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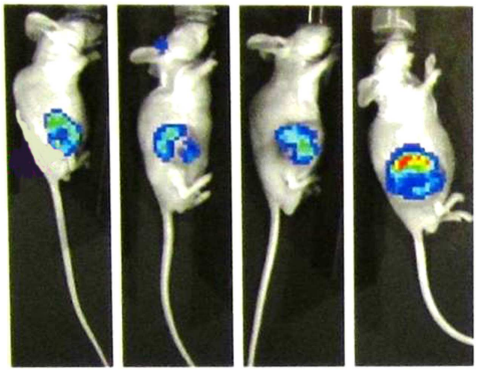
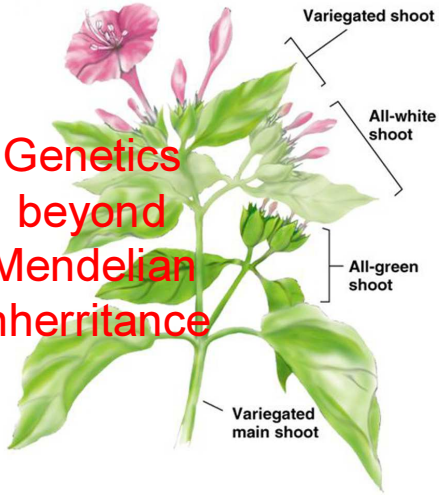
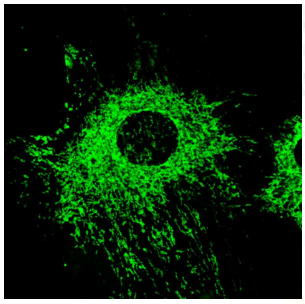
Cell Biology Newsletter

Tumor localization of luminescent Salmonella



Genetics beyond Mendelian inherritance





Mitochondria revisited

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Forty Years of Indian Society of Cell Biology

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This year the Indian Society of Cell Biology (ISCB) is completing four decades of its existence. A series of Cell Biology Conferences organized during 1960s and early 1970s by the Department of Zoology of Delhi University under the leadership of Prof. B. R. Seshachar and his colleagues (Drs. C. M. S. Dass, V. C. Shah and S. R. V. Rao) catalyzed the establishment of Indian Society of Cell Biology. For someone like me, who has been associated with the Cell Biology meetings since late 1960s and with the ISCB since its inception, the growth of the Society is indeed greatly satisfying. During the four decades of its existence, the ISCB has witnessed a remarkable transformation in its subject coverage from mostly Cytology and Cytogenetics to more contemporary Cell and Molecular Biology. Its membership has increased substantially and now covers almost the entire geographical area of the country. Expertise of its members spans all the contemporary areas that relate to Cell Biology. It is indeed a very healthy sign of growth that the annual meetings of the ISCB are held regularly and each meeting enriches the membership of the society through enrolment of new younger colleagues. The increasing numbers of Endowment lectures and young scientists' awards have also enriched the academic quality of presentations at the annual meetings.

The ISCB is poised for tremendous growth in the coming years as the overall quality of research in the country improves and diversifies. The Society must continue to enlarge its base through the continued expansion of its membership. However, as it grows, its management also needs equally involved participation of all its members. The founders of ISCB ensured a much wider participation of its fraternity in management by ensuring that the election of its office-bearers is held regularly and no individual or group can continuously hold its reins. This must continue through enthusiastic coming forward of new members to take the responsibility. Elections for the new office-bearers are due this year: let more groups come forward to offer themselves to take the leadership and let an increasing number of members participate in this democratic election process.

I would like to also note some disconcerting trends noticed in recent annual meetings. Some of the invited speakers attend the meeting only to deliver their talks with little time for the off-stage interactions with other members, especially the younger ones. This not only deprives the eager younger members to learn from the experienced researchers but, in my view, the invited speaker also misses the remarkable opportunities to think beyond his/her own research. I think the meeting organizers should make all efforts to impress upon the invited speakers to stay beyond their talks and interact more freely with other participants. The other concern is the limited time available for poster sessions. In spite of the ISCB guidelines, the local organizers feel tempted to have a larger number of invited talks which finally cuts into the poster session time. This gets compounded by speakers over-shooting their allotted time. The time allotted for poster sessions comes handy to the organizers to buffer the delays. This is indeed an unfortunate situation. We need to seriously curb this practice and ensure that young students, who are the main contributors to the posters, have equal opportunity to share their findings with others and also have the advantage of good peer-review by more experienced researchers. I may also note that the "senior" members should also seriously visit the posters rather than taking these sessions as “leisure time”.

I congratulate all members of ISCB and the generations of office-bearers that have steered the Society during the past forty years to the present forward-looking and continuously growing phase. A very good opportunity to show-case the strength of Cell Biology in the country is provided by the proposed IFCB congress in India in 2018. We all need to put our strengths together to not only ensure that this congress is organized well but also to provide adequate opportunities to our young cell biologists so that they take full advantage of the presence of internationally acclaimed experts.

I have no hesitation in stating that attending the annual Cell Biology meetings has been a great learning experience for me – sitting through the lectures and discussing the studies carried out by young researchers during the poster sessions have greatly enriched my own understanding of the rapidly growing discipline of Cell Biology. These have also provided new perspectives to my own research. I am sure many more members would have had, and would continue to have the same pleasure.

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Professor Jyotirmoy Das
(1939-1998)

Professor Jyotirmoy Das was born in 1939 in old Calcutta. He was an archetypical Bengalee youth of those days with a streak of idealism, respect for a scholarly life and love for poetry and Rabindra Sangeet. Tagore and Elliot were his lifelong favorites. With a brilliant academic record, he inevitably went for engineering but promptly returned to basic sciences and obtained his master's degree in physics from Calcutta University in 1960.

He obtained his doctorate degree in biological sciences from Calcutta School of Tropical Medicine where he extensively worked on electron microscopy of *Vibrio cholerae* an organism that fascinated him throughout his life. His post Ph.D. exposure in the Department of Microbiology in the University of Rochester and a long stay in United States made him a hardcore molecular biologist. He returned to India in 1977 and joined as a faculty in Bose Institute for short period and then moved to IICB as Head of the Biophysics Division in 1979. Thereafter, he led original and innovative research work both on molecular biology of *Vibrio cholerae* and in theoretical biology, which quickly distinguished him as a scientist of great talent and remarkable drive. He became the director of IICB in December 1995 and continued till 26th July 1998. His major research interest was elucidation of the molecular basis of pathogenicity of *V. cholerae*. He was one of the scientists at the forefront to establish recombinant DNA technology in this country during the late seventies. Once again in nineties, he initiated pioneering work on the newly emerging areas of bacterial genome mapping and comparative genomics with *V. cholerae,* as a model organism. Continuing with his work on *V. cholerae* genetics, he showed remarkable originality, freshness of mind and with his love for abstract thinking, developed a totally diverse project on theoretical biology and mathematical modeling. He proposed a new theory of self-organization in non-ideal biochemical system and contributed significantly.

Professor Das was an extraordinarily dynamic person whose commitment towards research and science was total. His ultimate passion was always to be personally in the frontiers of international biotechnological research. He was very closely involved with the growth of the Department of Biotechnology (DBT) from the very beginning and believed to be one of the architects of Modern Biology and Biotechnology in India. Professor Das was a fellow of the Indian National Science Academy, the Indian Academy of Science, Bangalore and the National Academy of Sciences India, Allahabad. His outstanding contributions were honored with a large number of prestigious awards. He also served as an advisory capacity in many scientific bodies, funding agencies and research institutes. Hesuddenly passed away on July 26, 1998 at the age of 59 after a brief illness and respiratory failures.

Indian Society of Cell Biology immortalized Professor Das contributions in modern biology and biotechnology by instituting "Prof. Jyotirmoy Das Memorial Lecture" in year 2000 and its first lecture was delivered by notable eminent scientist and academician Professor P. Balram in year 2001.

To honor Professor Jyotirmoy Das, Indian Society of Cell Biology at its 39th meeting at IISER-TVM, Thiruvananthapuram, has decided to deliberate a talk by the eminent scientist and renowned academician Professor Jaya Sivaswami Tyagi.

The TB bug:
From gene discovery to strategies for the control of tuberculosis

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Area of research interest
Molecular and Cellular Biology of Infectious disease (Tuberculosis)

Tuberculosis (TB) is an enormous public health challenge world-wide. Approximately one-third of the world's population harbors a latent TB infection which greatly complicates efforts aimed at TB control. The success of the TB pathogen (Mtb) is attributed in significant measure to its ability to survive indefinitely in a dormant state within the host as a latent infection. Therefore, a priority research goal is to understand the properties of dormant bacteria in order to devise more effective strategies for TB control and to prevent reactivation and clinical disease.

DevR is a transcriptional regulator that was discovered by subtractive RNA hybridization in my laboratory. Together with DevS, it forms a bonafide two-component signaling system of Mtb, which controls the expression of the DevR regulon in dormancy models in response to hypoxia and other gaseous signals. We have characterized this signal transduction pathway and established that its interception blocks hypoxia-mediated dormancy adaptation of TB bacilli.

There is an urgent need in India and other countries for sensitive, specific and rapid diagnostic tools for tuberculous meningitis (TBM), the most common form of neurotuberculosis. Early diagnosis and prompt treatment are the cornerstones of effective TBM management. The accurate diagnosis of TBM poses a challenge due to an extensive differential diagnosis, low bacterial load and paucity of cerebrospinal fluid (CSF), especially in children. We have demonstrated that DNA and TB antigen based assays accurately detected TBM samples at a specificity of ~90 % and sensitivity >92 %. The development of rapid and sensitive point-of-care TB antigen based diagnostic tests is in progress. Apart from its diagnostic value, the detection of HspX dormancy antigen discloses the presence of metabolically heterogeneous bacterial populations in CSF of TBM subjects.

