzottius subanomalus Biserov, 1985)
- Ramazzottius szeptycki Dastych, 1980)
- Ramazzottius theroni Dastych, 1993
- Ramazzottius thulini Pilato, 1970)
- Ramazzottius tribulosus Bertolani and Rebecchi, 1988
- Ramazzottius valaamis Biserov and Tumanov, 1993
- Ramazzottius varieornatus (sv) Bertolani and Kinchin, 1993

Ramazzottius tribulosus Bertolani and Rebecchi, 1988

- Original description
- Biserov, V. I.; Tumanov, D. V. (1993). Ramazzottius valaamis sp. n.(Tardigrada, Hypsibiidae), a new species of tardigrads from Valaam Island, Karelia, Russia. Zoologicheskii Zhurnal. 72, 35-39. Taxonomic citationGuidetti, R.; McInnes, J. S.; Kristensen, M. R. (2018). World List of Tardigrada. Ramazzottius valaamis Biserov & Tumanov, 1993. Accessed through: World Register

Ramazzottius varieornatus (sv) Bertolani and Kinchin, 1993

- They are extracted from the sediments of rain gutter and can be readily distinguished by the shell morphology, placcoids and cuticle type. (21)

Ramazzottius andreevi Biserov, 1998

Original description

- Biserov, V. I. (1998). Tardigrades of the Caucasus with a taxonomic analysis of the genus Ramazzottius (Parachela: Hypsibiidae). Zoologischer Anzeiger. 236(2-3), 139-159. Taxonomic citation
- Guidetti, R.; McInnes, J. S.; Kristensen, M. R. (2018). World List of Tardigrada. Ramazzottius andreevi Biserov, 1997/98. Accessed through: World Register of Marine Species at: (22)

In this R. variornatus is showing significant tolerance to radiation than other species.

R. variornatus genome sequencing was done by sanger and Illumina technologies. To avoid contamination, mitochondrial DNA was to be removed and hence 56 Mbp of DNA was obtained. It was observed that most of the gene is contaminated with alien genome. In evolutionary biology this is known to be called horizontal gene transfer. Now it is left with 55.6Mbp. Later on Blast searching on expressing sequence shown results to be 98% of the gene is expressible and produce up to 19,521 proteins. *R. variornatus* is said to perform anhydrobiosis during drought or subzero temperatures. During drought conditions, they roll up to form a ball shaped object. Almost all metabolic reactions shut down. It will be completely dehydrated. After hydration they will resume to normal metabolism. But nobody knows how they do it. Many researches regarding these are still going on and the sequencing of the expressible genome of R. variornatus is to be done.

These species are known to be active in space also. With all the vacuum and dryness of outer space, it still

shows normal life activity. This could mean astrobiological studies can be held in its name and prove the fact that life can exist out there also.

Later a study has revealed that UVC radiation on other organisms has shown significant thymine dimer(8), or thymine cyclobutane pyrimidine dimers. The experiment was conducted on other species of tardigrades such as Milnesium tardigradum and has found that they are stress tolerance but for a fewer time. It has been noted that not only resistance is the key to but simultaneous repairing also. Terrestrial species of R. variornatus has shown no significant thymine dimmers from UVC irradiation (9).

The general DSUP protein shows no relevance to other forms of proteins. The protein revealed to have putative long α-helical region in the middle and a putative nuclear localization signal at the C terminus. The protein is highly basic and its interaction with the DNA is purely electrostatic. A gel shift assay experiment by interagating the DSUP gene with bacterial genome has given that, the migration of plasmid DNA is inhibited. This shows the affinity of DSUP towards DNA. Presence of C-terminal in the protein enabled it to band shift the DNA bind by histoneH1 protein. These findings show that the C-terminal regions enable the DSUP to bind to the DNA and form strong bonds.

DSUP protein suppresses DNA damage in human cultured cells

A team of experts came with hypothesis suggests that DSUP protein can protect nuclear DNA. For this they made a HEK293 cell line expressing DSUP under the control of CAG promoter. The co-localization of DSUP and DNA was established and was confirmed by immunocytochemistry. The breakage of DNA was confirmed by more distant location from nuclei (comet tail region). The untransfected cell line show 33% localization at the tail region while 16% showed in transfected. This clearly proved that DSUP is protecting the DNA of the tardigrade or more specifically towards X-Rays. It was found that, the protein could also protect DNA from ROS (hydrogen peroxide) also, up to 18% localization.

It was found that not only there are proteins that protect the DNA but other enzymes that act as anti-oxidants. Total analysis of genome revealed that about 19000 protein was found translated by the genome. The presence of C terminal enable the DSUP to firmly attach to the DNA, and several experiments related to the repairing property of DSUP has proven a failure. A human cultured cell was engineered with DSUP and was irradiated with X-rays and results show substantial suppression of fragmentation and was detected before DNA repair. The experiment was performed on ice and the fragmentation was detected immediately after irradiation and later repairing occurred. Thus proving the fact that DSUP is a shielding agent for DNA. Proliferative ability in mammalian cells will be lost when an X-ray of 4 Gy was irradiated but surprisingly, the cells that express DSUP increase their number over time. All these support the fact that such proteins can help us survive many type of extreme events. Future experiments involve taking tardigrades to mars for further research.

Discussion

Although its showing such extraordinary characteristics and not to mention a 5 time mass extinction champion, very few people know about these wonderful creation of nature. The research of tardigrade tolerance is still under pursuit. The application of this skill is numerous. What if the common man can be saved from the harmful radiations he is being surrounded with? What if we could somehow manufacture this protein by under taking recombinant DNA tech to extract the DSUP protein which binds the DNA of tardigrade, and

use it for making say, a body lotion? Or clothing which is similar to the coat used in nuclear power plants? The death because of cancer increasing year by year. So as per the quote, "prevention is better than cure" let's make history. It has been noted that scientists actually don't know or not providing sufficient details about how the protein is able to protect the DNA from harm's way As per the present data, I can only provide with assumptions and practical researches have to be done. As per the scientists the protein is bided the DNA. With the current knowledge of physics the protein DSUP is either absorbing the radiation or reflecting it.

CASE-1

If its absorption then it's evident that Compton Effect has taken place. Compton Effect refers to the activity in which a high frequency radiation is absorbed by the material and a low frequency radiation is emitted with a photon. If it's Compton Effect then it would be useful for making lotions, creams, which would act as protective agents from harmful radiations and would be cheaper than SPF. Also it has been noted that the presence of nitrogen is vital for absorption of sunlight in chlorophyll.

CASE-2

If it's reflection, then it's evident that the structural composition does matter. So we would do electro spinning and incorporate it with silk or other clothing material which could be used in textile industry. Another reason why we should look upon the structural aspects of DSUP is that, there are many types of proteins that found in the blue butterflies that have this peculiar property that allows them to diffract white light. The structural composition is so formed as that only blue color escapes the wings. They act as heat reflectors and thus maintaining body temperature. (16)

It is possible that either of the two can happen

Also another question left is that how does this protein bind to the whole DNA? The answer is left with some unaccepted conclusions and assumptions.

No protein has been found to bind to the whole DNA physically, and to be radio tolerant the protein has to cover the histones as well and conventional proteins don't show such properties.

If it covers the whole DNA with the histones with it, the protein is predominantly positive at some places and predominantly negative at other, which would make it a Zwitter ion, but experiments suggests that the protein is basic and has to be negatively charged.

Or the DNA is enclosed within a protein shell. Like viruses.

If all the above stated is wrong, the protein is entirely alien.

If the protein can absorb such huge amount of radiation, then it is evident that the most amino group has high content of reduced form of reduced nitrogen or predominantly amide.

Hence research based on tardigrde protein research should be undertaken.

Another key mystery of tardigrades is that it possesses the ability to travel through space which no other species have in common. Theories regarding the evolution of tardigrades are still going. The interesting theory is that tardigrades are "aliens". It is more believable and even if it's wise to think that since such extremophiles could exist, it does mean that life could happen elsewhere also.

It is noted that tardigrades tend to roll into a ball shaped structure during dehydrated conditions. This ia survival advantage which is similar to hibernation in bears. During winter they consume a lot of food which is then converted to fat and this allows them to survive the whole winter. During hibernation, the metabolic rate decreases which contribute to low energy use, heart beat rate is also low during this period.

Another key component used by other animals is using high content of glucose, the American toad will entirely stop its metabolism and even the heart beat and will come out of this partial death once the winter is over. But tardigrades show tolerance to various types of stresses so it is illogical to think that tardigrade secrete glucose to escape freezing. The only species of birds which hibernate is the common poorwill. They also hibernate like bears and its body temperature drops drastically.

Hibernation in tardigrade is versatile one. there are proteins that enable some species to be cryopreserved. But whether its protein or carbohydrate or high concentration lipid is still unknown.

REFERENCE

- ✓ 1)Brigit Kartz smithsonian.com (Stec et al., PLOS One 2018)
- ✓ 2) https://www.livescience.com › Animals
- ✓ 3) Horikawa, Daiki D.; Sakashita, Tetsuya; Katagiri, Chihiro; Watanabe, Masahiko; Kikawada, Takahiro; Nakahara, Yuichi; Hamada, Nobuyuki; Wada, Seiichi; et al. (1 January 2006). "Radiation tolerance in the tardigrade Milnesium tardigradum". International Journal of Radiation Biology.
- ✓ 4) UniProtKB/Swiss-Prot (reviewed).
- ✓ 5) Parra, G., Bradnam, K., Ning, Z., Keane, T. & Korf, I. Assessing the gene space in draft genomes. Nucleic Acids Res. 37, 289–297 (2009).
- ✓ 6) Ralph O. Schill Zoology, Biological Institute, Universität Stuttgart, Pfaffenwaldring 57, 70569 Stuttgart, Germany
- ✓ 7) Jönsson KI, Rabbow E, Schill RO, Harms-Ringdahl M, Rettberg P. Curr Biol. 2008 Sep 9;18(17):R729-R73
- ✓ 8) Westh P, Ramløv H (1991) Trehalose accumulation in the tardigrade Adorybiofus coronifer during anhydrobiosis. J Exp Zool 258: 303–311.
- ✓ 9) john Cumbers Affiliations Biospheric Science Branch, NASA Ames Research Center, Moffett Field, California, United States of America, Department of Molecular Biology, Cell Biology and Biochemistry, Brown University, Providence, Rhode Island, United States of America
- ✓ 10) Rogakou E.P., Pilch D.R., Orr A.H., Ivanova V.S., Bonner W.M. DNA double-stranded breaks induce histone H2AX phosphorylation on serine 139. J. Biol. Chem. 1998;273:5858–5868. doi: 1074/jbc.273.10.5858

- ✓ 11) Rogakou E.P., Boon C., Redon C., Bonner W.M. Megabase chromatin domains involved in DNA double-strand breaks in vivo. J. Cell Biol. 1999;146:905–916. doi: 10.1083/jcb.146.5.905.
- ✓ 12) Andrievski A., Wilkins R.C. The response of gamma-H2AX in human lymphocytes and lymphocytes subsets measured in whole blood cultures. Int. J. Radiat. Biol. 2009;85:369–376. doi: 0.1080/09553000902781147
- ✓ 13) Taneja N., Davis M., Choy J.S., Beckett M.A., Singh R., Kron S.J., Weichselbaum R.R. Histone H2AX Phosphorylation as a Predictor of Radiosensitivity and Target for Radiotherapy. J. Biol. Chem. 2004;279:2273–2280. doi: 10.1074/jbc.M310030200.
- ✓ 14) Spurio R., Dürrenberger M., Falconi M., La Teana A., Pon C.L., Gualerzi C.O. Lethal overproduction of the Escherichia coli nucleoid protein H-NS: Ultramicroscopic and molecular autopsy. Mol. Gen. Genet. 1992;231:201–211. doi: 10.1007/BF00279792.
- ✓ 15) Setlow B., Hand A.R., Setlow P. Synthesis of a Bacillus subtilis small, acid-soluble spore protein in Escherichia coli causes cell DNA to assume some characteristics of spore DNA. J. Bacteriol. 1991;173:1642–1653. doi: 10.1128/jb.173.5.1642-1653.1991
- ✓ 16) Hsu, Shao Ti. Engineering Heat Transfer. Blacksburg, Virginia:D. Van Nostrand Company, Inc.,1962.
- ✓ 17) Pabo CO, Sauer RT (1984). "Protein-DNA recognition". Annu. Rev. Biochem. 53 (1): 293–321
- ✓ 18) Patton JT, Vasquez-Del Carpio R, Spencer E. Replication and transcription of the rotavirus genome. Current Pharmaceutica
- ✓ 19) Mark Blaxter and Kazuharu Arakawa from the universities of Edinburgh, Scotland and Keio, Japan https://www.sciencealert.com.
- ✓ 20) Nelson, Diane R. Ecology and Classification of North American Freshwater Invertebrates. New York: Academic Press, 1991https://www.amnh.org/learn.../tardigrades
- ✓ 21) https://onlinelibrary.wiley.com/doi/abs/10.1111/j.1096-3642.1993.tb02538.x
- ✓ 22) www.marinespecies.org/aphia.php?p=taxdetails&id=342610
- ✓ 23) hibernationstation.weebly.com/the-common-poorwill.htm
- ✓ 24) https://www.scientificamerican.com/article/how-do-frogs-survive-wint/

VIDYARTHI VIGYAN MANTHAN : 2018 - 19

"INDIA'S LARGEST SCIENCE TALENT SEARCH FOR NEW INDIA USING DIGITAL DEVICES"

Vidyarthi Vigyan Manthan (VVM) is a national science talent search programme for New India organised by VIBHA (Vijnana Bharati), in collaboration with Vigyan Prasar-an autonomous organisation under the Department of Science and Technology, Government of India and NCERT- Ministry of Human Resource Development. VVM is a National program for educating and popularizing science among school students of VI to XI standards. VVM aims to identify and nurture the bright minds among the student community, who are keen on subjects related to science.