39th All Indian Cell Biology conference on

"Cellular Organisation and Dynamics"

6th -8th December 2015 | KTDC Samudra, Kovalam

39th All Indian Cell Biology conference entitled **"Cellular Organisation and Dynamics"** was organised by Indian Institute of Science Education and Research Thiruvananthapuram (IISER-TVM) and Rajiv Gandhi Centre for Biotechnology (RGCB) at Kovalam during Dec. 6-8, 2015.. Prof. Radhakrishna Pillai, Director of the Rajiv Gandhi Centre for Biotechnology and Prof V Ramakrishnan, Director, Indian Institute of Science Education and Research Thiruvananthapuram, extended a warm welcome followed by release of conference souvenir by Prof Ramakrishnan. Prof Nagaraja, President of the Indian Society of Cell Biology, Prof. Hari Misra, Secretary, ISCB, Prof Srinivasa M Srinivasula, organising secretary of the conference along with Director, RGCB and IISER-TVM, light the lamp and conference was inaugurated and opened by deliberations.

The scientific sessions started with first talk by President Prof V. Nagaraja, who intrigued everyone by asking a question that shook the fundamentals of cell biology as we have been learning it. Bacteria produce special enzymes called Restriction Enzymes, which cut DNA. It has long been thought that these enzymes cleave DNA at very specific locations. Prof Nagaraja questioned this assumption, by giving the example of one such enzyme isolated from the bacteria *Klebsiella pneumoniae*. This enzyme is 'promiscuous' it does not cleave at

specific locations! What are the advantages of such promiscuity was well conveyed through his lecture. Readers are advised to read his recent publications on this topic.

The Keynote Address of the conference was delivered by Carl Philipp-Heisenberg, a Group Leader at IST Austria, who works on Zebrafish model system. Heisenberg demonstrated the mechanisms by which the outermost layer of the embryos is formed. Heisenberg also showed that the spreading of the cells triggers the embryo to develop into the next stage; the formation of a dome-like layer of cells, called the blastoderm, on top of the yolk sac.

Satinath Mukhopadhyay from the Institute of Post Graduate Medical Education and Research, Kolkata, spoke on a topic of grave concern in the Indian context. He emphasized that diabetes is fast becoming an epidemic, with 415 million adults affected worldwide, with about 69 million in India. Mukhopadhyay and his colleagues have shown that a particular molecule secreted by the liver, called FetuinA, binds to free fatty acid molecules in the blood. This complex of fatty acids and FetuinA can together bind to certain structures on the cell membrane, leading to a condition called insulin resistance. Apurva Sarin from the National Centre for Biological Sciences spoke about her group's work on the mechanisms that control cell number. Sanjeev Gupta from the National University of Ireland, Galway spoke about the role of tiny messenger molecules in the cell called miRNAs and their role in adaptations to stress. Ravi Manjithaya from the Jawaharlal Nehru Center for Advanced Scientific Research spoke on the clean up mechanisms found in cells.

The second day of the conference witnessed high quality deliberations by many who covered topics focusing research on different processes that form the basis of life – from within cells to between cells, at the earliest stages of an organism's life to adulthood. How does a tiny one-celled embryo develop into an entire large organism? As the cells of the embryo divide after fertilization, all cells are the same in the initial stages. With time, different cells start making different proteins, and end up in different parts of an organism's body – the cells in your heart perform functions completely different from the cells in your brain, for example. These different functions require different 'hardware' – proteins on the cell membrane, in the cellular matrix; and different 'software' – different parts of the genome are active.

Apart from conference proceedings, Indian Society of Cell Biology also conducted one of the very important sessions on Prof. Jyotirmoy Das Memorial Lecture by Professor Jaya S Tyagi, AIIMS, New Delhi followed by

Annual General Body Meeting of the society. Prof. Nagaraja, the president of the society presented a Silver Medal and Citation to Prof. Tyagi.

Using fruitfly *Drosophila melanogaster* as a model system, labs have been studying the mechanisms that give a particular size and shape to an organ. In the fruitfly, the cells that go on to make the thin transparent wings and rigid supporting structures called halteres are exactly the same in the larval stage. How do they produce such different structures were narrated to audience with high quality research. Prof. Jagat Kumar Roy from Banaras Hindu University spoke about his lab's work on Rab11, a small protein found in *Drosophila*. They have shown the role of Rab11 in making muscle cells and the Malphigian tubules – the organ involved in excretion in the insect. Different organisms have different machineries for sensing their environment. Within our eyes for example are specialised cells that are sensitive to light; within our ears the cells on the eardrum respond to sound waves. The interaction between the stimulus and the outermost membrane of the receptor cells is a main determinant of the sensitivity of the sensory system. Raghu Padinjat from the National Centre for Biological Sciences, Bangalore, spoke about his group's work on how stimuli regulate membrane structure in photosensitive membranes in *Drosophila*. When we breathe in, special cells that line our respiratory tract help to filter out impurities. These cells are lined with 'cilia' – hair like outgrowths that beat continuously in the mucous lining our respiratory tract, and keep out bacteria and dust particles. Female ovaries also have hair-lined cells – they deliver the fertilized egg to the uterus. How are these cells made? – this was the thrust of Sudipto Roy's talk. Affiliated to the Institute of Molecular and Cellular Biology, Singapore, Roy also spoke about the defects that arise from improper development of cilia.

Our cells have genetic material within an area called the nucleus. To pack the material into the nucleus, there is a matrix of proteins. Rakesh Mishra from the Centre for Cellular and Molecular Biology has been working on how the matrix reorganises during cell division. Maithreyi Narasimha from the Tata Institute of Fundamental Research in Mumbai spoke of her research on developing embryos – how processes within a cell dictate the development of an embryo. Kaustuv Sanyal from the Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore works on yeast. More specifically, he works on how yeast chromosomes are pulled apart during cell division. He presented work on how this process occurs in two yeasts, which cause diseases: *Candida albicans* and *Cryptococcus neoformans*. The Japanese encephalitis virus (JEV) causes brain fever in humans, and is transmitted to humans through the bite of *Culex* mosquitoes. There have been frequent epidemics of encephalitis in much of South East Asia, China and India. The virus uses the host cell's protein synthesis machinery for itself, which is obviously detrimental to the host. Sudhanshu Vrati from the Translational Health Science and Technology Institute spoke about a specific aspect of the JEV – how exactly the JEV uses host proteins during its life cycle.

Conference also witnessed the vibrant poster session one each of the first two days. Several students presented their work in poster sessions and indeed pleasure to see that all the participants took parts in brain storming with young colleagues. A constructive criticism that poster session should have been longer duration business indicates the enthusiasm of people like to interaction directly with actual researcher s in our laboratories.

On 3rd and final day of the conference the lectures included on “An in planta model for the identification of combinatorial anti-cancer therapy regimens that target stemness”, by JianXu from the National University of Singapore. The ability to regenerate is essential after any injury, in both plants and animals. Xu will talk about

the interaction of plant-derived anti-cancer drugs with regenerating plant cells and their environment. “The phytohormonesabscisic acid and auxin crosstalk to mediate plant stress responses” by Prakash Kumar from the National University of Singapore. “Role of host cell proteins in Japanese Encephalitis Virus replication” by Sudhanshu Vrati from Translational Health Science and Technology Institute (THSTI), New Delhi. Japanese encephalitis virus (JEV) that is transmitted to human beings by mosquitoes is responsible for frequent epidemics of encephalitis in much of South East Asia, China and India. Vrati spoke about mechanisms in the virus replication, which can potentially help in finding ways to combat the virus.

In the afternoon, the successful conclusion of the conference witnessed prize distribution to young participants, words of praise for organizing a wonderful conference to conveners. On behalf of the Organizers, Professor S. Murty Srinivasula proposed vote of thanks, gratefully acknowledging the generous financial support received from, IISER Thiruvananthapuram, RGCB, KSCSTE, DST, Welcome DBT, JNCASR and various Corporations, members of various committees and participants.

LINKS

http://conference.iisertvm.ac.in/cbc/

Detailed schedule: http://conference.iisertvm.ac.in/cbc/?page_id=3610

ISCB: http://iscb.org.in/homepage.htm

IISER-TVM: http://www.iisertvm.ac.in

RGCB: http://rgcb.res.in

Mitochondria dynamics: the "moves" and "moods" of mitochondria

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Abstract

The power-house of the cell-mitochondrion is the dynamic organelle which exists in a form of network. Mitochondria can change its shape by continuous dividing, fusion and movement from one place to another along cytoskeletal machinery. Hence, the shape and length of mitochondria are dependent on fusion and fission rates. An increased fusion rate would lead to the mitochondrial elongation; whereas, an increases fission rate would lead to the mitochondrial fragmentation. Inside the cell, there are various factors or processes, which can influence the rate of fusion and fission. For example, during high glucose condition, fission takes over the fusion and mitochondrial fragmentation is seen. On the other hand, during starvation fusion takes over and we do see elongated mitochondria. The process of fusion and fission of mitochondria is governed by a several GTPases such as Dynamin-related GTPase 1 (DRP-1 controls fission), Mitofusin 1/2 (Mfn1 and Mfn2 controls inner membrane fusion) and OPA1 (controls outer membrane fusion). The balance between fusion and fission is very crucial as the disturbance in these processes is directly or indirectly linked with several neurodegenerative diseases. In this review, we will discuss in detail the process of mitochondrial dynamics and its players

Introduction:

The mitochondria are first described by Richard Altmann in 1890 as an "elementary organism" living inside the cell and termed them "bioblasts". The term "mitochondrion" was coined by Benda in 1898; it derives from Greek words, which means thread (mito) and granule (chondros), depicting to their heterogeneous morphology (O'Rourke et al., 2010). In the year 1914, Lewis and Lewis's observations laid the foundation of mitochondrial dynamics (Lewis, 1914). They observe the ever changing shape of a mitochondrion from granule to rod or thread and also that it can fuse with another mitochondrion. Mitochondria contain their own genome which is circular, similar to bacteria and have their own transcriptional and translational machinery (Schnare and Gray 1982; Spencer et al. 1984). Not only mitochondrial ribosomes and mRNA but also mitochondrial membrane is very much similar to that of bacteria. These observations laid the foundation of "endosymbiotic theory" of mitochondrial origin by

Dr. Lynn Margulis in the year 1970, according to that mitochondria were once a free-living organism, engulfed by the eukaryotic cell since they provide an evolutionary advantage in term of energy production, hence survived and live inside the host in a symbiosis (Margulis, 1970). The "endosymbiotic theory" is the widely accepted theory of the evolution and origin of the mitochondrial with no experimental evidence. Moreover, the majority of mitochondrial proteins are encoded by the nucleus, those involving mitochondrial dynamics as well. Mitochondrial DNA in humans is of 16,569 base pairs, encodes only 37 genes (Anderson et al. 1981, 1982;). Mutations in several genes are reported wherein mitochondrial dynamics plays a central role in the disease pathogenesis (Koopman et al., 2012). Interestingly, the emerging research suggests the involvement of disturbed mitochondrial dynamics in already well-known diseases those were thought of not involving mitochondria. Examples are cardiovascular diseases, neurodegenerative diseases, and cancer (Liesa et al., 2009).

Mitochondrial dynamics

As stated earlier, mitochondria can divide, fuse, move and can be degraded, if required. All these processes together fall under mitochondrial dynamics. The question is why each of these processes are important. What if mitochondrial be a static organelle, what is the need of it being dynamic. We can understand the importance of mitochondrial dynamics better in neurons, since neurons are the metabolically very active, with the long process and high energy demands at the end. Neurons are the most unique and specialized cells of the human body, where the axons can be as long as several feet. Since neurons have high energy demands; they are dependent on mitochondria for the functions (Kuznetsov et al., 2009). In the absence of fission, the mitochondrial would be long and interconnected which would result in the hindrance of their movements to the axonal terminus, where high energy is required (Chen et al, 2007). Fusion ensures the mixing of mitochondrial content by complementing the function of defective mitochondria, if fusion is absent mitochondria will be small and non-functional, leading to the energy deficit in the affected neuron. If the mitochondrial movement is absent there will be no distribution of mitochondria to the nerve endings, which will eventually lead to the compromised neuronal function. The clearing of damaged mitochondria known as "mitophagy" is the fourth arm of mitochondrial dynamics. In the absence of mitophagy, the cell would accumulate dysfunctional mitochondria eventually leading to energy deficit. The fine-tuned mitochondrial dynamics is very much required for the cells to perform the normal task assigned to them.

Fission

Fission produces smaller fragmented mitochondria, depending on the cellular demands. Fission can take place to serve the several purposes such as the distribution of organelles during division, makes smaller subunit of the mitochondria to make them easy to translocate to the site of high energy demand and the release of "cytochrome-c" to the cytoplasm during apoptosis. Interestingly, Fission can take place to eliminate the damaged portion from already existing mitochondria. Small fragmented mitochondrial are easy to clear off by mitophagy, so it is speculated that excessive fission preceded mitophagy. This is supported by the experiment wherein mitochondria are fluorescently labeled in cultured cell and after fission out of two, one mitochondrion was always found to have low mitochondrial potential and low in the mitochondrial fusion protein, hence less likely to fuse. Moreover, such mitochondria are subsequently degraded by the autophagy (Twig et al, 2008). At the molecular level, fission is mediated by a large GTPase called Drp1 (dynamin-related protein 1), which was identified by the genetic screen for abnormal mitochondrial morphology in yeast as Dnm1 (Smirnova et al., 2001, Bleazard et al., 1999). Drp1 is a cytosolic protein, which when required translocates to mitochondrial outer membranes and forms multimeric spiral rings wrapping the membrane. It constricts the membrane and eventually divides the mitochondria (Zhu et al., 2004, Ingerman et al., 2005). Other proteins which play a role in mitochondrial fission are Fis1 (mitochondrial fission protein 1), MFF (mitochondrial fission factor), and MEF-1 (mitochondrial elongation factor 1), which are non-GTPase proteins. These proteins target DRP1 to the outer mitochondrial membrane for fission (Lee et al., 2004; Otera et al., 2010; Zhao et al., 2011). Other than these three proteins, the activity of DRP1 can be regulated by kinases, which can phosphorylate it at different residues and can modulate its activity. Phosphorylation of DRP1 at serine 616 by cyclin B1-CDK1 (cyclin B1- cyclin dependent kinase) which is a mitosis initiator, activates DRP1 and co-ordinates its activity to cell division eventually coordinating mitochondrial division to cell division for efficient segregation of organelle following cell division (Taguchi et al., 2007). Recently, another kinase ERK2 has also been shown to phosphorylate DRP1 at serine 616 position and activates it (Kashatus et al., 2015). Another residue which is known to get phosphorylated in DRP1 is 637 by CamK (Calcium-calmodulin-dependent kinase) activates DRP1 upon increased intracellular concentration (Han et al., 2008). Phosphorylation at the S-637 residue of DRP1 is also done by Protein kinase A, which inhibits the activity of DRP1 in a cyclic AMP-dependent manner (Cribbs et al., 2007). However, dephosphorylation of DRP1 at S-637 by calcineurin activates it (Cereghetti et al., 2008).

DRP1 can be post-translationally regulated through ubiquitination by two of the ubiquitin-ligases known so far, which are Parkin and MARCH5 (membrane–associated RING-CH protein 5) (Park et al., 2010; Wang et al., 2011). Sumoylation also plays a regulatory role upon Drp1, desumoylation of DRP1 by SENP5 (SUMO protease sentrin-specific peptidase 5) activates DRP1 (Zunino et al., 2009). Inhibiting the activity of DRP1 using small molecule chemical inhibitors Midivi-1 (mitochondrial division inhibitor-1) and P-110-TAT has been proved to be of therapeutic potential in case of neurodegenerative disorders associated with increased fission (Cui et al., 2010; Guo et al., 2013).

Fusion

Mitochondrial fusion produces large elongated mitochondria, which allows mixing of mitochondrial content thereby diluting the damaged that accumulate due to mitochondrial DNA mutation or damaged proteins due to reactive oxygen species. Mitochondrial fusion makes mitochondria escape from the degradation which is particularly helpful under the conditions of high energy demands. Disruption of mitochondrial fusion results in decreased cellular growth, cellular respiration and loss of mitochondrial membrane potential, both in yeast and mammalian cells (Chen et al., 2005; Chen et al., 2003). Three GTPases, MFN1, MFN2, (Mitofusin1/2)and OPA-1 (optic atrophy 1) play an important role in mitochondrial fusion (Ciplot et al., 2004). MFN1 and MFN2 are present in the mitochondrial outer membrane and brings the fusion of outer membrane (Chen et al., 2003). While, OPA-1 is present in the inner mitochondrial membrane and make them fuse together. MFN2 is also located in the ER, it brings ER-mitochondria tethering thereby increasing calcium uptake in the mitochondria (Rojo et al., 2002, de Brito et al., 2008). In humans, mutations in MFN2 and OPA-1 are known to cause a peripheral neuropathy known as Charcot-Marie-tooth type 2A (CMT2A) and most common optic neuropathy known as dominant optic atrophy, respectively. It is characterized by muscular atrophy and axonal degeneration. disease Like DRP1, Mitofusins and OPA-1 are also regulated post-translationally via ubiquitination and phosphorylation. An E3-ubiquitn ligase Parkin ubiquitinates both MFN1 and MFN2. On the other hand, deubiquitylase USP30 deubiquitinates and stabilizes mitofusins, thereby promoting mitochondrial fusion (Escobar-Henriques et al., 2014; Cunningham et al., 2015). Whereas, OPA-1, on the other hand, is alternatively spliced into three long forms (L-OPA, a and b) which are cleaved to S-OPA-c, d, and e, by two proteases YMEl1 and OMA-1 present in the inner membrane, upon metabolic stimuli and stress respectively (Ishihara et al., 2006). It is the balance between L-OPA1 and S-OPA1 makes tubular and reticular mitochondrial morphology. However, upon metabolic imbalance and stress

the proteases YME1L and OMA-1 become active and cleave L-OPA1 to S-OPA1, which accelerates fission thereby making mitochondria fragment (Anand et al., 2014).