STRUCTURE OF VVM (JUNIOR AND SENIOR):

1. **School Level Examination:** VVM is a unique online examination to be conducted at national level. The registered students will take the exam using his/her own device namely a laptop/ tablet / smart phone (mobile with any OS) AND HIS/HER OWN INTERNET CONNECTIVITY. The school level examination will be conducted nationwide, on 25 November or on 28 November 2018 (option to choose) at the given time. Evaluation of student will be based on their individual performance at every level.
2. **State Level Camp (SLC) :** Top 20 rankers per class per state will be identified to participate in the one or two days State Level Camp (SLC). The camp will be organised anywhere within the state.
3. **National Camp (NC) :** From each State Camp, top two students from each class i.e. total 12 students per state, will be invited to a two-day National Camp.

SYLLABUS FOR VVM:

Content	Contribution			Curriculum
	Junior & Senior (Class VI to XI) (Multiple Choice Questions)			
	Questions	Marks	Duration	
Science and Mathematics from text books	50 (1 marks each)	50	120 minutes	NCERT Curriculum
Indian Contributions to Science	20 (1 marks each)	20		VVM Study Material*
Life stories of Dr. Meghnad Saha and Srinivasa Ramanujan	20 (1 marks each)	20		VVM Study Material*
Logic & Reasoning	10 (1 marks each)	10		General Reading
Total	100	100		

*VVM Study Materials will be made available in PDF format on www.vvm.org.in by 30 August 2018. No printed copies will be provided

KEY POINTS:

1. **Eligibility** - Students from classes VI to XI studying under CBSE, ICSE, and State Boards.
2. **Language of Exam** - English, Hindi, Tamil, Telugu & Marathi
3. **Exam Centre** - Registered School & specified centres
4. **Fee** - Rs. 100/- (without late fee) , Rs. 120/- (with late fee)
5. **Registration** - Online on www.vvm.org.in
6. **Mode of Payment** - 1) ONLINE payment on website 2) RTGS / NEFT/ CHALLAN PAYMENT
   * No Cash / DD / Cheque will be accepted

Press Release

Blueberry Therapeutics Limited Completes £10m Series B Fundraising

Alderley Park, UK, 14 August 2018 – Blueberry Therapeutics Limited ("Blueberry Therapeutics"), a drug discovery and development company focused on developing innovative nanomedicines for difficult to treat skin and nail infections, today announces that it has successfully completed its £10m Series B Fundraising with investment from China Medical Venture Investment (HK) Limited, a wholly owned subsidiary of China Medical System Holdings Limited ("CMS"), and A&B (HK) Company Limited ("A&B").

Blueberry Therapeutics will use the net proceeds of the Series B Fundraising to fund its development programme for BB2603 for the treatment of onychomycosis and tinea pedis, as well as progressing its earlier stage acne and atopic dermatitis programmes. Dr. Huaizheng Peng, General Manager of International Operations at CMS and Chief Executive Officer of A&B, joins the board of Blueberry.

Blueberry Therapeutics and CMS Medical Limited ([a wholly owned subsidiary of CMS]) have also today entered into a licensing deal whereby CMS Medical Limited has acquired the rights to develop and commercialise BB2603 in certain defined Asian territories in return for which Blueberry Therapeutics receives an upfront payment and further payments conditional upon achieving certain regulatory milestones and performance payments based on commercial sales. Blueberry Therapeutics retains rest of world rights to develop and commercialise BB2603 and all pipeline products.

Bryan, Garnier & Co. Limited acted as Financial Adviser to Blueberry, with Slater Heelis LLP providing legal advice to the company on the fundraising investment.

Dr. John Ridden, Chief Executive Officer of Blueberry Therapeutics said: "I am delighted to have completed the Series B Fundraising which enables us to progress all of our programmes to the next stages of development. In addition, I got to know the CMS team well during negotiations and I firmly believe they are the ideal partner to help us develop and commercialise our products in the Asia region and we look forward to working closely with them."

Mr. Lam Kong, Chairman, Chief Executive and President of CMS, commented: "We are very pleased to be shareholders in Blueberry Therapeutics and to be able to support the management team in its quest to deliver high value innovative medicines for patients suffering from a range of dermatological disorders. We look forward to collaborating in the development of the company's products."

For further information contact:
Blueberry Therapeutics Limited, Karen Winterhalter – Onyx Health PR
Tel: +44 (0)7917 571238

Press Release

Pall Corporation and Aetos Biologics Partner to Deliver Integrated, Off-the-Shelf Biosimilar Manufacturing Solutions

www.whitemattercomm.com

PORT WASHINGTON, NY – September 12, 2018 – Pall Corporation, a global leader in filtration, separation and purification, has announced a strategic partnership between its Pall Biotech business unit and Aetos Biologics, a biosimilar cell line development company.

The companies will collaborate to offer biosimilar manufacturing solutions to the global biosimilars market. Pall Biotech will provide access to next generation bioprocess equipment, such as the Allegro™ STR Single-use Stirred Tank Bioreactor for good manufacturing practices (GMP) manufacturing, and consumables to enable efficient biosimilar production. Aetos Biologics will provide high-quality/high-titer cell lines, and scalable manufacturing processes.

"Biosimilars are a replication of a successful biopharmaceutical product. While they are much less expensive than innovator molecules, the complexities in their development make it critical to work with the right equipment and service providers," said Mario Philips, VP & General Manager at Pall Biotech. "We are excited to partner with the Aetos Biologics team to advance the market impact of biosimilars and deliver lower priced, high-quality options to end users."

"Our team is constantly working to optimize a growing pipeline of high-yield biosimilars with outstanding quality," said Amita Goel, founder and CEO of Aetos Biologics. "Through this strategic partnership with Pall Biotech, we can ensure that the exceptional quality we achieve in scaled-up processes is efficiently transferred and reproduced by the client."

By aligning Pall Biotech equipment, including bioreactors, mixing and storage, and downstream technologies with Aetos Biologics' cell lines and manufacturing processes, customers benefit from access to integrated solutions for expedited biosimilars development.

About Aetos Biologics

Located in the heart of the San Francisco Bay Area in California, Aetos Biologics has assembled a formidable gene to product team comprised of seasoned industry veterans experienced in biosimilar development, manufacturing, clinical trials, global regulatory requirements and successful commercialization. Aetos Biologics serves partners engaged in commercialization of biosimilars for the global market.

For more information visit: www.aetosbio.com or email info@aetosbio.com.

Guest Article

Whole Exome Sequencing: An Alternate way to WGS

Deepak Agarwal[1]*, A. K. Singh[1],Bhartendu Vimal[1], Adnan Gora[2], Shubham Varshney[3]
*[1]CoFS, BAU, Ranchi; [2]CMFRI, Kochi; [3]CIFE, Mumbai

*[Email: Deepakbfsc@gmail.com]

Introduction

The exome is the sum of all regions in the genome comprised of exons. The term exon was derived from "EXpressed regiON," since these are the regions that get translated, as opposed to the intron, or "INTRagenic regiON" which is not represented in the final protein. Exome sequencing is a capture based method developed to identify variants in the coding region of genes that havea wide range of applications, including population genetics, genetic disease, and cancer studies.

In 2001 human genome project required more than 200 scientists working for more than a decade with almost $3 billion cost while today, sequencing a whole genome is done over a period of a few days and is soon projected to cost less than $10 000. Human genome comprises about $3x10^9$ bases, and contains approximately 180,000 coding regions (exome), constituting about 1.7% of a human genome. It is estimated that 85% of the disease (both Mendelian and common diseases such as cancer and diabetes) causing mutations occur in the coding and functional regions of the genome. For this reason, sequencing of the whole exome has the potential to uncover higher yield of relevant variants at far lower cost making it a cost-effective alternative to whole genome sequencing.

Whole Exome Sequencing (WES) utilizes sequence capturing or targeting technology to enrich and then to sequence the exome regions of the whole genome. DNA samples are fragmented and biotinylated oligonucleotide probes (baits) are used to selectively hybridize to exome in the genome, magnetic streptavidin beads are used to bind tothe biotinylated probes, the non-targeted portion of the genome is washed away, and the samples for DNA are enriched by PCR. The sample is then sequenced before proceeding to bioinformatics analysis (Fig. 1). This strategy can result in up to a 100-fold improvement in gene coverage for the human genome.

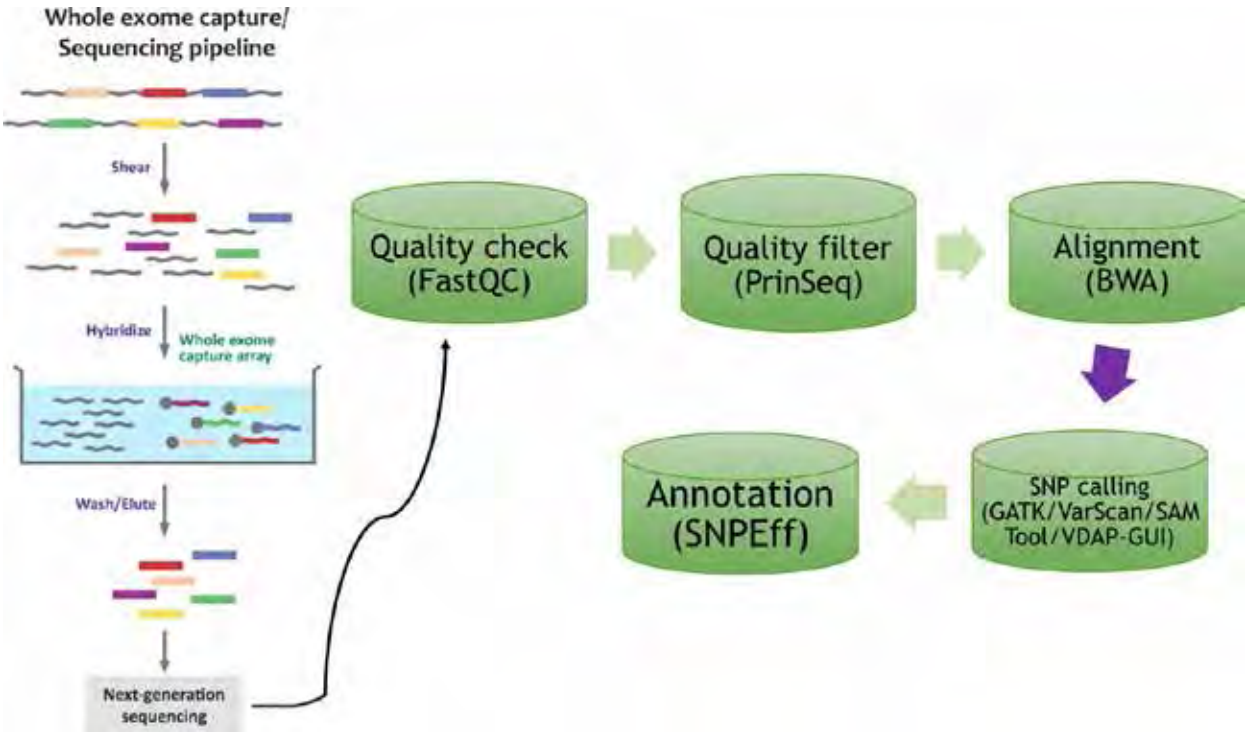


Fig.1. Workflow of WES

Capture Methods

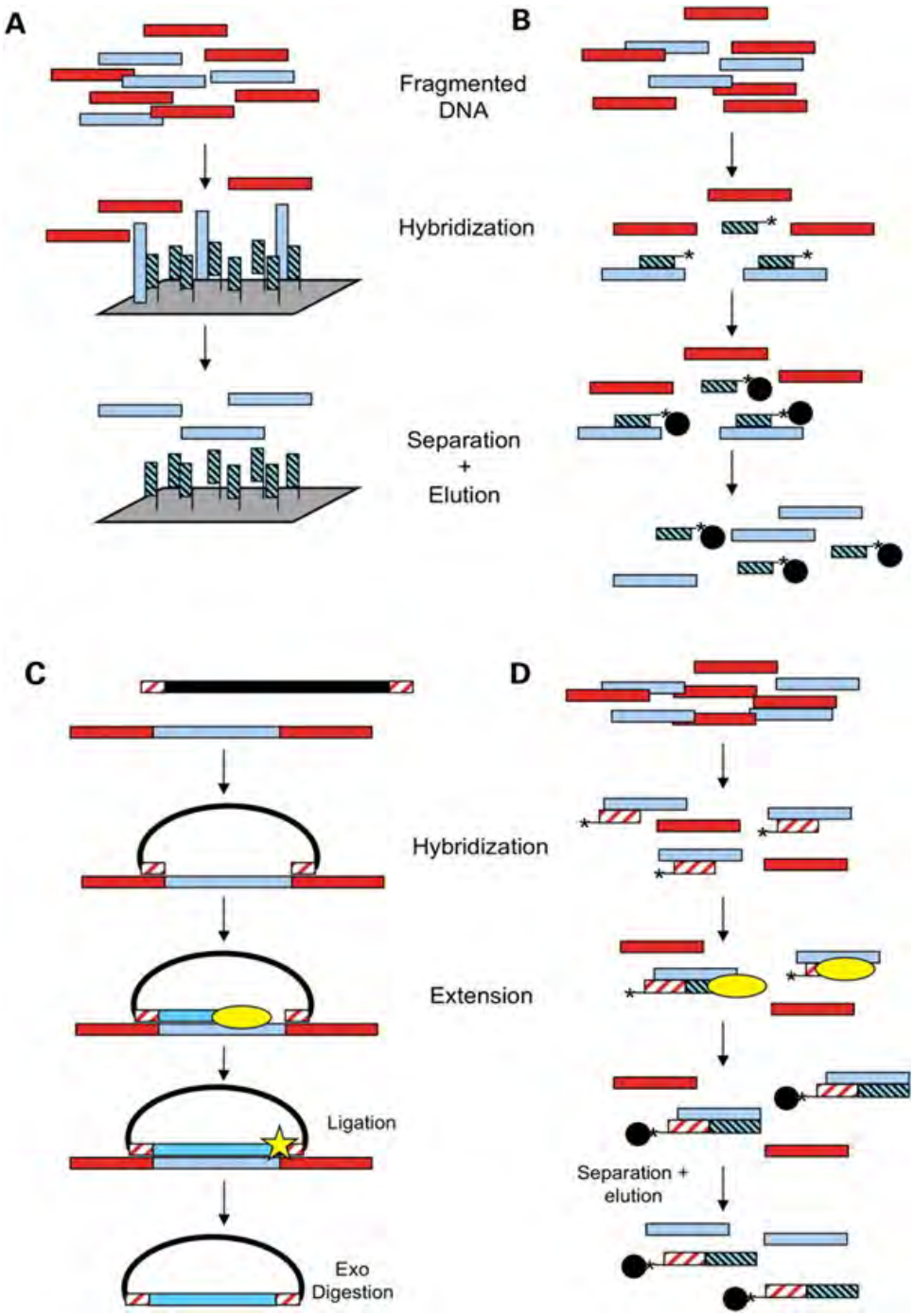
Several methods have been extended to capture the exome, eliminating the need to choose a subset of genes for interrogation and focussing on the best understood 1% of the genome, the protein-coding exons.

A. Solid-phase hybridization

Solid-phase hybridization methods generally utilize probes complementary to the sequences of interest affixed to a solid support, such as microarrays (Fig. 2A). The total DNA is applied to the probes, where the desired fragments hybridize. The non-targeted fragments are subsequently washed away, and the enriched DNA is eluted for sequencing. Recently, these methods have been improved using multiple enrichment cycles. Agilent, Roche/Nimblegen,andFebit offer commercial kits implementing these methods.

B. Liquid-phase hybridization

Liquid-phase hybridization is similar to a solid phase; the probes in this method are not attached to a solid matrix, but insteadare biotinylated (Fig. 2B). Following hybridization, the biotinylated probes (with the complementary desired genomic DNA) are bound to magnetic streptavidin beads and are separated from the undesired DNA by washing. After elution, enriched DNA can be sequenced. Initial reports on this method used biotinylated RNA probes (commercially available from Agilent), and recent methods use DNA probes (commercially available from Roche/Nimblegen).

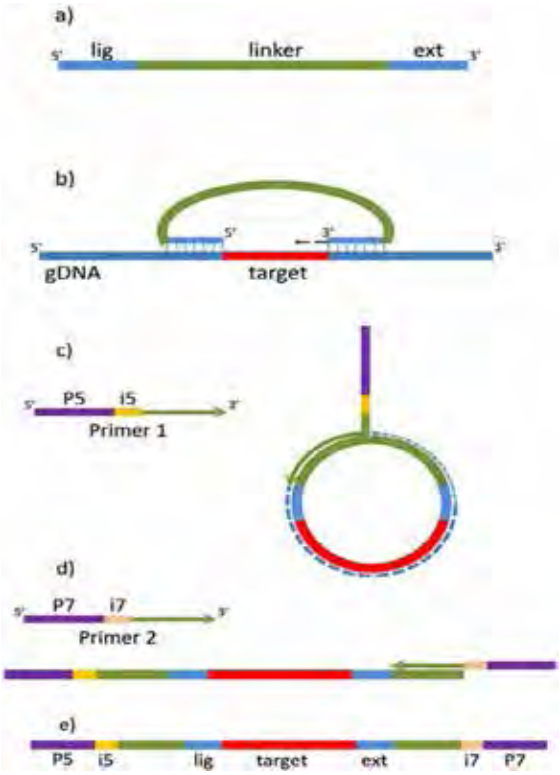


(a) The structure of a MIP; lig -ligation arm, ext -extension arm,
(b) Hybridization of the MIP to the target, gap-filling and ligation
(c) 1st cycle of library amplification, P5–P5 Illumina adaptor, i5 - Nextera index
(d) 2nd cycle of library amplification, P7–P7 Illumina adaptor, i7 - Nextera index
Fragments of the Primers 1 and 2 complementary to the custom sequencing primers are in green
(e) The final product ready for Illumina sequencing.

Fig. 2. Capture Methods

C. Polymerase-mediated capture

Although all capture methods use polymerases to amplify captured fragments, these methods use polymerases in a more integral way. Padlock probe technology has been extended to develop Molecular Inversion Probes (MIP; Fig. 2C).MIP appear particularly well suited for targeted resequencing of tens, hundreds or thousands of short genomic regions. They can be used in any organism with partial genomic information available.



MIPs are single-stranded DNA molecules containing on their ends sequences complementary to two regions flanking the target of up to several hundred bp. Following hybridization of MIPs to the target, gap-filling and ligation result in circularized DNA molecules containing a sequence of the target together with adaptors and barcodes ready for downstream analyses (Fig. 3). MIP technique was a popular solution at early stages of large-scale human SNP genotyping. More recently MIPs have been used for resequencing large sets of human exons and medically relevant gene panels. Specialized applications of MIPs include detection of low-frequencyvariants, copy-number variation (CNV), accurate genotyping of highly similar paralogs and quantification of alternative splicing

Fig.3. Molecular Inversion Probe (MIP) and the principle of the method

D. Primer extension capture (PEC)

Primer extension capture (PEC) was developed with small amounts of DNA in mind (Fig. 2D). This method uses a biotinylated primer with a complementarysequence to the DNA of interest. After annealing, the primer is extended, effectively generating a hybridization probe to capture the sequence of interest like other hybridization methods. Highly parallel PCR has been an effective method to prepare samples for capillary sequencing, and recent work has extended this idea using microfluidics.

Instead of using plates with hundreds of wells, aqueous microdroplets can segregate thousands of individual reactions in the same tube, allowing for a much more highly parallel use of PCR (commercially available from Raindance). Another commercially available kit uses restriction enzymes to fragment DNA; probes specific to the ends of desired fragments are used to amplify the desired sequence (Olink Genomics).

Why WES?

With the price of sequencing decreasing as rapidly as it has during the past decade, questions have been raised concerning WES's usefulness in the era of affordable WGS. The costs of WES consist of the cost of the capture plus the cost of sequencing, whereas WGS consists only of the sequencing costs. If we assume that the cost of capture remains fixed, then as the costs of sequencing decrease, the cost of WGS will approach the cost of WES. However, at present that is not the case, and it would be unwise to assume that the cost of sequence capture will

not decrease. WGS, however, is still more expensive than WES. Also, interpretation of variants, particularly in the non-protein-coding portion of the genome is extremely challenging.

Less Expensive than WGS

Most functional related disease variants can be detected at a depth of between 100-120X which definitely makes the cost case for exome sequencing.Today on Genohub if we want to perform whole human genome sequencing at a depth of ~35X, the cost is roughly $1700/sample. If we were to request human exome-sequencing services with 100x coverage, using a 62 Mb target region, the cost would be $550/sample. Both of these prices include library preparation. So in terms of producing data WES is still significantly cheaper than WGS. It's important to note that this doesn't include your data storage and analysis costs which can also be quite a bit higher with whole-genome sequencing.

Human genomes are a special case, HiSeq X platform offers a cost-per-Gb far less than other platforms yet is limited to 30X WGS human genomes (Watson 2014). However, even given that advantage, the $1000 price tag for a 30X human genome is two to three times the cost of a 40X human exome.

In other species, the price difference is even greater, for example, in pigs (a similarly sized genome to human but currently without the benefit of access to the HiSeq X platform) the estimated cost of WGS was 9-10 times the cost of WES (Robert et al. 2014).

Produce Manageable Data

The amount of data produced by WES is far more manageable than WGS. Although sequencing technology has been improving at a much faster rate the technology for storing and analyzing the data has not seen a matching acceleration in improvement (Mardis 2010; Sboner et al. 2011).For example, whereas 90 Gb of the sequence is required to obtain 60x average coverage of the zebrafish genome (genome size 1.5 Gb), 100x average coverage is achieved for the exome (50 Mb) with only 5 Gb of the sequence using the current state-of-the-art platforms for targeting.

Afford number of samples

WES still costs a lot less than WGS, which may be advantageous to sequence more number of samples (an important factor for large population studies) to gain statistical power, than to sequence more of the genome.If the capacity of an Illumina chip is to produce 100 Gb data, only one sample can be used for WGS to get 100X coverage while 20 samples could be used at a time for WES to get the same coverage.

More advantageous than GWAS

Exome sequencing offers a look into the genome that large-scale studies of common variation, such as the genome-wide association study (GWAS) cannot provide. GWAS can only identify variation in DNA that is common in the population, in at least one percent of people. But sequencing determines every letter in a DNA sequence, not just the ones known to vary, so it can reveal rare mutations that GWAS wouldn't uncover. Exome sequencing is a good choice for scientists today who are looking for rare mutations, especially when used as a complement to studies of common variation like GWAS (Gilbert et al., 1978).

WES constraints and solutions

The probes in the sequence capture method are designed based on information from gene annotation databases such as the consensus coding sequence (CCDS) database and RefSeq database. Therefore, unknown or yet-to-be-annotated exons are not typically captured. WES is not a successful method for the species having

uncompleted reference genome or only a draft genome.Poor annotation of genomes means that in the design of capture probes, causative genes may be missed because they are not annotated. Additionally, errors in the reference genome will greatly increase the number of false-positive variant calls in the species. This increases computational burden forces more stringent filtering which may lead to unintentional discard of causative variants. Inefficient targeting process, e.g. uneven capture efficiency across exons can result in off-target hybridization means that at least 20% of reads come from genomic DNA outside the exome.

Where available, including predicted genes identified from RNA-sequencing data may be beneficial to maximize coverage of functional elements in poorly annotated genomes. For example, Robert *et al.* (2014) added an additional 14Mb of data to the capture region in pigs using EST evidence.

Recent studies have highlighted and suggested roles for promoters (The Fantom Consortium and the RIKEN PMI and CLST 2014) and enhancers (Andersson *et al.* 2014) in a range of different cell types. These evolutionarily conserved non-coding regions and regulatory sequences are not typically captured by exome sequencing. It is therefore important to take care when designing the capture region or purchasing a commercial kit to ensure any specific regions of interest are included.

Partly to address these issues of coverage, the latest commercially available capture kits provide nearly complete coverage of the well-annotated genes but also allow the user to add custom content by designing capture probes targeted to additional regions of interest such as promoters or highly conserved sequences. Newer kits have also expanded the regions captured to include micro-RNA sites and untranslated regions of genes, thus increasing the regions captured from 30 Mb to as high as 62 Mb.

Exome sequencing involves a PCR stage that is known to create the amplification artifacts and reduce coverage of GC-rich regions (Kozarewa *et al.,* 2009; Veal *et al.,* 2012). New sequencing technologies are being developed for sequencing of DNA without the need for DNA amplification, generating sequences from single molecules. This technology can produce accurate, longer reads without the artifacts and biases associated with the amplification process in other sequencing methods (Shin *et al.*, 2013). The longer read length is particularly beneficial for detecting structural variants and for resolving repetition in assemblies and copy number variable regions. However, for now, the price of this long-read sequencing is still prohibitively expensive and is not commonly in use for analysis of genetic variation. In future, as these sequencers improve and prices come down they may make WES more attractive to researchers.

Factors affecting capture efficiency

Quality of DNA - Poor quality DNA, typical with extractions from FFPE, can introduce bias as certain regions tend to be more fragmented than others. If capture isn't balanced, this results in bias and complications during downstream SNP calling and other forms of analysis.

The quantity of DNA - Low amounts of input DNA usually require a lot more PCR cycles in order to get enough library for the hybridization of capture probes to be efficient. Higher PCR cycles can result in a significant amount of PCR duplicates, making conclusions from data analysis less informative.

Pseudogenes - Can reduce evenness of coverage.
Repeat elements - Will reduce the evenness with which reads are distributed across the exome, resulting in the need for more sequencing to call de novo SNPs.

Exome capture platforms

There are several differences between the available platforms, which are constantly being updated and improved. The major providers of exome capture platforms are NimbleGen, Agilent, and Illumina, and each has different designs and strengths.

xome-Seq Kits	Targeted Region	Number of Probes	Probe Type	Genomic DNA input required	Fragmentation method	Probe Length (mer)	Probe Design	Price per capture (negotiable)	Reads remaining after filtering	Hybridization time (hours)
Agilent SureSelect XT2 V6 Exome	60 Mb	~758,086	biotinylated cRNA baits	100 ng	Ultrasonication	120	Non-overlapping, paired-end reads used to fill gaps	$270	71.7%	16
Agilent SureSelect QXT	51 Mb	~655,872	biotinylated cRNA baits	50 ng	Transposase	120	Non-overlapping, paired-end reads used to fill gaps	-	-	90 minutes
Agilent HaloPlex	37 Mb	2.5 M	biotinylated cRNA baits	250 ng	Restriction enzymes digestion	120	Non-overlapping (adjacent to each other)	-	-	1.5 days (overall work flow)
Roche Nimblegen SeqCap EZ Exome v3.0	64 Mb	~2,100,000	biotinylated DNA bait	1 ug	Ultrasonication	60 - 90	Overlapping baits	$600	66%	72

xome-Seq Kits	Targeted Region	Number of Probes	Probe Type	Genomic DNA input required	Fragmentation method	Probe Length (mer)	Targeted exons	Price per capture (negotiable)	overall work flow time (Days)
Illumina Nextera Rapid Capture Expanded Exome	62 Mb (After filter 40.1%)	>340,000	biotinylated DNA bait non-coding DNA in exon flanking regions, UTRs and miRNA	30 ng	Transposase	95	Non-overlapping (adjacent to each other	$250	Hybridization 24-48 h
Illumina's TruSeq Exome Enrichment Kit	64 Mb	~340,427	biotinylated DNA bait, non-coding DNA in exon flanking regions, UTRs and promoters	50 ng	Ultrasonication	95	Non-overlapping 201,121 (20,794 genes)	-	Hybridization24-48 h
IDT xGEN Exome Panel	39 Mb	429,826	biotinylated DNA bait	500 ng	Ultrasonication	-	19,396 genes	$250	Hybridization 4 hours

Kits for Non-human Species

Currently, in addition to human kits, NimbleGen offers capture kits for maize, barley, wheat, soy, mouse, and pig exomes, and Agilent offers capture kits for mouse, cattle, and zebrafish exomes. Both providers also offer the opportunity to design custom kits for other species. Both manufacturers offer a flexible design process that allows for modifications to improve coverage for specific regions and purposes.