Quality control

As stated earlier that after fission one of the two mitochondria has always a low mitochondrial potential and also that the mitochondria are the active site of ATP production, ROS production being the by-product can damage mitochondrial proteins, DNA, and lipids; thereby making mitochondria dysfunctional (Scherz-Shouval et al., 2010). If the damage mitochondria accumulate in the cell can lead to energy deficits and metabolic imbalance, hence the elimination fo damage mitochondria become an important process. The process of elimination of dysfunctional and damaged mitochondrial via the autophagy is called “mitophagy”. Loss of mitochondrial potential is the trigger for mitophagy, LC3 (an autophagy marker) decorates mitochondrial following the treatment of chemical CCCP (carbonyl cyanide m-chlorophenylhydrazone) which causes the decrease in mitochondrial potential. In a widely accepted model of mitophagy, PINK1 (PTEN-induced kinase 1) and Parkin (both are mutated in an autosomal recessive form of a neurodegenerative disorder Parkinson’s disease) play a central role. In healthy mitochondria, PINK1 is degraded however in damaged mitochondria PINK1 is accumulated, which causes phosphorylation of Parkin thereby recruiting Parkin to the damaged mitochondria where it subsequently brings about the mitochondrial degradation. In the healthy mitochondria, PINK1 is cleaved by two proteases present in the inner membrane of mitochondria forms a shorter PINK1 (52 KDa) which is rapidly degraded. However, such a cleavage does not take place in the damaged mitochondria leading to the accumulation of a full form of PINK1 (64 KDa) and thereby recruiting parkin (Narendra et al., 2008, 2010; Deas et al., 2011; Whitworth et al., 2008). Parkin decorates the damaged mitochondria with the ubiquitin molecules which serve as an adaptor for autophagy plays p62 and LC3.Other than PINK1-parkin pathway, NIX or BNIP3-L (BNIP3 like protein)- a Bcl-2 family member plays an important role in the removal of mitochondria during reticulocyte development. *Nix-/-* mice shows reduced life span and anemia with the loss of entry mitochondria to the autophagosomes for clearance, in their RBCs (Sandoval et al., 2008). This suggests that Nix is very important for targeting the mitochondria to the autophagosomes for their removal during the reticulocyte maturation. The crosstalk between these two pathways of mitophagy has been explored and interestingly Nix can result in the recruitment of Parkin to the depolarized mitochondria for their removal (Ding et al., 2010).

Mitochondrial motility

Another important process in mitochondrial dynamics is the movement of mitochondria to the places where it needed most in a cell. Mitochondria travel on the microtubules using motor proteins kinesin and dynein/dynactin in the anterograde and retrograde directions, respectively. The adaptor protein Miro-1, which is anchored to the mitochondrial outer membrane using C-terminus, another protein Milton serves as an adaptor between miro and kinesin motor (Glater et al., 2006). Loss of miro results in fewer mitochondrial in the dendrites and axons. Interestingly, PINK1/Parkin as a complex regulates the miro-dependent mitochondrial movement. PINK1 phosphorylates miro, thereby making parkin act upon it for proteasomal degradation. Parkin-mediated degradation of miro stops the mitochondrial movement, as it detaches mitochondria from motor proteins. PINK1-parkin pathway actually makes sure only healthy mitochondria travels, and degrades the unhealthy ones via mitophagy, suggesting a cross-talk between mitophagy and mitochondrial movement (Wang et al., 2011).

Perspective

Many significant discoveries are made in the field of mitochondrial dynamics and we know the mechanism of fusion, fission, mitophagy and mitochondrial movement. However, many questions ares still needs to be answered. How the damaged mitochondrial are cleared in parkin-deficent cells? Indentification of parkin-independent pathways of mitophagy will help us to understand mitophagy better. How mitochondrial dynamics is affected by aging is another important question. Since, mitochondria get damaged by aging, whether or not mitochondrial dynamics is affected by aging. The cross-talk between aging and mitochondrial dynamics would be interesting to explore.

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Prof. A. S. Mukherjee Award

Rudhira stabilizes microtubules to regulate focal adhesion turnover during endothelial cell migration

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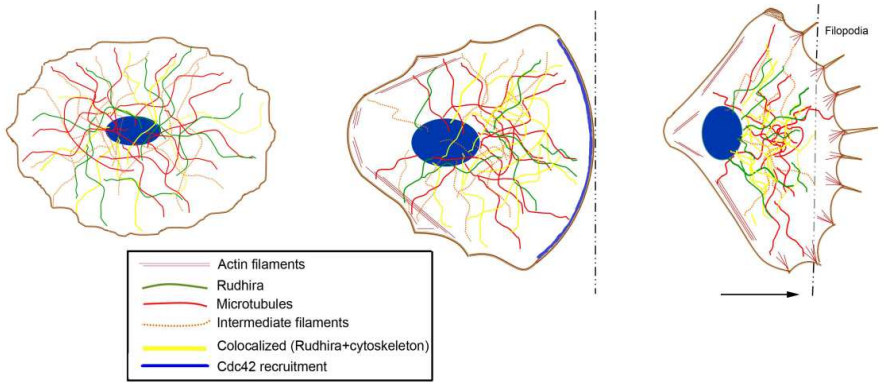
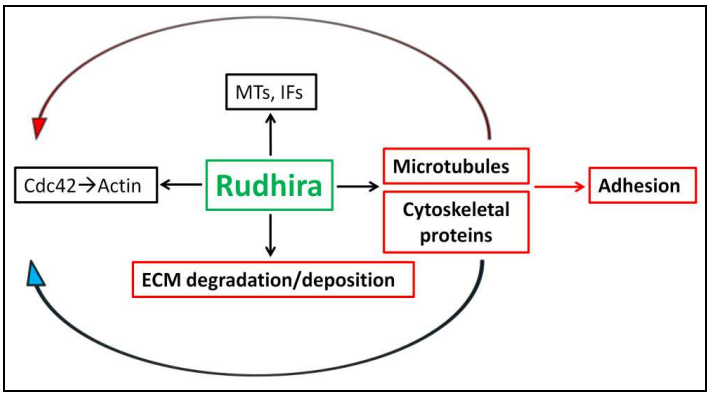
Cell migration is a process common to development and cancer metastasis. It is essential for and tightly regulated during development. Cell migration requires dynamic remodeling of the cytoskeleton and extra-cellular matrix (ECM) and the concerted interplay of multiple signaling pathways. Slight misregulation in any of these can have dramatic effects on organism development and viability. Cell migration has been widely studied at the cellular level. However, further studies are required to understand the specific molecular mechanisms. In this context, identifying and targeting cell-specific regulators of migration and understanding their spatio-temporal position in the events thereof would be helpful in disease control.

Earlier studies from our lab have identified a molecule, Rudhira/BCAS3 (Breast Carcinoma Amplified Sequence 3), as an endothelial cell specific positive regulator of migration. Endothelial cell migration is a key process in the development of the cardio-vascular system. Consequently, *rudhira* knockout mice display gross cardio-vascular defects.



Schematic showing the co-localization of Rudhira with microtubules in non-migrating, pro-migratory and migrating cells.

Here, we investigate the mechanism by which Rudhira regulates cell migration. Through transcriptome analysis we identify that processes such as cell migration, adhesion, angiogenesis and ECM organization are highly affected. Detailed analysis of the events in cell migration shows that Rudhira positively regulates migration by affecting cell adhesion and microtubule stability. Rudhira is also important in maintaining proper ECM organization and the regulation of AKT and ERK pathways, which are shown to be important during endothelial cell migration. Finally, we show that Rudhira interacts with other cytoskeletal and scaffold proteins which could be important for regulating microtubule dynamics and cell migration. Our study identifies a cell type-specific modulator of microtubule dynamics and migration which can be targeted in cancer.



Schematic showing the regulation of cell adhesion and ECM organization by Rudhira. Rudhira interacts with microtubules and other cytoskeletal proteins. This interaction could be required for microtubule mediated cell adhesion regulation and Cdc42 mediated actin reorganization.

Deltex and Hrp48 cooperatively downregulate Notch Signaling and induce Apoptosis in *Drosophila*

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Introduction: Notch signaling is an evolutionarily conserved pathway that is found to be involved in a number of cellular events including cell fate determination, cellular differentiation, proliferation, apoptotic events and self renewal process of different tissues. The deployment of Notch signaling pathway in numerous cellular contexts to influence varied aspects of development is possible due to its multiple levels of regulation. Notch signaling is regulated at the levels of expression of ligand and receptor, post-translational modifications, ligand-receptor interactions and its trafficking (Bray, 2006). Deregulation of Notch pathway leads to variety of pathological conditions including developmental disorders and cancer (Bolos et al., 2007).

Results: In an effort to identify novel components integrated into the molecular circuitry affecting Notch signaling, we carried out a protein-protein interaction screen based on the identification of cellular protein complexes using co-immunoprecipitation followed by mass-spectrometry. We identified Hrp48, *Drosophila* homologue of human DAZAP1, as a novel interacting partner of Deltex (Dx), a cytoplasmic modulator of Notch signaling. Immunocytochemical analysis reveals that Dx and Hrp48 colocalized in cytoplasmic vesicles. *dx* mutants also show strong genetic interactions with *Hrp48* mutant alleles. Co-expression of Dx and Hrp48 results in depletion of Notch in larval wing imaginal discs and downregulation of Notch targets, Cut and Wingless (Fig. 1). In addition, Dx and Hrp48 display synergistic effect on caspase mediated cell death. Taken together our results suggest that Dx and Hrp48 together negatively regulate Notch signalling.

Discussion: Dx was initially identified as a positive regulator of Notch (Matsuno et al., 1995) and later it has been shown that being an E3 ubiquitin ligase, Dx can also negatively regulate Notch signaling depending on the cellular context. It helps internalization of full length Notch and subsequently target Notch receptor to late endosome where it gets processed and finally the NICD is released. Earlier studies have

also shown that along with Kurtz, a non-visual beta-arrestin, Dx induces poly-ubiquitination followed by proteasome-mediated degradation of Notch receptor (Mukherjee et al., 2005). Here we show that Hrp48 directly interacts with Dx and this interaction results into depletion of NICD. This may be due to either defective vesicular trafficking or degradation of Notch. Further investigation is going on to pinpoint the actual mechanism.