Application in Agricultural Species

Plant genomes are extremely complex, repetitive, often polyploidy and not well suited for genome re-sequencing studies. For example, Bread Wheat (*Triticum aestivum)* has an allohexaploid (AABBDD) genome around 17Gb in size. An exome capture kit has been designed for wheat based on the accumulated transcriptome data (Winfield *et al.*, 2012). The capture region for this kit is 56.5 Mb and because of similarity between the three genomes may be sufficient to capture most of the exome data from the whole allohexaploid genome.

The genome of barley (*Hordeum vulgare L.*) is around 5 Gb and has not been fully sequenced. A gene space assembly has been produced (The International Barley Genome Sequencing Consortium 2012) and a barley exome capture kit has been developed based on this assembly (Mascher *et al.,* 2013). The kit has since been used to identify a mutation involved in early maturation, a trait relevant to production (Pankin *et al.,* 2014).

Exome Capture Transferability between Species

The kit designed for cattle also can be applied to other bovid species. Cosart *et al.* (2011) demonstrated that the kit could be successfully used to capture the exomes and identify SNPs in zebu (*Bos indicus*) and American Bison (*Bison bison*). This transferability of exome capture kits is also demonstrated in studies involving the sequencing of Neanderthals and nonhuman primates using human capture kits (Burbano *et al.* 2010). This is possible because, despite millions of years of divergence, functional elements tend to be highly conserved.

Application in Fish Species

Till date, no one has applied WES in any fish species except in zebrafish. McConnell *et al.* (2016) used whole-exome sequencing of clonal zebrafish to identify potential variants in immune loci. They first performed whole-exome sequencing of two different lines of homozygous diploid, clonal golden zebrafish: CG1 and CG2. They also mined SNPs using WES. They used Agilent SureSelect Target Enrichment kit to capture the exome and Illumina HiSeq2000 instrument for sequencing. After using BWA for mapping against Zv9 reference genome they mined approximately 400,000–500,000 SNPs for each clonal line through GATK pipeline.

Major Applications

Identification of rare genetic variants
Disease association studies
Genetic marker development
Determination of important disease-related variations
Profile low-frequency genotypes at the population level

Conclusion

Exome sequencing is a cost-effective approach when whole-genome sequencing is not practical or necessary. Sequencing only the coding regions of the genome enables researchers to focus their resources on the genes most likely to affect phenotype and offers an accessible combination of turnaround time and price. Exome sequencing detects variants in coding exons, with the capability to expand targeted content to include untranslated regions (UTRs) and microRNA for a more comprehensive view of gene regulation. The amount of data produced by WES is far more manageable than WGS, particularly for small research groups and groups studying organisms with large genomes. WES has been established as an important method in disease gene identification in humans and increasingly in domestic species. DNA libraries can be prepared in as little as 1 day and require only 4–5 Gb of sequencing per exome.

References

Andersson, R., Gebhard, C., Miguel-Escalada, I., Hoof, I., Bornholdt, J., Boyd, M., ... & Ntini, E. (2014). An atlas of active enhancers across human cell types and tissues. Nature, 507(7493), 455-461.

Burbano, H. A., Hodges, E., Green, R. E., Briggs, A. W., Krause, J., Meyer, M., ... & Rooks, M. (2010). Targeted investigation of the Neandertal genome by array- based sequence capture. science, 328(5979), 723-725.

Cosart, T., Beja-Pereira, A., Chen, S., Ng, S. B., Shendure, J., & Luikart, G. (2011). Exome-wide DNA capture and next generation sequencing in domestic and wild species. BMC genomics, 12(1), 347.

Gilbert W (February 1978). "Why genes in pieces?". Nature 271 (5645): 501.

Mascher, M., Richmond, T. A., Gerhardt, D. J., Himmelbach, A., Clissold, L., Sampath, D., ... & Akhunov, E. D. (2013). Barley whole exome capture: a tool for genomic research in the genus Hordeum and beyond. The Plant Journal, 76(3), 494- 505.

McConnell, S. C., Hernandez, K. M., Wcisel, D. J., Kettleborough, R. N., Stemple, D. L., Yoder, J. A., ... & de Jong, J. L. (2016). Alternative haplotypes of antigen processing genes in zebrafish diverged early in vertebrate evolution. Proceedings of the National Academy of Sciences, 113(34), E5014-E5023.

Niedzicka, M., Fijarczyk, A., Dudek, K., Stuglik, M., & Babik, W. (2016). Molecular Inversion Probes for targeted resequencing in non-model organisms. Scientific reports, 6.

Pankin, A., Campoli, C., Dong, X., Kilian, B., Sharma, R., Himmelbach, A., ... & von Korff, M. (2014). Mapping-by-sequencing identifies HvPHYTOCHROME C as a candidate gene for the early maturity 5 locus modulating the circadian clock and photoperiodic flowering in barley. Genetics, 198(1), 383-396.

Robert, C., Fuentes-Utrilla, P., Troup, K., Loecherbach, J., Turner, F., Talbot, R., ... & Watson, M. (2014). Design and development of exome capture sequencing for the domestic pig (Sus scrofa). BMC genomics, 15(1), 550.

Winfield, M. O., Wilkinson, P. A., Allen, A. M., Barker, G. L., Coghill, J. A., Burridge, A., ... & Bevan, M. W. (2012). Targeted re-sequencing of the allohexaploid wheat exome. Plant biotechnology journal, 10(6), 733-742.

"I accept any challenge, so challenge me" Shane Koyezan

PharmaAQ
Pharmaceutical Analysis and Quality

Advances in Food & Beverage Analysis

Co-located Conferences

REGISTER NOW!

11-12 OCTOBER 2018 - MUMBAI, INDIA

- Method Development
- Analytical Techniques
- Control Strategies
- Quality Control
- Pharma/ Bioanalysis
- Data Interpretation

- Food Analysis
- Food Pathogens
- Nutrients & Supplements
- Technologies & Instruments
- Food Regulations
- Nanotechnology

FOR DETAILS, CONTACT

PAQ: p.sharma@selectbio.in | 7696325050 | **FBA:** g.sharma@selectbio.in | 7696025050

Registration: f.zainab@selectbio.in | 7696125050 | **Exhibition:** mjsingh@selectbio.in | 7696225050

For a quick response, just **WhatsApp: 9041725050**

SELECT BIOSCIENCES INDIA PVT LTD

Guest Article

"Bioterrorism: Exploitation of Microorganisms"

Utkarsh Singh*[1] and Preeti Sachan[2]

[1]Department of Biotechnology, Baba Farid Institute of Technology, Dehradun
[2]Department of Environmental Science, Kanya gurugul Campus, Gurukul Kangri Vishvavidyalaya, Haridwar

*Email: utkarshbiotech@yahoo.com

Terrorism is the most prevalent word in the developing countries. They have been fighting terror, whether it is intra or inter, since time immemorial. During the World War I, apart from human fighting against human, the resources required for livelihood was also targeted. Its impact was directly related to the food which could impair the basic skeleton of a country. Biologically active microorganisms were exploited in the form of biological weapons.

Science has been proved to be a boon as well as a curse for the mankind. Biological weapons have been utilized in numerous battles and are a topic of interest for centuries. This is how 'Bioterrorism' comes into play. Innovations in molecular biological techniques have resulted in successful manipulation of bacteria and viruses, making it more susceptible to the diseases, so as to use it for human desolation.

Bioterrorism, as defined by the Centers for Disease Control, is the "international or threatened use of bacteria, fungi, or toxins from living organisms to produce death or disease in humans, animals and plants". A number of diseases can be used as a weapon, in different ways. Either it may be spread via air or it may contaminate drinking water. Both ways can target a huge population.

The term bioterrorism may include biological, nuclear and chemical agents. The hazardous chemicals like nitrogen mustard, phosgene, chlorine gas etc. have been used during the World War I and the effects were not under carpet.

A new era of disaster begins with the end of a war. Different diseases are spread all around. Infectious diseases are the leading cause of death. The influenza epidemic and the avian flu are the unforgettable examples of the devastating consequences.

Bioweapons being easy to obtain and inexpensive to produce, compared to nuclear and chemical weapons, makes them beneficial to the terrorists.

Terrorists may sometimes try to target the agriculture by targeting crops which result in good national economy. Though it may not result in a direct massive loss to agriculture but it would benefit the terrorists in gaining attention of a large population without killing them.

The widespread effect of contamination on agriculture could increase the public attention, enough to meet the demands of the terrorists.

The advent of molecular techniques has brought a revolution in fighting the undesired attacks of microorganisms. Viral diseases are not so approachable to produce as a weapon, since viruses can only produce inside a body or cell. So it becomes technically difficult and expensive. Bacteria and fungus are comparatively easier to produce than the viruses. Therefore such diseases are most harmful.

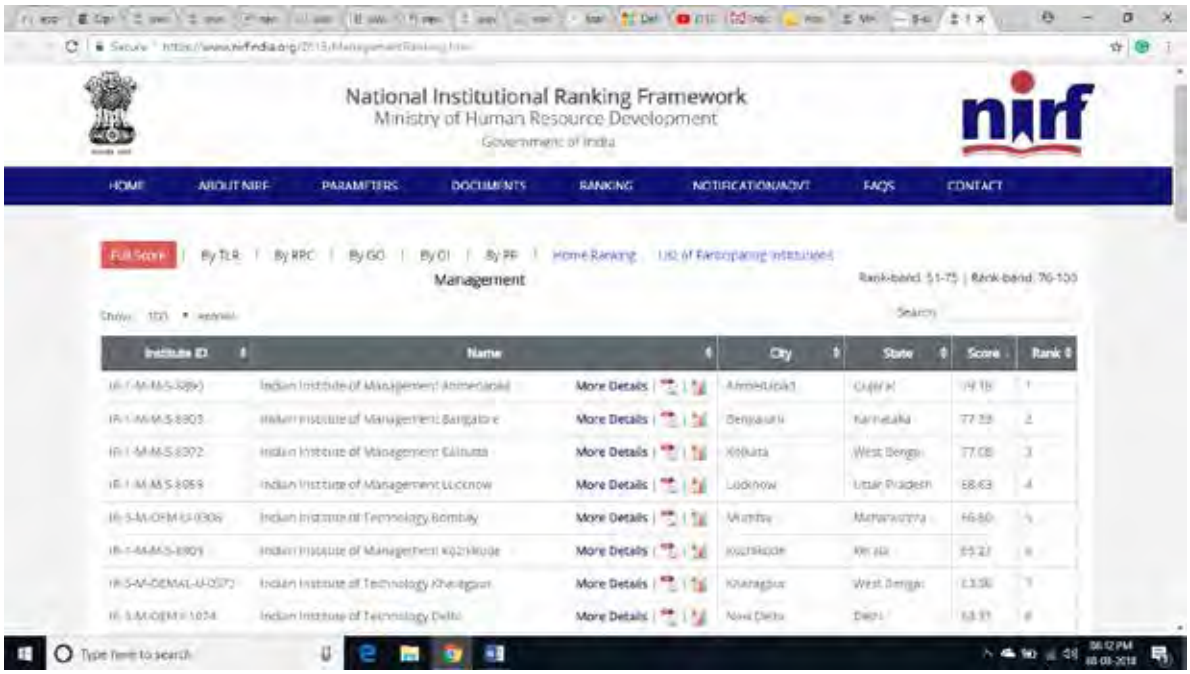
To fight the possible peril of the 'Bioterror', people must be made aware of the diseases and its causative agents. Misuse of the new emerging techniques must be stopped. Serious steps must be taken by authorities for proper accurate diagnoses and effective treatment of diseases. Increasing terror of biological and chemical agents has to be stopped. We must work upon new techniques for prevention against fatal diseases. We pray for the world to become a terror free environment, so that the coming generations would live in peace.

Guest Article

National Institutional Ranking Framework: An aspiration without essentials

Rahul Bhandari, Assistant Director at O.P. Jindal Global University
E-mail: rahulbhandari1983@gmail.com

National Institutional Ranking Framework released its 3rd edition of Indian University Rankings. The higher education world in India and its stakeholders in various capacities expected eminent Institutions of the country like IIMs and IITs continue to be on top of these rankings. On a contrary, it was quite surprising to see few private institutions are ranked even above some IITs and NITs like Vellore Institute of Technology, Birla Institute of Technology and Science, Pilani, College of Engineering, Pune and much more which were missing in 2017 were able to secure positions in best 10.



The idea of India's own ranking system came into existence after HRD ministry noticed the continuous poor performance of Indian universities in the top 3 recognized world university rankings i.e., QS, ARWU, also known as Shanghai Ranking and Times Higher Education (THE) World University Rankings.

On October 2014, the framework of National Institutional Ranking was laid by a 16 member core committee which included Chairman NBA, Chairman AICTE, Chairman NAAC, Former Director, IIT Bombay, Director, INFLIBNET center and other prominent personalities of MHRD and NBA. It took almost a year to formalize it.

On 29th September 2015, Smt. Smriti Irani, Former Minister for Human Resource Development publically announced India's own ranking system list for Engineering and Management categories and later on ranking of the pharmacy and architecture and other institutions were released.

Total 22 parameters in five major categories are used to rank universities across the country, most of them are handpicked from the recognized world university ranking systems such as Teaching, Learning and Research Excellence. However, the committee brought few country-specific parameters like regional diversity, a facility for physically challenged and the percentage of economically and socially disadvantaged students under the head of Outreach and Inclusivity.

NIRF envisaged separate ranking for different universities/colleges/ institutions, within each discipline, there are separate ranking in two different categories- Category A for institutions who are engaged in Teaching & Research and Category B for only teaching institutions.

In 2016, NIRF published India's first universities ranking. During its initial stage, NIRF ranked only engineering, management and pharmacy institutions from government funded, privately- funded or self-financing institutions had participated, the Architecture and general degree were exempted due to no or less response. The core committee did few significant changes in few sub-parameters but the main ranking parameters unchanged.

One of the paradoxes or moreover an irony is that the MHRD felt the need to have India's own ranking system when our universities are struggling with basic necessities like shortage of faculty members, efficient staff members, basic infrastructure, job oriented course curriculum and minimum fund for research & innovation.

These current state of affairs seems familiar, a decade back when China found that its Universities are struggling to be amongst the top world universities of the world, the Chinese policymakers decided to start their own ranking system i.e., ***Academic Ranking of World Universities*** (***ARWU***), also known as **Shanghai Ranking,** focusing on Science and Research. While framing parameters, they focused and gave more weightage on Quality of Education and Quality of faculty with the indicators focused on Alumni & staff as Nobel Laureates

and the projects like 985 & 211 to improved the overall quality of China's higher education as a result two Chinese universities -- Peking University (PKU) and Tsinghua University are in the world's top 30 (According to the World University Rankings 2018 published by the Times Higher Education Supplement) and included 12 Chinese universities in the world's top 100 (QS World University Rankings).

Another initiative was taken by the Chinese Central Government to promote the development and reputation of higher education was to develop the C9 League, an official alliance of 9 universities through Project 985, the C9 League together account for 3% of the country›s researchers but receive 10% of national research expenditures. They produce 20% of the nation›s academic publications and 30% of total citations that's why China is responsible for 17% of Global Research Output as compare to Indian universities, which contributes a measly 3.5% only. On its earlier time, ARWU faced serious criticism for its criterion which heavily focused on scientific research but at present ARWU is considered one of the best 3 world university ranking and it's highly appreciated for its transparency and objectivity. On the other side, MHRD took the same initiative but while drafting the framework and while establishing the parameters for ranking, the policymakers perhaps neglected that most of the Indian universities are struggling to keep up with the basic requirements of a higher education institutions.

Challenges

1. **Voluntary exercise**

Participation in NIRF ranking is a voluntary exercise due to which there is a huge imbalance in participation number and it's really hard for MHRD to produce the entire list. In 2017, the second list of NIRF ranking had witnessed the decline of 16% and participation of only 6% of the total institutes around the country. Point to keep in mind that in 2016 only Engineering, Management, Pharmaceutical universities/institutes were ranked but in 2017 they increased the dimension by adding Subject stream colleges and best General Degree colleges. The latest rankings in 2018, new category rankings being introduced in Medical, Architecture, and Law.

	Total No. of Institutes participated	**Growth/Decline Ratio**
	3,563	NA
	2,995	-16%
	4500	44%

Although, while announcing NIRF 2018 ranking, Union Minister for Human Resource Development (HRD) Prakash Javadekar raised his concern on participation and said that it would be mandatory for public institutes to participate in the ranking framework from next year and those public institutions which will not take part in it will face fund cut.

Data authentication issue:

There is no way anyone can verify the data which is submitted by universities across the country (Note: the ranking heavily based on these data). NIRF has not authorized any company or individuals to verify the submitted data. At present whether private or public or any institution, are required to submit their data on their own. There are possibilities of errors in the submitted data (intentionally or unintentionally). In a recent NIRF 2018 ranking list, Times of India accessed the data from NIRF website and found that Bishop Heber College (BHC) Trichy had submitted false data about the total student strength. This is only one incident which came into light, we really don't know how many more such cases. Who is responsible if a potential student blindly trusts NIRF ranking, take admission and later on finds the truth.

All fruits in the same basket

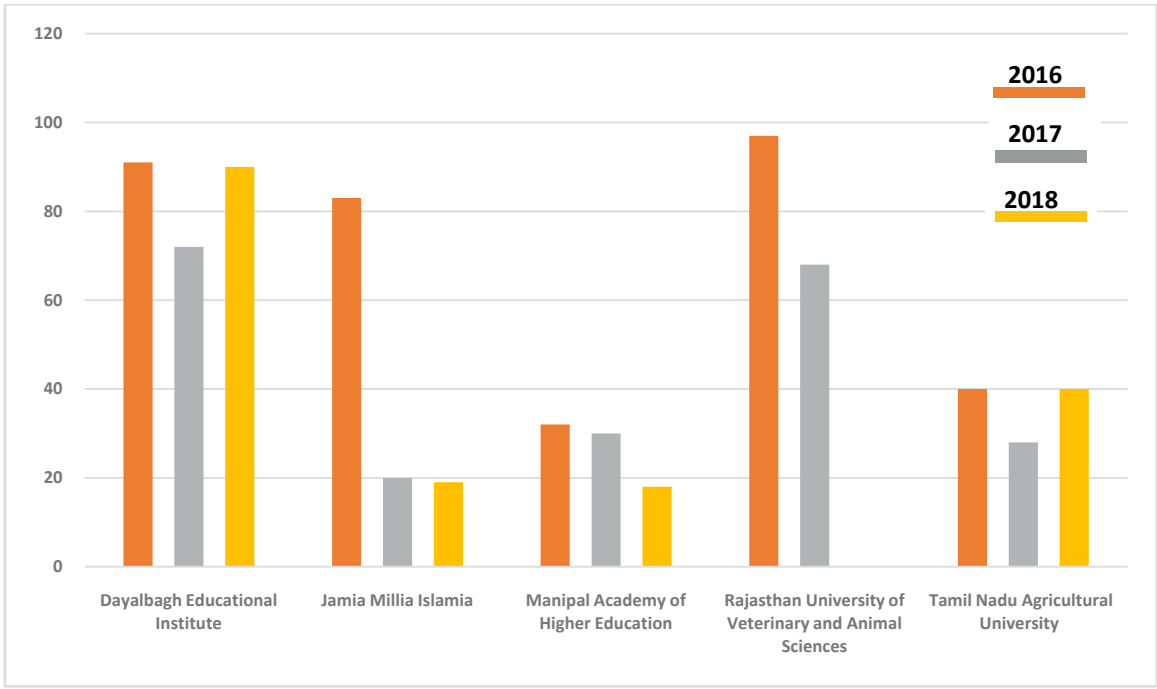
There are huge structural issues in the framework of NIRF ranking, as it allows to rank all the universities on the same scale. How a public university like Indian Institute of Science which is established in 1909 and fully supported & funded by the government for its research can compare with a self-funded university which is decade old and have a very limited source of fund for research. There should be a process where the performance of university is evaluated by keeping its establishment, quality publication and community engagement activity in mind.

A roll coaster ride

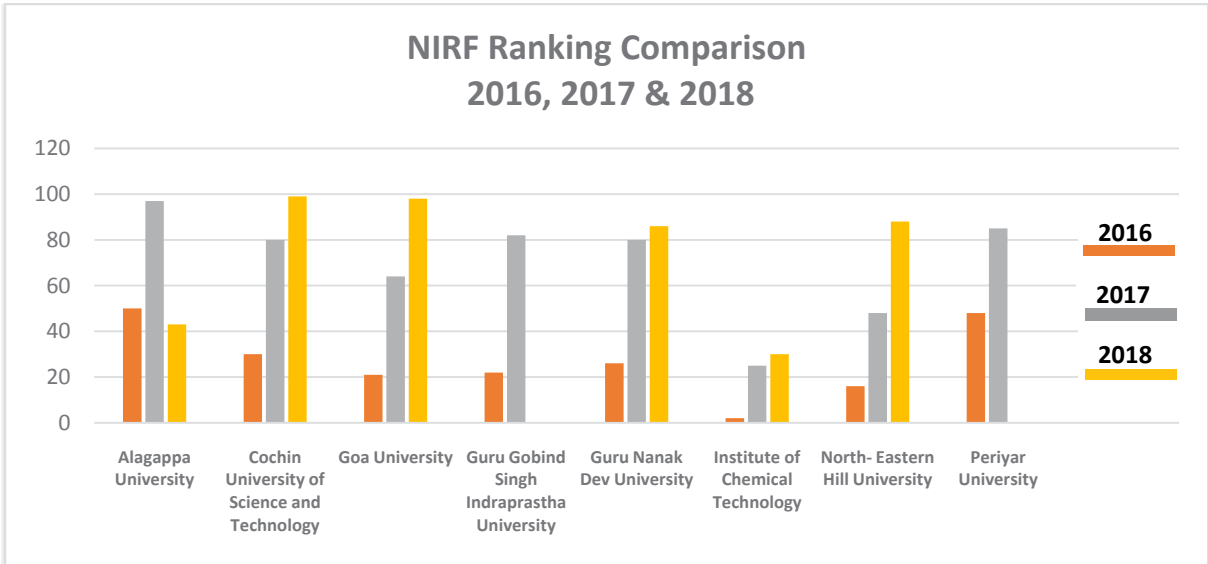
Below graphs clearly, show the unrealistic difference in universities position at NIRF ranking between 2016 to 2018. Few universities like Jamia Milia & Tamil Nadu Agricultural University really enjoyed the ride of NIRF ranking. In a span of a year, they suspiciously improve their positions from 83 to 20 and 40 to 28 respectively.

What can be possibly done

1. **Introduce new parameters in NIRF**: Keeping in mind the social obligation we have in our education system, it's time to give more weightage to parameters which are more human-centric rather than following the western way which is more process-centric. Factors like happiness, job satisfaction, work-life balance, Equal pay, Entrepreneurial ecosystem and equal opportunity can be the game changer.
2. **Allocating more Research fund to Privately funded institutions**: Most of the Indian universities don't get sufficient funding from the government. Few handful universities majorly Public/Government universities are getting funds which are not sufficient.
3. **Fair selection process**: Currently all the university is keeping on the same level which sounds not write for example how any university which is established in 10 years back have the same level of research and publication s compare to a university which was established on 60 years back. The only way to give a fair chance to all universities across the country by adding the human-centric factors in ranking parameters.
4. **Mandatory participation**: At present participation in NIRF ranking is absolutely on the desire of institutions.



Universities who faced steep slopes during NIRF ranking



To improve the quality of education, research, and learning, MHRF needs to make mandatory for all institutions to participate.

It's a long way to go but I believe it is a great initiative by our government to improve the quality of institutions across the county. To get to the top, institutions definitely need to improve practices that will make them stronger and ultimately affect their ranking.

B4

Building Bharat-Boston Biosciences Program

Call for Applications for the 2019-20 B4 Fellowship

Deadline to Apply: Sept. 25, 2018

Apply at:
https://mittalsouthasiainstitute.harvard.edu/b4-harvard-fellowships/

Starting Date: January 20, 2019
Duration of the Program: 18 months
Stipend: INR 195,000/month for 18 months

**Health insurance & round trip economy travel expenses to & from Boston will also be provided.*

ABOUT

Up to 8 Science & Technology Fellowships for 2019-20 will be offered in fields related to the biosciences at Harvard University and other institutions in the Boston area. The Mittal institute will organize seminars at Harvard for Fellows to discuss their research with the broader community at Harvard and beyond.

Fellows are expected to reside in the Cambridge vicinity and to actively participate in the events and intellectual life of the Institute. In addition, Fellows are expected to contribute to the greater Harvard community by teaching, mentoring, or advising students.

ELIGIBILITY

Scholars who have completed their PhD within the last five years from an institution in India in a bioscience-related field are eligible. Exceptional senior doctoral students, with demonstrated independence and maturity, may be considered. Applicants must be Indian citizens currently residing in India (from program start date). For applicable areas of study, please visit the program's website.

This program is a collaboration between IBAB (Bengaluru, India) & The Lakshmi Mittal and Family South Asia Institute (Harvard University, Cambridge, MA). Funded by the Dept. of Biotechnology, Govt. of India.

SOUTH ASIA INSTITUTE

IBAB

Questions? Please email the Program Manager, Savitha G. Ananth at savitha_ananth@fas.harvard.edu

Biotech Express

Submit Articles

WRITE FOR BEM

General Topics

Field of Biological Sciences - Its spread, boundaries and correlation with other sciences. Specializations and updates of Individual subjects. Sc-fi thinking, Biographies of famous Scientists, History and advancement of BioScience.
Trending topics - Science and its unseen benefits to society Science, Plagiarism, Pitfalls in research papers. Open access or not.
Book Reviews (column) Any book relevant to field – its existence, reporting and review.

Topics For students

Choosing science as career, Top rules for choosing institution, How to adapt to college academics, Character Education – Science ethics, Beating the examination stress. Driving habits, experience with colleagues, Challenges and power to overcome, Life lessons, Grading system, Mobile Phones and students, Probable secrets of success in science career, GRE TOEFL preparation, How successful students manage their time, How to get academic help in college, Many benefits of campus life, Online degrees and classes.