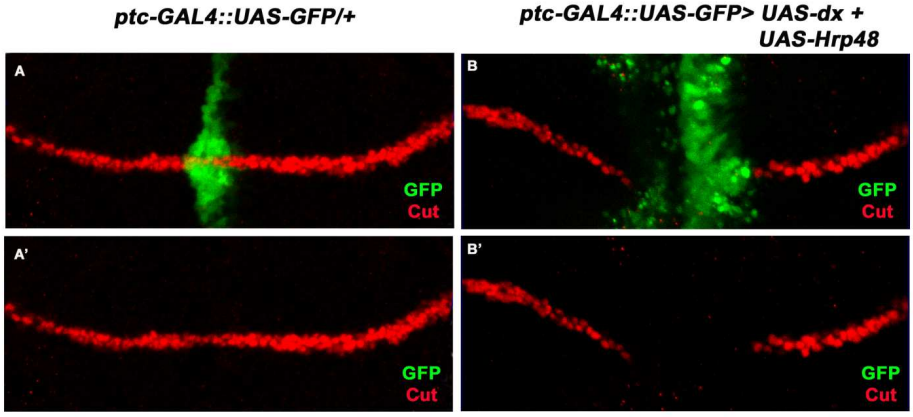

Fig 1. Dx and Hrp48 together results in loss of Cut expression. Wing imaginal disc showing wild type cut expression at A/P boundary (A, A'). Co-expression of Dx and hrp48 results in complete loss of Cut expression (B, B').

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SKR is a Novel Meiotic Gene Required for Male gametophyte Development in *Arabidopsis thaliana*

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Meiosis is a special type of cell division which demarcates the dominant sporophyte from gametophytic generation in angiosperms.

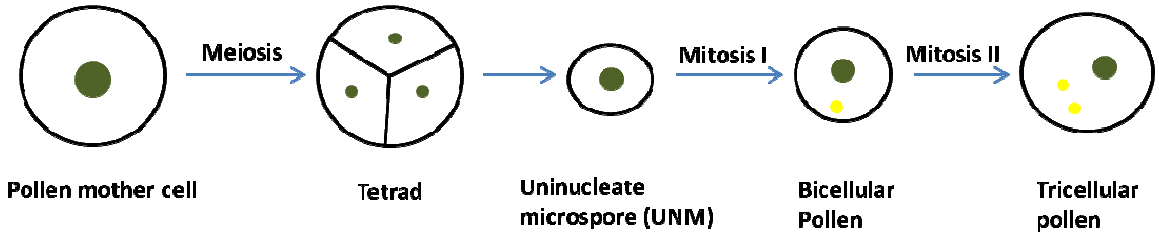

Fig1. Schematic representation of developmental stages of male gametophyte in *Arabidopsis thaliana*

The process of gamete development in plants is unique as meiosis is followed by mitoses for the development of fully functional male and female gametes. Production of functional male gametophyte relies on precisely controlled, sequential and distinct stages of microsporogenesis and microgametogenesis (Fig. 1). During microsporogenesis, diploid meiocyte generates tetrad of haploid microspores through reductional cell division. Microgametogenesis involves mitotic divisions and differentiation of microspores and formation of pollen wall to produce functional pollen grains. In Arabidopsis, the diploid pollen mother cell undergoes meiosis to form four haploid spores enclosed in callose wall, which forms tetrad stage after the dissolution of callose the uninucleate microspores (UNM) are released. These UNM later undergo two

rounds of mitosis to eventually form the functional tricellular pollen (Borg et al., 2009). In this study, we attempted to identify new genes involved in meiosis and gametophyte development through co-expression analysis using an *in-silico* approach. Candidate genes were identified using Expression Angler tool (Toufighi et al., 2005) based on co-expression with known meiotic genes and other criteria's like developmental and tissue specific expression and copy number of the gene.

Fig2: a) WT plants with elongated siliques b) skr plant is sterile with stunted sylique.

The knockout lines for the candidate genes were checked for the sterility/ reduced fertility phenotype. In the screening, we identified a mutant that shows male sterile phenotype. We named the gene *SHUKR (SKR)* because of the sterile phenotype of the mutant; the name represents a fertility god from Hindu mythology. *SKR* is a sporophytic recessive gene, which expresses from mid prophase of meiosis till UNM stage. In spite of being expressing during meiotic stages, there was no observable defect till the tetrad formation in *skr*. The cause of male sterility in the mutant was found to be defective pollen development starting at the uninucleate microspore stage following meiosis, without affecting normal development and function of the tapetum. SKR protein is found to expresses specifically in the male meiocyte and its daughter cells from mid prophase to early uni-nucleate microspore stage and displays dynamic nuclear-cytoplasmic enrichment. Further cytological studies show that it is probably a chromatin

associated protein. Additionally SKR is also required for proper formation of Aperture length. In certain percentage of microspores in *skr* the length of apertures is reduced, moreover the transcript level of the gene known to be required for proper aperture formation, *INAPERTURATE1* (*INP1*) (Dobritsa et al., 2012) is down regulated in the *skr*. Overall our findings indicate that there is a meiotic control over the gamete development in the plants and *SKR* could be one of the major player regulating the process.

*contributed equally to the work

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Prof. B R. Sheshachar Memorial Award (Best Poster)

Plakoglobin localization to the cell border rescues desmosome assembly in cells lacking 14-3-3γ.

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Desmosomes are cell-cell junctions present in epithelial cell lines and tissues and provide mechanical strength and rigidity to the tissue. Loss of desmosomes leads to a disruption of tissue organization and function. It was observed in our laboratory that the absence of 14-3-3γ in testis, affected cell-cell adhesion between developing spermatocytes and sertoli cells leading to sterility. Loss of 14-3-3γ in HCT116 cells lead to a defect in the transport of the desmosomal plaque protein, Plakoglobin (PG), to the cell border leading to defects in desmosome assembly and the mislocalization of other desmosomal proteins to the cytoplasm [1]. To determine whether PG mis-localization was the only defect affecting desmosome formation upon 14-3-3γ loss, PG was constitutively targeted to the cell border by fusing it to a farnesylated GFP (PG-GFP-f) and expressed in 14-3-3γ knockdown cells to study the localization of desmosomal proteins. It was found that 14-3-3γ knockdown cells expressing PG-GFP-f showed cell border localization of desmosomal proteins Desmoplakin (DP), Desmoglein 2 (DSG2) whereas Plakophilin 3 was partially localized to the cell border and the localization of Desmocollin 2 was not altered in comparison to the 14-3-3γ knockdown cells transfected with EGFP-f. It has been reported in the literature that border localization of desmosomal protein increases their stability therefore we checked the desmosomal protein levels using western blot and we found that there was more protein levels of DP, DSG2, DSC2, PKP3 and endogenous PG when compared to the desmosomal protein levels of 14-3-3γ knockdown cells transfected with EGFP-f. Taken together, these results suggest that localization of PG to the cell border is sufficient for the induction of desmosome assembly in the absence of 14-3-3γ.

Plakoglobin 14-3-3γ complex is transported to the cell border by kinesin motor protein Kif5B and therefore in the absence of Kif5B the cell border localization of desmosomal proteins is affected [1]. We hypothesized if we could rescue the cell border localization

of desmosomal protein by expression of PG-GFP-f in Kif5 B knockdown cells also. To test this hypothesis, we expressed PG-GFP-f in Kif5B knockdown cells but we found that PG-GFP-f expression in these cells only rescued DP localization and the localization of other desmosomal proteins was not altered significantly. Moreover, desmosomal protein levels were also not significantly altered in PG-GFP-f expressing Kif5B knockdown cells in comparison to EGFP-f expressing Kif5B knockdown cells. These data suggest PG-GFP-f cannot completely rescue desmosomal protein localization in the absence of Kif5B and Kif5B is required for the transport of DSG2, DSC2 and PKP3.

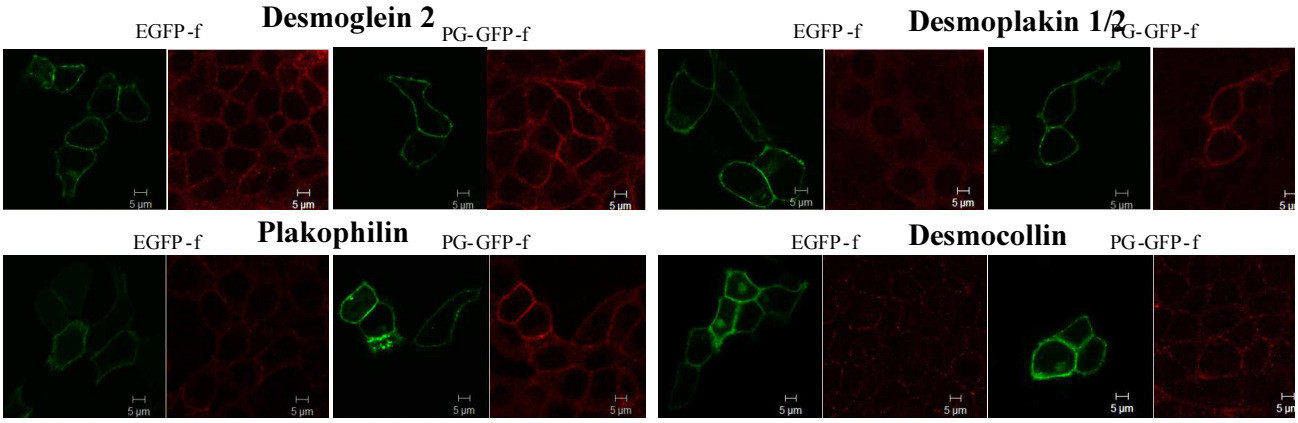

Fig. 1. Immunofluorescence was done for different desmosomal proteins to check their localization in the 14-3-3γ knockdown cell line transfected with EGFP-f or Plakoglobin GFP-f (PG-GFP-f).

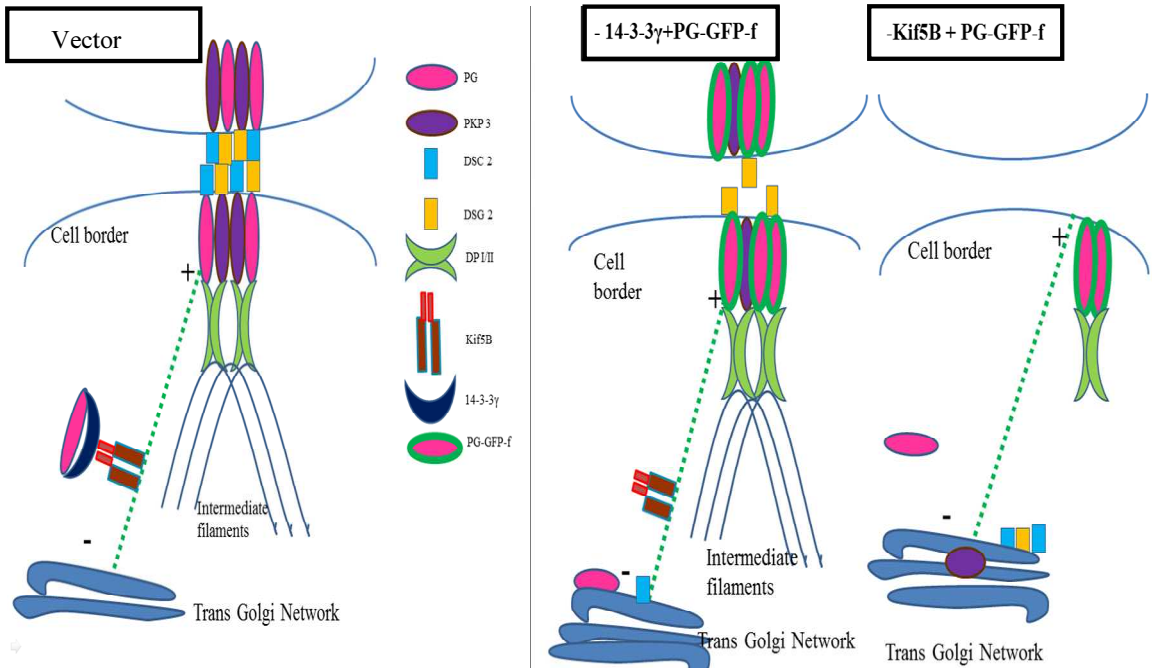

Fig 2. Model of Desmosome assembly in the i) vector control, ii) in the absence of 14-3-3γ with the expression of PG-GFP-f and iii) in the absence of Kif5B with the expression of PG-GFP-f.

Sehgal L, Mukhopadhyay A, Rajan A, Khapare N, Sawant M, Vishal SS, Bhatt K, Ambatipudi S, Antao N, Alam H *et al*: **14-3-3gamma-Mediated transport of plakoglobin to the cell border is required for the initiation of desmosome assembly in vitro and in vivo**. *J Cell Sci* 2014, **127**(Pt 10):2174-2188.

Prof. Manasi Ram Memorial Award (Best Poster)

Roles of WD-Repeat proteins in Zebrafish Development

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WD-repeat (WDR) domain containing proteins are a family of proteins that are characterized by widespread and abundant occurrence, low levels of sequence conservation, common structural conformation and high levels of functional diversity. There are a large number of WDR proteins of unknown functions that have been implicated in human disorders. One such protein is WDR8. Although previous studies have provided clues about the functions of WDR8, the exact role of this protein in development is still unclear. Investigating the role played by WDR8 in zebrafish development provides an opportunity to elucidate its exact function and interacting partners.

WDR8 is ubiquitously expressed in adult tissues of zebrafish as well as during different stages of embryonic development. Knockdown of WDR8, by gene specific Morpholinos (MO) during development causes reduction in eye size but does not affect eye structure. Co-injection of WDR8 MO and plasmid carrying complete WDR8 cDNA lacking the morpholino binding site rescues the decrease in eye size, showing that the phenotype is a result of gene specific knockdown effects. Further cell counts from the eyes of embryos indicate that the number of cell nuclei in the retinal layers is significantly reduced in WDR8 morphants compared to that in control embryos, suggesting that WDR8 may be involved in regulating cell numbers in the analysis for mitotic cell markers as well as assays for apoptosis indicate a difference in the number of mitotic cells and apoptotic cells between the control and morphant embryos. This suggests that WDR8 may be involved in regulation of the cell number by regulating rather cell division and /or apoptosis.

The zebrafish WDR8 protein is highly similar to its human ortholog. In order to understand if the human WDR8 carries out similar functions during development, experiments to rescue the knockdown phenotype by co-injecting zerbafish embryos with WDR8 MO and plasmid carrying either the wild type or mutant human WDR8 cDNA are underway. Future plans include attempting to identify interacting partners of WDR8 by co-immunoprecipitation.

AICB conference Award (Best Poster)

Phosphorylation of Ku70 by cell cycle kinases modulates its replication related function

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Ku protein - a heterodimer of Ku70 and Ku80, was originally identified as an autoantigen recognized by the sera of patients with autoimmune diseases. Ku functions as a DNA binding protein complex holding broken DNA ends during the repair process of double-strand breaks (DSBs) as its role in DNA-PKcs dependent non-homologous end joining (NHEJ) pathway (1). In addition, Ku has also been found to be involved in various cellular processes including repair, apoptosis, telomere maintenance and replication (2,3). The involvement of Ku protein in DNA replication has been implicated by virtue of its purification through the binding to the monkey replication origin Ors8 (4,5). Its interaction with several other chromosomal replication origins in a sequence-specific and cell cycle dependent manner has further established the role of Ku in replication (6,7). It is found that after initial binding of initiation protein Orc2 to replication origin subsequent loading of Orc3, -4 and -6 requires the association of Ku-heterodimer with the origin demonstrating its critical role at the initiation step of DNA replication (8). Ku also interacts with other DNA replication proteins including DNA polymerases, PCNA, topoisomerase II, RFC and RPA (9). Thus, the involvement of Ku in initiation of DNA replication is well-established, but how the protein is regulated in a cell cycle dependent manner remains unclear.

Previously, a substrate was identified during a search for potential substrates of the S-phase LdCyc1 / CRK3 kinase from the disease causing parasite *Leishmania donovani* that contained Ku70 related conserved domains (10). Interestingly, human Ku70 protein

also contains four putative Cdk target sites along with several potential cyclin binding Cy-motifs, leading us to hypothesize the possibility of its functional regulation through cell cycle dependent phosphorylation.

In this context we show that human Ku70 protein interacts with Cyclin B1 *in vitro* and *in vivo* in a Cy-motif dependent manner. Strikingly, the interaction of Ku70 with cyclin B1 disrupts the Ku70/Ku80 dimer, possibly explaining the reported independent localization of Ku70 and Ku80 in mammalian cells during mitosis. It has also been shown that human Ku70 protein is a novel target of cyclin B1/Cdk1 kinase, which phosphorylates the threonine residues at 401, 428 and 455 positions of the protein. Interestingly, cyclin A2/Cdk2, which is also known to phosphorylate Ku70, targets the same sites, but the S-phase kinase cyclin E1/Cdk2 phosphorylates additional target residues. Our result from the experiments in HeLa cells further confirmed that Ku70 remains in phosphorylated state during S, G2 and M phases of cell cycle and is dephosphorylated during G1 phase, strongly suggesting the critical role of the post-translational modification in regulating the periodic activity of the protein. Strikingly, the modified Ku70 containing alanine mutations at Cdk phosphorylation sites (kinase-dead mutant) enhanced the episomal replication of human origin containing plasmid in HeLa cells as well as that of its genomic DNA. Also, the binding of Ku to replication origin containing DNA is completely abolished due to its phosphorylation by cyclin/Cdks which has been shown by EMSA. Based on these results it has been hypothesized that the phosphorylation of Ku70 has prevented Ku from interacting with replication origin due to high Cdk activities during S, G2 and M phases of cell cycle, and its dephosphorylation on exit from mitosis facilitates the role of Ku in formation of functional pre-replication complex during G1 phase. The kinase-dead mutant of Ku70 jeopardises such a role in licensing mechanism most likely resulting in rereplication. This possibility is supported by our further observation of increased nuclear DNA content in the cells overexpressing the kinase-dead mutant of Ku70. Moreover, in such

cells, enhanced binding of the mutant Ku70 to origin DNA has also been observed by chromatin immunoprecipitation along with increased abundance of replication initiation factor Cdt1, which is normally expected to be absent after origin firing in S-phase.