Topics For Researchers

Education Policies, Accomplishments and projections of Ministries, Departments and Organizations, Rules and regulations Amendments/Updates, Research status in India with global comparison, Scope of excellence in Research and Education

Topics For Industries

Big News- Product Launch, Merger & Acquisition, Annual Budget info etc. Advertorials- Articles for company/ professionals

Submit News Article @

Online: http://kashbiotech.com/biotech-express-magazine/submit-article/
Email: biotechexpressindia@gmail.com

Subscribe

Biotech Express

TERM	Print		Digital	
USER PROFILE	INSTITUTIONAL	INDIVIDUAL	INSTITUTIONAL	INDIVIDUAL
Annual	₹ 10,000	₹ 5,000	₹ 5000	₹ 1200

For payment:

Contact:
"BIOTECH EXPRESS"

Note:
Print subscription includes digital subscription as gratis (no extra cost) for the subscribed period.

Terms and Conditions:

1. Please fill the form in CAPITAL letters.
2. Print Subscription is valid in India only. Outside India Subscriber may subscribe Digital version.
3. Print Subscription cost includes first class courier charges.
4. Print subscription includes digital subscription as gratis (no extra cost) for the subcribed period.
4. The mode of payment should be cheque/DD/favouring "Biotech Express". Please write your name and contact details on the back side of cheque/DD.
5. Your subscription will commence from the next available Issue OR within four weeks.
6. For Multiple Subscriptions/error use seprate forms (Photocopies allowed).
7. Biotech Express will not entertain cancellation of subscription after commencement of the same. No request for refund will be entertained.
8. In case of changing address, kindly send us in writing one month in advance.
9. Non delivery should be reported within 20 days of publishing of monthly issue to consider repost by us. After which no request will be entertain under any circumstances.
10. Annual Subscription can be avail throughout the year.
11. Previous Volumes are available on request.

My Details !

Name of Individual/Institution.....

Address (correspondence).....

Pin..... Mobile..... enclosing Cheque/DD of ₹ .....

..... (in figures).....

Drawn on .....in favour of Biotech Express for the subscription plan.....

Please submit this form after filling the details and send it to :
BIOTECH EXPRESS - V-31/4, Ext-1, Shalimar Garden, Sahibabad, Ghaziabad, U.P- 201005, India.

SUBSCRIBE INFO ON WEBSITE @ www.kashbiotech.com

NEWS: Govt & Industry

FIRST HUB: Facilitation of Innovation and Regulation for Start-ups and Innovators

To promote government initiatives on Start-up India & Make in India, BIRAC a Public Sector Undertaking of Department of Biotechnology, GoI has set up a Facilitation unit which will act as FIRST HUB to address the queries of Start –ups, Entrepreneurs, Researchers, Academicians, Incubation Centres, SMEs etc.

The policies, rules and regulations are dynamic and keeping pace with the fast changing ecosystem is next to impossible for small companies and young entrepreneurs. BIRAC through its various programs is already facilitating research and innovation and to complete the 360 degree start-up facilitation, setting up of FIRST HUB is envisaged.

First Hub will be open on every first Friday of the Month at BIRAC office from 3:00 pm to 5:00 pm. Officers from DBT, BIRAC, ICMR, CDSCO and other relevant government organisation will be available for taking queries related to;

Regulatory pathways and Regulation
Funding opportunities
Mentorship
Investment opportunities
Market access
Industry Academia partnerships
Intellectual Property

Prior appointment is essential as only 5-6 Innovator slots are available. Innovators are encouraged to take prior appointment with details on Company Name, Address, Contact Details, Technology/ Innovation Summary, Stage of development and specific queries through online portal available at First Hub.

BIRAC is also facilitating "Testing and Standardisation of Medical Devices" in collaboration with KIHT.

For any further details e-request may be sent to Sonia Gandhi, Senior Manager – Investments, BIRAC at sgandhi.birac@nic.in.

India bans 328 combination drugs in setback for pharma companies

NEW DELHI (Reuters) - The Indian government has banned 328 combination drugs in a blow to both domestic and foreign pharmaceutical firms, but the ban has been cheered by health activists worried about growing antibiotic resistance due to the misuse of medicines.

The Indian government had in 2016 banned about 350 such drugs, referred to as fixed-dose combinations (FDCs), but the industry mounted various legal challenges that prompted the Supreme Court to call for a review by an advisory board.

The health ministry on Wednesday said the board had found there was "no therapeutic justification for the ingredients contained in 328 FDCs and that these FDCs may involve risk to human beings".

It said it was prohibiting the "manufacture for sale, sale or distribution for human use" of the 328 FDCs with immediate effect. It did not name the drugs or give any brands.

The president of the Indian Drug Manufacturers' Association, Deepnath Roychowdhury, said the order would have an impact on a market worth an estimated 16 billion rupees ($222 million) a year for such drugs, which are produced by both small and large pharmaceutical companies. He said the verdict would be respected.
Combination drugs are used to improve patients' compliance, as it is easier to get patients to take one drug rather than several.

SpiceJet operates India's first biofuel-powered flight from Dehradun to Delhi

SpiceJet today operated India's first test flight powered by biojet fuel, marking a new chapter in the fast-growing domestic aviation sector.

The nearly 45-minute flight from Dehradun to the national capital was operated with a Bombardier Q400 aircraft, partially powered by biojet fuel made from Jatropha plant, according to an airline official. With the test flight, India has become one of the few countries and probably the first among the developing nations to use biofuel for flying planes.

For the test flight, which carried 28 people, including five crew members, the aircraft's right engine was filled with 75 per cent aviation turbine fuel (ATF) and 25 per cent of biojet fuel, made from Jatropha plant, the airline official said. The fuel was prepared by the CSIR-Indian Institute of Petroleum (IIP), Dehradun. The institute's Director Anjan Ray said around 330 kg of biojet fuel was made for the little over 40-minute flight.

At a function to mark the successful operation of the test flight here, Civil Aviation Minister Suresh Prabhu said efforts are on to have a consumer-friendly, affordable and environment-friendly aviation sector.

Road Transport Minister Nitin Gadkari said the government plans to come out with a "special policy" for use of biofuel in the aviation sector.

"Taking our biofuel mission forward @PetroleumMin will be bringing a new Bio- ATF Policy soon," Petroleum and Natural Gas Minis ..

Scientists at Institute of Life Sciences (ILS), Bhubaneswar discovers a drug target for neurodegenerative diseases and cancer

Accumulation of protein aggregates is a hallmark of neurodegenerative diseases. For therapeutic interventions of neurodegenerative diseases, it is important to understand the mechanism involved in the formation and degradation of protein aggregates.

At the Institute of Life Sciences (ILS) Scientsts led led by Dr. Santosh Chuahan, have unrevealed mechanisms by which the protein aggregates are formed and degraded. They found that a protein named, TRIM16 governs the cell stress machineries to safely dispose the protein aggregates which otherwise could be cytotoxic. The work suggests that pharmacological activation of TRIM16 could be a useful strategy for therapeutic interventions of neurodegenerative diseases. This work is published in the recent issue of "The EMBO Journal".

The study showed that the cancer cells can highjack the TRIM16 governed cell stress machinery so that they can survive under harsh cellular stress conditions including oxidative stress. They found that knocking out this protein in cancer cells make them vulnerable and cannot tolerate the oxidative stress succumbing them to death. Hence, the pharmacological down-regulation of TRIM16 could have direct implication in cancer therapy. The study was financially supported by DBT and The Wellcome Trust/DBT India Alliance.

Enzyme in milk production identified as target for novel breast cancer drugs

Charles Clevenger, M.D., Ph.D., and a team of researchers discovered that the enzyme cyclophilin A (CypA) regulates the Jak2/Stat5 genetic pathway. This pathway is responsible for the natural maturation of mammary glands as well as the development of breast cancer cells.

"This research identifies cyclophilin A as a relevant target for therapeutic intervention in breast cancer. Because FDA-approved drugs are available to inhibit the action of CypA, translation of these findings to breast cancer patients should be rapid," said Clevenger, interim associate director for basic research, member of the Cancer Cell Signaling research program and Carolyn Wingate Endowed Chair in Cancer Research at VCU Massey Cancer Center. "No study to date had previously examined the loss of CypA func-

tion during mammary development and the formation of cancer."

By deleting the CypA enzyme in mouse models with ER-positive and ER-negative breast cancer, Clevenger and his team were able to inhibit the activation of the Stat5 pathway. This inhibition correlated to an increase in mammary tumor latency, which means they were able to slow or completely halt the growth of breast cancer cells.

The discovery of CypA's contribution to the development of breast cancer was helped by previous observations of prolactin receptor (PRLr) signaling. Prolactin is the hormone that is primarily responsible for the production of milk during pregnancy, and earlier research by Clevenger has also linked it to the growth of breast tumors. By more closely analyzing the genetic pathways associated with PRLr signaling (including Jak2 and Stat5), CypA was revealed to be a major participant in the activation of those pathways.

"This study demonstrated many similarities to other loss-of-function mouse models of the PRL-PRLr-Jak2-Stat5 signaling pathway. However, what distinguishes the CypA-deprived mouse models from the other genetic deletion models was the mice's ability to still successfully lactate and nurse their offspring, despite the loss of an enzyme critical to mammary gland development," said Clevenger, who is also the chair of pathology at the VCU School of Medicine.

Clevenger believes the mice's continued ability to lactate is related to the fact that there is a significant, but not complete, deactivation of the Jak2/Stat5 signaling pathways.

The research, published in Cancer Research, builds upon a decade of work performed in Clevenger's labs at Massey and Northwestern University. He said he and his team will continue to conduct further studies in pre-clinical models.

Clevenger collaborated on this research with Sonja Volker and Shannon Hedrick of Massey and the VCU Department of Pathology, and Yvonne Feeney of Northwestern University.

Journal Reference:
Sonja E. Volker, Shannon E. Hedrick, Yvonne B. Feeney, Charles V. Clevenger. Cyclophilin A Function in Mammary Epithelium Impacts Jak2/Stat5 Signaling, Morphogenesis, Differentiation, and Tumorigenesis in the Mammary Gland. Cancer Research, 2018; 78 (14): 3877 DOI: 10.1158/0008-5472.CAN-17-2892

First interactive model of human cell division

In 2010, a large study led by the same EMBL group identified which parts of the human genome are required for a human cell to divide, as part of the EU MitoCheck project. But cells don't run on genomic DNA; they run on the proteins it encodes. Proteins carry out most of the work in a cell, forming the cell's operational level. Processes like mitosis require the tight coordination of hundreds of different proteins in space and time. Proteins often work in groups, similar to the specialist teams of construction workers on a large building site.

"Until now, individual labs have mostly been looking at single proteins in living cells," says Jan Ellenberg, the group leader at EMBL who led the project. "Supported by the follow-up EU project MitoSys we were now able to take a systems approach, and look at the bigger picture by studying the dynamic networks many proteins form in living human cells."

The resulting Mitotic Cell Atlas integrates these data in an interactive 4D computer model. In this public resource, scientists can freely choose any combination of mitotic proteins and see in real time where and with whom they work during cell division.

Five different proteins are tracked during cell division (from metaphase to telophase): AURKB (red), NUP107 (green), CENPA (purple), CEP192 (yellow), and TUBB4B (cyan). The video* represents what users could create by themselves when using the mitotic cell atlas homepage: http://www.mitocheck.org/mitotic_cell_atlas/

The current study looked at HeLa cells, a widely used line of human cancer cells. 28 proteins that are important for mitosis were made fluorescent mostly by CRISPR/Cas genome editing. These proteins were then tracked using 3D confocal microscopy, to see where in the cell they're located at each point in time. The microscope is so sensitive that it's even possible to count the proteins, so researchers know now if there are 100, 1000 or 10.000 proteins in a certain location. For all proteins, these data were integrated into an interactive computer model -- the creation of which was actually the largest part of the project.

In total, there are about 600 different proteins involved in mitosis in human cells. Completing the dataset for all 600 would allow scientists to fully understand the transmission of information within a dividing cell, and how decisions -- like going from one cell cycle phase to the next -- are made. This will take several more years of work. "At EMBL, we're constantly adding information to the atlas by imaging more proteins in the same standardized way" says Stephanie Alexander, research manager in EMBL's Ellenberg group. "In the long run, a full overview of all the cell's proteins will allow us to see how different important processes of life, like cell division and cell death for example, are linked to one another. You can only understand this from a network point of view."

Journal Reference:
Yin Cai, M. Julius Hossain, Jean-Karim Hériché, Antonio Z. Politi, Nike Walther, Birgit Koch, Malte Wachsmuth, Bianca Nijmeijer, Moritz Kueblbeck, Marina Martinic-Kavur, Rene Ladurner, Stephanie Alexander, Jan-Michael Peters, Jan Ellenberg. Experimental and computational framework for a dynamic protein atlas of human cell division. Nature, 2018; DOI: 10.1038/s41586-018-0518-z

Genes are key to academic success, study suggests

For many years, research has linked educational achievement to life trajectories, such as occupational status, health or happiness. But if performing well in school predicts better life outcomes, what predicts how well someone will do throughout school?

"Around two-thirds of individual differences in school achievement are explained by differences in children's DNA," said Margherita Malanchini, a psychology postdoctoral fellow at the Population Research Center at UT Austin. "But less is known about how these factors contribute to an individual's academic success overtime."

Malanchini and Kaili Rimfeld, a postdoctoral researcher at the Institute of Psychiatry, Psychology and Neuroscience at King's College London, analyzed test scores from primary through the end of compulsory education of more than 6,000 pairs of twins.

Researchers found educational achievement to be highly stable throughout schooling, meaning that most students who started off well in primary school continued to do well until graduation. Genetic factors explained about 70 percent of this stability, while the twins shared environment contributed to about 25 percent, and their nonshared environment, such as different friends or teachers, contributed to the remaining 5 percent.

That's not to say that an individual was simply born smart, researchers explained. Even after accounting for intelligence, genes still explained about 60 percent of the continuity of academic achievement.

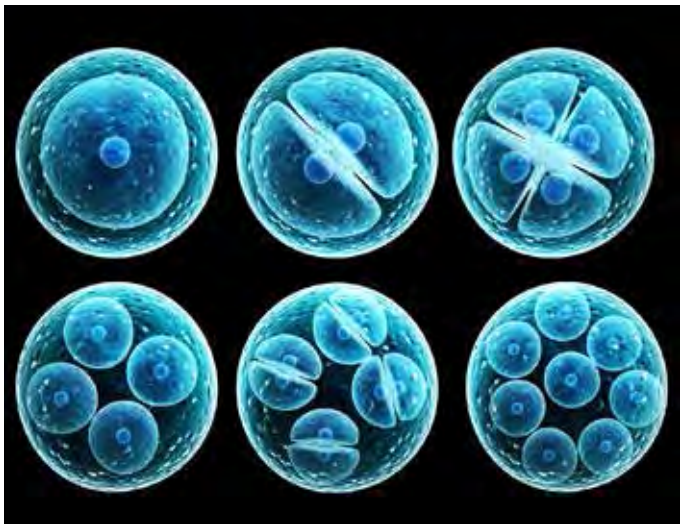
"Academic achievement is driven by a range of cognitive and noncognitive traits," Malanchini said. "Previously, studies have linked it to personality, behavioral problems, motivation, health and many other factors that are partly heritable."

However, at times grades did change, such as a drop in grades between primary and secondary school. Those changes, researchers said, can be explained largely by nonshared environmental factors.

"Our findings should provide additional motivation to identify children in need of interventions as early as possible, as the problems are likely to remain throughout the school years," said Rimfeld.

Journal Reference:
Kaili Rimfeld, Margherita Malanchini, Eva Krapohl, Laurie J. Hannigan, Philip S. Dale, Robert Plomin. The stability of educational achievement across school years is largely explained by genetic factors. npj Science of Learning, 2018; 3 (1) DOI: 10.1038/s41539-018-0030-0

Properties of stem cells that determine cell fate identified



Published in Stem Cell Reports, the study was led by Lisa A. Flanagan, PhD, an associate professor of neurology at UCI School of Medicine, and revealed that neural stem cells differing in fate potential expressed distinct patterns of sugars on the cell surface. These sugars contribute to neural stem cell membrane electrical properties and ultimately cell fate. "Stem cells hold great promise for treating disease, but it can be difficult to tell what a stem cell will become after it has been transplanted," said Flanagan. "We can transplant the same number of stem cells in one patient as in another, but the outcomes will be significantly different if the transplanted cells in the first patient become neurons and those in the second patient become astrocytes. With this new discovery, we will be able to predict what a neural stem cell will become and possibly direct cell fate, which will greatly enhance the success of stem cell transplant therapies for a wide variety of diseases."

In research initially published in 2008, Flanagan and colleagues discovered a new way to identify and sort neural stem cells that have different fates by using cell electrical properties. They now build on these findings by showing that differences in cell surface sugars are the reason that the cells have different electrical properties.

In this study, researchers examined several pathways that add sugars to cells and found one that differed between cells that make neurons and those making astrocytes. They stimulated this pathway in neural stem cells, changed cell electrical properties, and caused them to make more astrocytes and fewer neurons, showing that cell surface sugars can control fate. The pathway is active in cells grown for transplants and in cells of the developing brain, so this pathway may also control how neural stem cells form neurons and astrocytes when the brain is being formed during development.

The team is now testing whether modifying this pathway changes how cells behave in transplants or how the developing brain is formed. They are focusing on the machinery inside the cell that adds the sugars in the first place, to see how the process is regulated. They also are finding that particular proteins on the cell surface are changed by this pathway, which will help to uncover how the sugars are telling stem cells which type of cell to form. The long-term goal of these studies is to find ways to improve the effectiveness of stem cell transplants to treat injury and disease.

Journal Reference:
Zihao Sun, Minzhe Zhu, Pin Lv, Lu Cheng, Qianfeng Wang, Pengxiang Tian, Zixiang Yan, Bo Wen. The Long Noncoding RNA Lncenc1 Maintains Naive States of Mouse ESCs by Promoting the Glycolysis Pathway. Stem Cell Reports, 2018; DOI: 10.1016/j.stemcr.2018.08.001

Scientists develop new drug treatment for TB

The team hope the compound -developed after 10 years of painstaking research will be trialled on humans within three to four years.

The drug- which works by targeting Mycobacterium tuberculosis' defences rather than the bacteria itself -- can also take out its increasingly commonly antibiotic resistant strains.

The research funded by the Medical Research Council -- is published today in the Journal of Medicinal Chemistry.

Although a vaccine for TB was developed 100 years ago, one in three people across the world are thought to be infected with the infectious disease.

About 1.7 million die from the bug each year worldwide and 7.3 million people were diagnosed and treated in 2018, up from the 6.3 million in 2016.

It is most common in Africa, India and China, but on the rise in the UK with London often described as the TB capital of Europe.

Patients are forced to take a cocktail of strong antibiotics over 6 to 8 months, often enduring unpleasant side effects with a 20% risk that the disease will return.

But now The University of Manchester team's discovery has been proven effective in guinea pigs at Rutgers University in the United States.

The animals with acute and chronic TB infection were treated with the compound, which was discovered after investigating dozens of other derivatives and compounds thought to have similar properties.

Professor Lydia Tabernero is the project leader. She said: "The fact that the animal studies showed our compound, which doesn't kill the bacteria directly, resulted in a significant reduction in the bacterial burden is remarkable.

"For more than 60 years, the only weapon doctors have been able to use against TB is antibiotics. But resistance is becoming an increasingly worrying problem and the prolonged treatment is difficult and distressing for patients.

"And with current treatments, there's no guarantee the disease will be eliminated: antibiotics do not clear the infection and the risk of being infected with drug-resistant bacteria is very high.

"But by disabling this clandestine bacteria's defences we're thrilled to find a way that enhances the chances of the body's immune system to do its job, and thus eliminate the pathogen."

Mycobacterium Tuberculosis secretes molecules called Virulence Factors -- the cell's secret weapon -which block out the immune response to the infection, making it difficult to treat.

The team identified one Virulence Factor called MptpB as a suitable target, which when blocked allows white blood cells to kill Mycobacterium Tuberculosis in a more efficient way

Professor Tabernero added: "The great thing about MptpB is that there's nothing similar in humans -- so our compound which blocks it is not toxic to the human cells.

"Because the bacteria hasn't been threatened directly, it is less likely to develop resistance against this new agent, and this will be a major advantage over current antibiotics, for which bacteria had already become resistant.

"TB is an amazingly difficult disease to treat so we feel this is a significant breakthrough.

"The next stage of our research is to optimise further the chemical compound, but we hope Clinical trials are up to four years away."

Publisher retracts two papers, will correct five more for lab with high "level of disorganization"

A lab at the University of Malaya has lost two papers and will have to correct five more — just from one publisher — over poor lab practices.

One of the retracted papers paper tested the effects of a plant on liver damage; its notice says the paper contains overlap with another paper from the same lab that tested a different plant for the same effect — but to save time and cut costs, the authors tested both plants in animals at the same time, and collected their tissues using one kit and protocol.

The publisher (Hindawi) decided to take a second look at the work coming out of the lab of Mahmood Ameen Abdulla after people raised questions about some of his previous work, including a Scientific Reports paper that was corrected for mistaken duplications, according to Matt Hodgkinson, the head of research integrity at Hindawi. After Hindawi spotted problems, it contacted the institution, which investigated.

This isn't the first time UM has had to deal with image problems from one of its labs; in 2016, the institution acted quickly after Twitter users posted concerns about some figures that appeared to be obviously duplicated. Within a week, UM posted a statement that reported four papers from the lab contained duplication and/or manipulation.

Researcher who once tried to sue critics has another dozen papers retracted

A cancer researcher who went to court — unsuccessfully — claiming that commenters on PubPeer had cost him a new job has just lost another 12 papers.

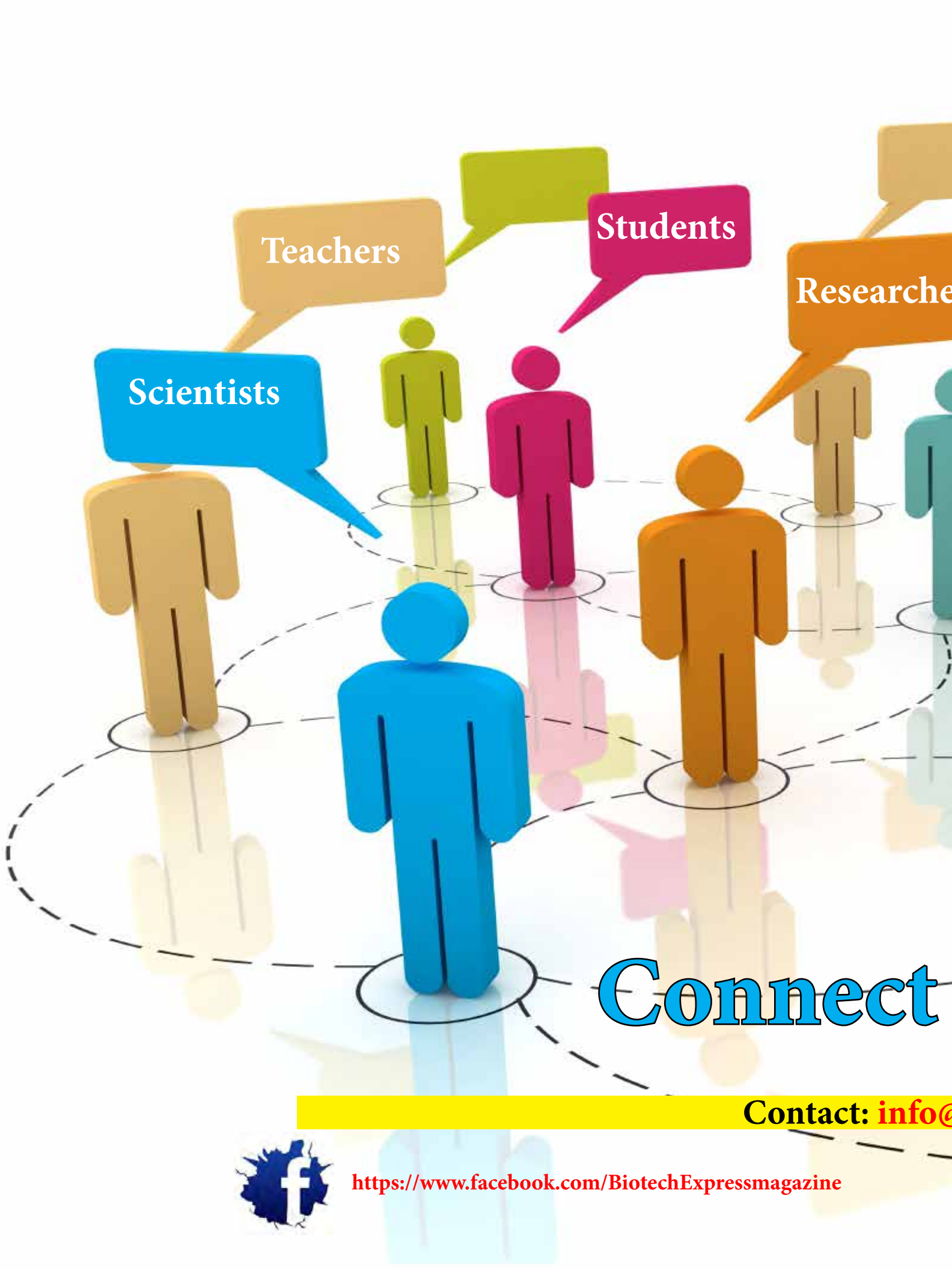
The twelve now-retracted papers by Fazlul Sarkar and colleagues — as well as another by Sarkar that is now subject to an editor's note — all appeared in Cancer Research, which made for a long table of contents in its September 15 issue.

The papers were cited anywhere from 39 to 276 times, according to Clarivate Analytics' Web of Science, with the top citation earner named a "highly cited paper," meaning it was cited more than 99% of all other papers in its field published the same year.

By our count, Sarkar is now up to 33 retractions, at least a dozen corrections and one editor's note. An investigation at Wayne State found that he had engaged in widespread misconduct, and recommended that 42 of his papers be retracted.

According to the retraction notices, the journal sent copies of all 12 to Sarkar's last known email address, but he did not respond. In most cases, at least one of the other authors agreed with the retractions.

Earlier this month, the American Association for Cancer Research, which publishes Cancer Research, retracted 10 papers from various journals and apologized for how slowly they had handled such cases. Publisher Christine Rullo also wrote that "It will take several months to publish various types of corrections related to a number of older cases on which we are working."