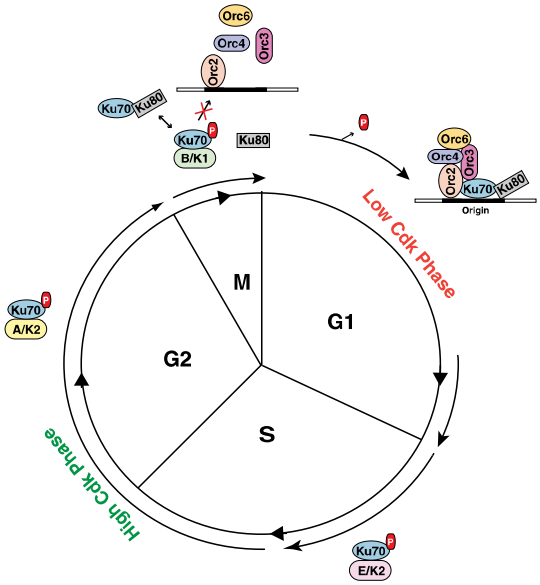

Figure 1. Regulation of replication related function of Ku by cyclin/Cdks

Therefore, our results elucidate the long unanswered question on the mechanism of regulation of replication related function of Ku periodically during cell cycle progression. Due to the formation of the complexes of Ku70 with cyclin-Cdks and its phosphorylation, the Ku dimer is disrupted (Figure 1). This results in the unavailability of functional Ku dimer for binding to replication origins during the high Cdk activity phases, thus preventing premature assembly of origin recognition complex till the end of mitosis. After the degradation of cyclin B1, Ku70 can be converted to dephosphorylated state and is able to form heterodimer with Ku80 for taking part in origin licensing during G1-phase.

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Identification of potential biomarkers for alcohol-induced impairment in neurogenesis

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Gestational alcohol exposure is known to have deleterious effect on the developing embryo, predominantly the nervous system owing to neural tube and crest abnormalities. Alcohol manifests neuronal developmental deformities collectively known as Fetal Alcohol Spectrum Disorders (FASD) which is characterised by craniofacial anomalies, defective CNS, growth retardation and organ dysmorphology. Depending on the developmental stage of the embryo, concentration, duration and frequency of alcohol exposure, the degree of developmental deformities varies. Alcohol is hypothesized to bring about this abnormal neurogenesis by modulating the expression of an array of crucial neural developmental genes. Identification of such an aberrant molecular signature at an early embryonic stage would be relevant from the translational perspective.

Since Human Embryonic Stem Cells (hESC) fairly recapitulate the invivo neurogenesis they were used as the in vitro model to delineate the molecular mechanism by which

ethanol disturbs the neural development. 5-6 day embryoid bodies (EBs) mimicking the gastrulation period were exposed to ethanol concentrations corresponding to the blood alcohol levels and were directed them to differentiate into neural progenitors and neural stem cells. Changes in mRNA expression profile of key genes were analysed using Real Time PCR at stages corresponding to gastrulation and neurulation. To validate the above, expression of protein level was studied using western blot. We also did monitor the brain development in Zebrafish model upon exposure with alcohol to vividly understand the phenomenon. Further investigation was done to understand epigenetic changes associated with this impairment in neuro specific genes.

The administration of 50mM and 100mM ethanol for 48 hrs led to spatiotemporal misregulation of neural/brain-tissue specific gene expression. Neurogenic genes such as Nestin, HES5, S100B and EN-1 exhibited an upregulation while Sox-2, Pax-6, Musashi-1 and GBX-2 were downregulated. Region specific brain markers such as HOXB2, PITX3, IRX3 and FOXG1 that are involved in SHH and WNT signalling were also found to be significantly affected. An array of neural specific genes such as N-cadherin, OTX-1/2, Sox-1, TUJ1, NR2F1, WNT1 and MAP2 also showcased an impaired expression when compared to the control. However ASCL1 a crucial neuro specific gene did exhibit a striking increase in the fold change upon alcohol exposure. Genes involved with the transcriptional activation of ASCL1 such as RBPJ, PARP1 HES1 and GLI1 associated with Notch and Shh signalling cascade showed an increase in its expression upon exposure. Evidently dysregulation of crucial genes did culminate in the impairment of the protein expression and ultimately the brain development in Zebra fish model upon exposure. Alteration observed in these genes might owe to the epigenetic constitution, since the methylation of H3K27 and H3K9 and the acetylation of H3K4 and H3K9along with expression levels of miR-96, miR-124 and miR-200c were perceived to be modulated.

The aberrant expression of neural specific genes upon alcohol insult could be a result of chromatin modification and miRNA intervention ultimately producing neurogenic defect like Fetal Alcoholic Syndrome Disorder (FASD). ASCL1 and S100B that were highly upregulated due to defective NOTCH and SHH signalling, could negatively impact embryonic neural development through premature neurogenesis resulting in deprivation of the stem cell pool. Our data suggest potential targets like ASCL1 and S100B as biomarkers for an early identification of FASD.

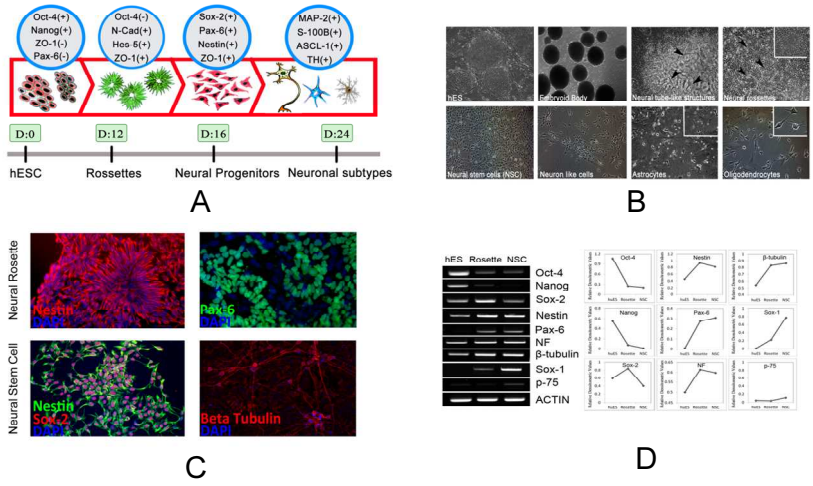

Figure 1: Neural differentiation of human embryonic stem cells. (A) Schematic representation of the neural differentiation protocol. (B) Phase contrast images of the differentiating cells at various stages of neural commitment via rosette formation followed by terminally differentiated neuronal and glial subtypes. (C) Characterization of the cells by Immunocytochemistry (co-staining) of Nestin and Pax-6 representing neural rosettes; Nestin, Sox-2 and β-tubulin representing neural stem cells. (D) Gene expression profiling to show temporal regulation key markers during the course of differentiation.

AICB conference Award (Best Poster)

Non-junctional adhesion-independent E-cadherin clusters regulate the actomyosin cortex and slow cytokinesis

Anup Padmanabhan[1] and Ronen Zaidel-Bar[1,2]

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Intercellular adhesion plays a vital role in achieving the shape control over a ball of cells during the development of multicellular organisms. How multicellular organisms achieve precise control on the growth and number of cells in time and space while adhering to one another is poorly understood. How is the load on cellular machinery divided to achieve the desired result? For example, cell-cell adhesion and cytokinesis are two cellular processes, which involve requirement and functioning of approximately 300 proteins, many of them with overlapping functions in the two processes [1]. Yet during cytokinesis in metazoan cells, the furrow ingression is resisted by intercellular adhesion mediated by cell-cell junctions. Therefore the outcome of the interactions between cell division and cell adhesion is critical to survival of the organism.

Although E-cadherins are best known for their essential role in mediating adhesion at cell junctions, a significant amount of E-cadherin on the cell surface is found outside of cell-cell junctions. The cellular function of these non-junctional cadherin clusters has not been addressed before. Here using live imaging and genetics we show that during in early *C. elegans* embryos E-cadherin/HMR-1 formed non-junctional puncta at the cell surface associated with cortical F-actin. Depletion of E-cadherin/HMR-1 puncta in 1-cell stage embryo lacking cell-cell junctions accelerated furrow ingression during the first cell division. At the molecular level we observed E-cadherin/HMR-1 and myosinII/NMY-2 to negatively regulate each other and localize to distinct regions both at the cortex and along the ingression furrow. This antagonistic interaction and spatial segregation of E-cadherin/HMR-1 and NMY-2 was dependent on the formin/CYK-1 polymerized F-actin. Finally, we discovered that the non-junctional E-cadherin/HMR-1 puncta localized at the cell surface helps in holding the cortex and membrane together, a hitherto unknown cellular function of non-junctional E-cadherin/HMR-1.

Our results thus show that surface localized non-junctional E-cadherin/HMR-1 could regulate cytokinesis beyond its canonical role in inter-cellular adhesion by (1)

regulating cortical myosin activity and (2) holding the membrane and cortex together thus resisting cortical deformations such as during furrow ingression.

Thus, our work uncovered a non-canonical role for E-cadherin clusters that is adhesion-independent and yet important for the regulation of cell shape dynamics. We speculate that these results might throw new light on our understanding of the metastasis, given that loss of E-cadherin expression is often associated with cells undergoing epithelial to mesenchymal transition (3). Therefore, future work on cadherin must also take into account the cortical functions of non-junctional cadherin clusters.