Connect

Contact: info@

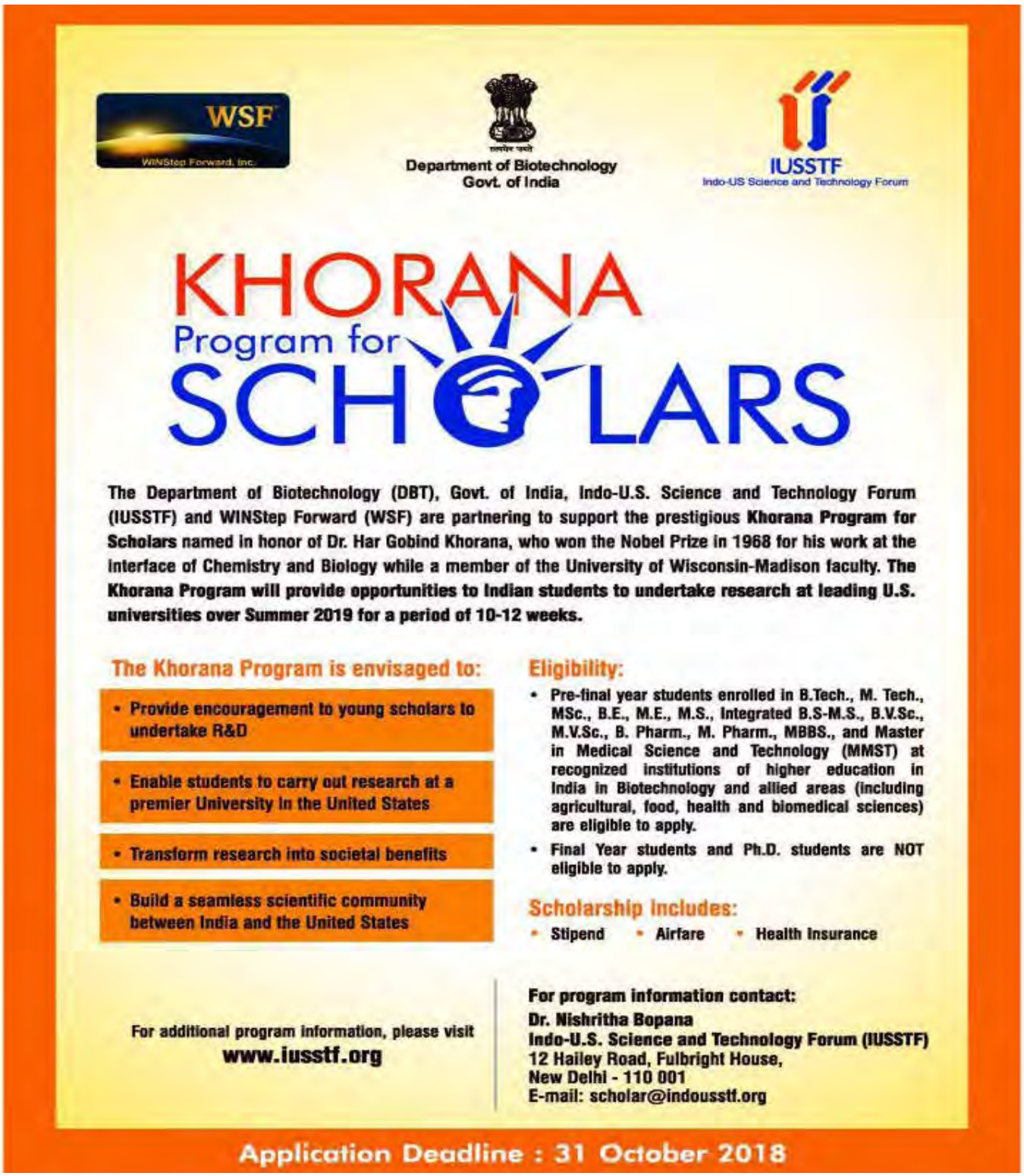
https://www.facebook.com/BiotechExpressmagazine

with peers

@kashbiotech.com

https://in.linkedin.com/in/kashbiotech

NOTIFICATIONS



SATHYABAMA

INSTITUTE OF SCIENCE AND TECHNOLOGY

(DEEMED TO BE UNIVERSITY)

NATIONAL CONFERENCE

ON

COMPUTATIONAL BIOLOGY & MEDICAL BIOTECHNOLOGY

IN

HEALTH CARE

(CBMH 18)

9th - 11th October 2018

ORGANISED BY

DEPARTMENT OF BIOINFORMATICS

SCHOOL OF BIO AND CHEMICAL ENGINEERING

SATHYABAMA INSTITUTE OF SCIENCE AND TECHNOLOGY

CHENNAI-600119

CHIEF PATRON

Smt. REMIBAI JEPPIAAR

CHANCELLOR

PATRONS

Dr. MARIE JOHNSON

B.E., M.B.A., Ph.D.,

PRESIDENT

Dr. MARIAZEENA JOHNSON

B.E., M.B.A., Ph.D.,

PRO - CHANCELLOR

CONVENORS

Dr. SWETHA SUNKAR

Dr. JEMMY CHRISTY

ADVISORY COMMITTEE

Dr. S.SUNDAR MANOHARAN Ph.D.,

VICE - CHANCELLOR

Dr. T.SASIPRABA Ph.D.,

PRO – VICE CHANCELLOR

Dr. S.S.RAU M.B.A Ph.D.,

REGISTRAR

Dr. B.SHEELA RANI Ph.D.,

DIRECTOR OF RESEARCH

Dr. S. IGNI SABASTI PRABU Ph.D.,

COE

ORGANIZING MEMBERS

Dr. C. JAYNTHY

Dr. ALEX ANAND

Dr. K. BALASANKAR

Organizing Institute: IIT Kharagpur

JAM 2019

Joint Admission Test for M.Sc.

ABOUT JAM

National test for admission to M.Sc. (Two years), Joint M.Sc.-Ph.D., M.Sc.-Ph.D. Dual Degree, M.Sc.-M.S. (Research)/Ph.D. Dual Degree and other Post-Bachelor Degree programmes at IITs (Bhubaneshwar, Bombay, Delhi, Dhanbad, Gandhinagar, Guwahati, Hyderabad, Indore, Jodhpur, Kanpur, Kharagpur, Madras, Patna, Roorkee, Ropar and Varanasi) for the Academic Session 2019-20. JAM score will be used by IISc Bangalore for admission to Integrated Ph.D. programmes. JAM score will also be used by other centrally funded technical institutions like NITs, IIEST Shibpur, SLIET Punjab and IISERs for admission to their programmes.

STRUCTURE AND MODE OF JAM 2019

JAM 2019 examination will be conducted ONLINE only. A candidate can appear in either one Test Paper or two Test Papers by paying an additional fee for the second test paper. Candidates opting to appear in two Test Papers must ensure that the opted Test Papers are not scheduled in the same session.

IMPORTANT DATES FOR JAM 2019

01 September 2018	ONLINE Registration and Application Process
01 October 2018	Closure of ONLINE Application Process
10 February 2019	JAM 2019 Examination
20 March 2019	Announcement of JAM 2019 Results

EXAMINATION CITIES & TOWNS

Agra, Ahmedabad, Allahabad, Asansol-Durgapur, Bareilly, Bengaluru, Bhopal, Bhubaneswar, Chennai, Coimbatore, Dehradun, Dhanbad, Dibrugarh, Ernakulam, Faridabad, Ghaziabad, Goa, Greater Noida, Gurugram, Guwahati, Hisar, Hubli, Hyderabad, Indore, Jaipur, Jalandhar, Jammu, Jodhpur, Jorhat, Kalyani, Kannur, Kanpur, Kharagpur, Kolkata, Kollam, Kottayam, Kozhikode, Kurukshetra, Lucknow, Madurai, Mangalore, Mohali, Moradabad, Mumbai, Nagpur, Nanded, Nasik, New Delhi, Noida, Palakkad, Patna, Pune, Raipur, Ranchi, Roorkee, Siliguri, Thiruvananthapuram, Thrissur, Tiruchirapalli, Tirunelveli, Vadodara, Varanasi, Vijayawada, Visakhapatnam and Warangal.

Note: The JAM 2019 Committee may add and/or drop any place as an examination city/town at its discretion.

INFORMATION BROCHURE AND APPLICATION PROCEDURE

Refer to http://jam.iitkgp.ac.in for the downloading of Information Brochure and the details of application procedure.

GROUP / CATEGORY	FEE DETAILS	
	One Test Paper	Two Test Papers
Female (All Categories)/ SC/ST/PwD	Rs. 750/-	Rs. 1050/-
All Others	Rs. 1500/-	Rs. 2100/-

PATTERN OF TEST PAPERS

JAM 2019 Test papers will be fully objective type, with three patterns of questions: (i) Multiple Choice Questions (MCQ), (ii) Multiple Select Questions (MSQ), and (iii) Numerical Answer Type (NAT) questions.

JOINT ADMISSION PROCEDURE

Admissions to various academic programmes at IITs for the Academic Session 2019-2020 shall be made based on the All India merit list of JAM 2019. Candidates who qualify in any test paper of JAM 2019 will be eligible to apply for admission to all the academic programmes corresponding to that test paper, provided they also satisfy the minimum educational qualifications and the eligibility requirements as specified by the institute(s) in which admission is sought. Admission shall be given in the order of merit depending on the number of seats available at the admitting institute(s). After the declaration of JAM 2019 results, qualified candidates should apply online at common admission portal (JOAPS) through the Organizing Institute (IIT Kharagpur) specifying preferences for the programmes of their interest. Further details regarding admission, prescribed fees, etc. are available on the JAM 2019 website. Reservation policy is as per the Government of India norms.

ELIGIBILITY REQUIREMENTS AND MINIMUM EDUCATIONAL QUALIFICATIONS (MEQ) FOR ADMISSION

In the qualifying degree, the aggregate marks or CGPA/CPI without rounding-off (taking into account all subjects, including languages and subsidiaries, all years combined) should be at least 55% or 5.5 out of 10 for General/OBC (NCL) category candidates and 50% or 5.0 out of 10 for SC/ST and PwD category candidates (If CGPA/CPI is on a different scale, it would be linearly mapped to a scale on 10) .

Refer to http://jam.iitkgp.ac.in for MEQ and other details. Proof of having passed the qualifying degree with the required eligibility, as specified by the admitting institute, should be submitted by September 30 , 2019.

JAM 2019 SCHEDULE

EXAM DATE	SESSION & TIME	TEST PAPERS & CODES
10 February 2019 (Sunday)	Session I 9:00 AM to 12:00 Noon	Biological Sciences (BL), Mathematics (MA) and Physics (PH)
	Session II 02:00 PM to 5:00 PM	Biotechnology (BT), Chemistry (CY), Geology (GG) and Mathematical Statistics (MS)

CONTACT DETAILS OF JAM OFFICES

Institute	Website	E-mail
IISc Bangalore	http://gate.iisc.ac.in/jam	jam@gate.iisc.ac.in
IIT Bombay	http://www.gate.iitb.ac.in/jam	jam@iitb.ac.in
IIT Delhi	http://jam.iitd.ac.in	jam@admin.iitd.ac.in
IIT Guwahati	http://iitg.ac.in/gate-jam	jam@iitg.ac.in
IIT Kanpur	http://gate.iitk.ac.in/jam	jam@iitk.ac.in
IIT Kharagpur	http://jam.iitkgp.ac.in	jam@adm.iitkgp.ac.in
IIT Madras	http://jam.iitm.ac.in/	jam@iitm.ac.in
IIT Roorkee	http://www.iitr.ac.in/jam	jam@iitr.ac.in

SELECTBIO *Conferences*

DRUG DISCOVERY INDIA 2019

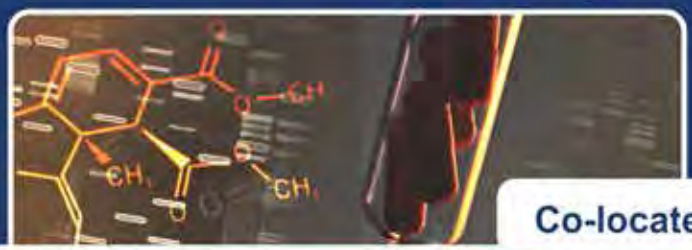
Breakthrough Research in

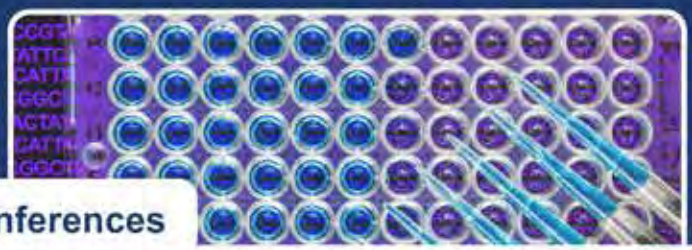
Medicinal Chemistry

11-12 October 2018

Advanced

Omics Technologies & Approaches





Co-located Conferences

FOR DETAILS, CONTACT

DDI: p.sharma@selectbio.in | 7696325050 | **AOTA:** g.sharma@selectbio.in | 7696025050

Registration: f.zainab@selectbio.in | 7696125050 | **Exhibition:** mjsingh@selectbio.in | 7696225050

For a quick response, just **WhatsApp: 9041725050**

SELECT BIOSCIENCES INDIA PVT LTD

"NGS has made it possible to derive meaningful information for potential clinical applications"

Translating NGS from Research to Clinical Genetic Testing

International Conference

Next Generation Sequencing *in* Clinical Genomics

Applications and Advances

29 - 30 November 2018 • Bengaluru, India

Organized by

SELECTBIO

www.selectbio.com

9041725050

AGENDA TOPICS

- **Oncology**
  - Hereditary Cancers, Liquid Biopsy, Tumor Mutation Burden
  - Precision Medicine
- **Genetic Disorder and Reproductive Medicine**
  - NIPT, PIGS, PTB, Rare Genetic Disorders
- **Genetic Disorder and Infectious Diseases**
  - Clinical Exome, Metagenomics, Twin Pregnancy - NIPS
- **NGS Data Analysis and Interpretation**
  - Data Quality and Interpretation, NGS Validation/Guidelines

5 BENEFITS OF ATTENDING

- Learn, Discuss and Collaborate
- Pertinent Talks, Panel Discussion and Technology Display
- Renowned Overseas and Indian Speakers
- Great Networking Opportunity
- Exclusive Gathering of Clinical and Diagnostic Fraternity

Register NOW!

For queries, contact

Talks & Topics: g.sharma@selectbio.in | 7696025050
Registration: f.zainab@selectbio.in | 7696125050
Exhibition: mjsingh@selectbio.in | 7696225050

RNI No. UPENG/2013/54102
ISSN: 2454-6968

Subscribe

Biotech Express

Go Green

Starting from @ Rs. 600 yearly and Rs. 6000 Lifetime only

Digital

Email delivery

Subscribe here: kashbiotech.com/biotech-express-magazine/biotech-express-subscription-plans/