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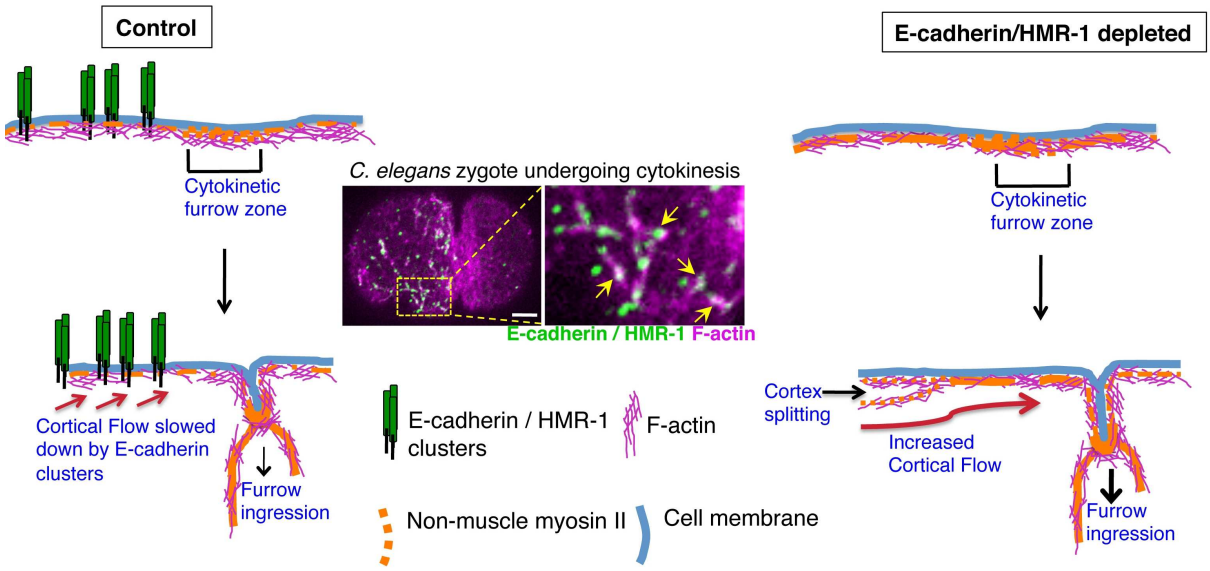

Non-junctional E-cadherin/HMR-1 clusters inhibits type-II myosin at the cortex , strengthens membrane – cortex association and slow down cytokinesis

Increased expression of SIRT2 is a novel marker of cellular senescence and is dependent on wild type p53 status

Tarique Anwar[1, 2], Sanjeev Khosla[1] and Gayatri Ramakrishna[3]

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Why Study Cellular Senescence?

The improvement in medical care has lead to increase in life expectancy. The process of ageing is imminent even with increasing lifespan. Organismal and cellular ageing is often associated with organ dysfunction and waning health. At the cellular level, the process of ageing is often referred as cellular senescence. Understanding the mechanisms leading to senescence is thus of utmost importance to prevent organ dysfunction with ageing. Further new markers of fraility are needed to assess the cellular homeostasis and organ health. Almost 50 years ago, Hayflick and Moorehead noted that with continuous passaging the primary fibroblasts show limited growth and stop dividing (Hayflick and Moorehead, 1961) which is often referred as Hayflicks limit. Later Leonard Hayflick referred that the finite lifetime of primary cells is due to ageing or cellular senescence. Hence cellular senescence is now defined as a process of irreversible growth arrest which is mainly results due to attrition of telomeres, and is commonly referred as replicative senescence. Usually replicative senescence is a slow process and in contrast under certain conditions, senescence can be accelerated due to oxidative stress or DNA damage and this is often referred as stress induced premature senescence (SIPS). Additionally, oncogenes such as *Ras* and loss of tumor suppressor

such as *PTEN* also results in premature senescence viz., Oncogene induced senescence (OIS) or *Pten*-loss-induced cellular senescence (PICS) respectively. Activation of p53-p21 or p16-pRb pathways are the two well-known mechanisms leading to cell cycle arrest during senescence (Campisi and d'Adda di Fagagna, 2007). However, these pathways are upregulated even in case of quiescence and p53 is often associated with programmed cell death. In general the senescence markers are limited and the most commonly used marker is the positivity to Senescence Associated beta galactosidase (SA-beta Gal) at pH 6, however this assay too has its limitation (Dimri et al., 1995). Further DNA damage markers like γH2AX and inactive chromatin mark such as H3K9 trimethylation has also been used but they are not very specific. Besides SA-beta Gal, a decrease in Lamin B1 is the only known specific marker of senescence (Freund et al., 2012). We made an explorative study to check if Sirtuins can be used as a marker of senescence.

Sirtuins and Ageing Connection

Sirtuins (SIRT) belonging to the NAD+ dependent histone deacetylase III class of enzymes have emerged as master regulators of metabolism and longevity. Atleast in the lower organisms Sirtuins have been shown to prevent ageing and increase the lifespan of the organism. The Mammalian Sirtuins is large family with seven distinct members (SIRT1-SIRT7). The existing data from lower organisms and knock-out mice in general is suggestive of role of Sirtuins in reversion of cellular aging. On the other hand, few studies have contradicted the role of Sirtuins in increasing longevity and prevention of aging (Burnett et al., 2011; Keneddy et al., 2005). However, their role in prevention of ageing and senescence remain controversial. Loss of SIRT6, a nuclear resulted in premature ageing in animal models implicating it in an anti-aging role. Recently our group demonstrated that replicative senescence is accompanied with loss of nucleolar

SIRT7 (Kiran et al, 2013). Further, using *in vitro* cell culture system we unraveled the role of SIRT7 in attenuating DNA damage and thereby delaying stress induced premature senescence (Kiran et al., 2015).

There is limited clarity with respect to expression of various Sirtuins isoforms in different forms of senescence such as replicative, oncogene induced and stress induced. Hence, the present study was attempted with an aim to evaluate changes in expression patterns of various Sirtuins under different conditions of cellular senescence. Briefly, our data supports the identification of SIRT2 as a novel senescence -associated marker which can be used in conjunction with LaminB1 to identify senescent cells with wild type p53 status (Fig.1). The major highlights of the study are:

- Among all the Situin family members, increased expression of SIRT2 is a specific feature associated with senescence but not with either quiescence or cell death.
- Further increase in SIRT2 expression is a feature associated with most forms of senescence viz., Replicative, Stress Induced and Oncogene induced senescence.
- Increase in SIRT2 expression during senescence was also associated with changes in deacetylation of its targets i.e α-tubulin at lysine 40, Histone H4 at lysine 16 (H4K16) and p65 at lysine 310.
- The SIRT2 expression during senescence is dependent on p53 status and using chromatin immunoprecipitation we noted a p53 binding site on SIRT2 promoter.
- Intriguingly, neither overexpression nor knockdown of SIRT2 had any effect on delaying or accelerating stress induced premature senescence. Thereby indicating that SIRT2 upregulation during senescence is not a cause of senescence; rather it is an effect linked to senescent associated changes.

Overall, our study supports the identification of SIRT2 as a novel senescence-associated marker which can be used in conjunction with Lamin B1 to identify senescent cells with wild type p53 status (Anwar et al, Cell Cycle, 2016 in press).

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Anwar T, Khosla S, and Ramakrishna, G (2016) Increased expression of SIRT2 is a novel marker of cellular senescence and is dependent on wild type p53 status. Cell Cycle : In press.

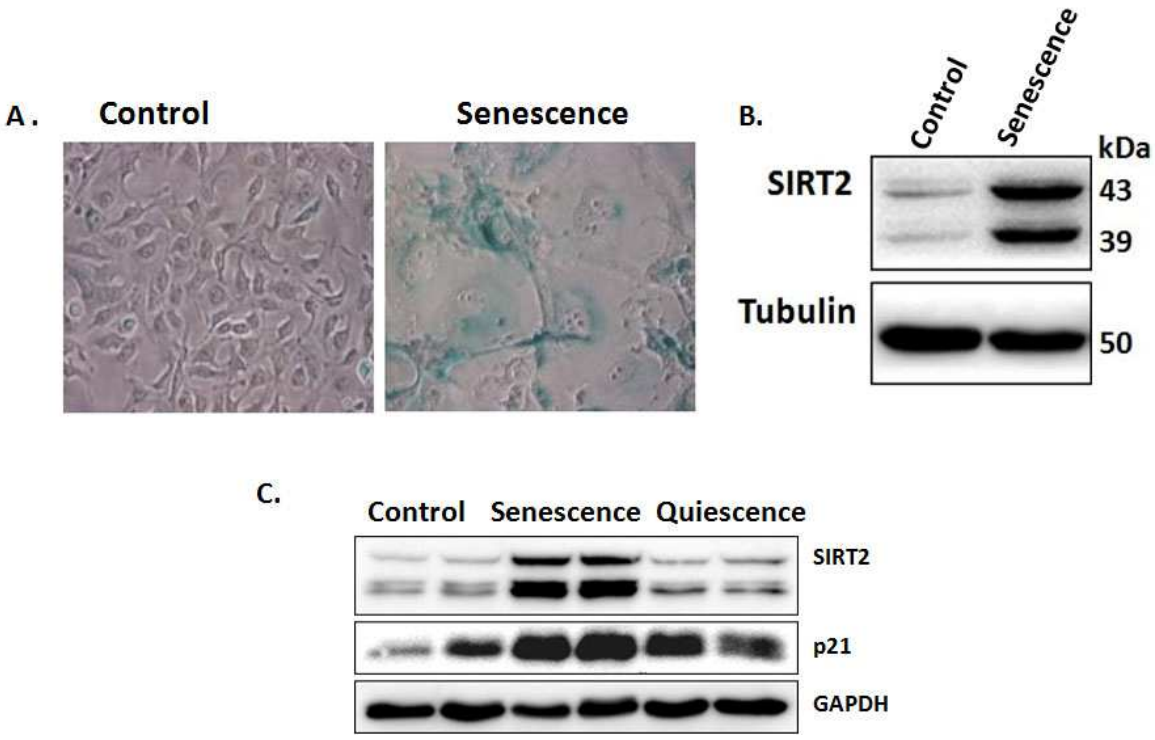

Figure 1. Increased SIRT2 expression in senescent cells. (A) U2OS cells were treated with doxorubicin to induce premature senescence and cells were evaluated for positivity to SA_beta galactosidase at pH 6.0. Note cells undergoing senescence show enlarged morphology and blue color intense staining for SA-beta galactosidase, but not the untreated control cells. (B) Immunoblot showing expression of SIRT2, and total-Tubulin was used as a loading control. (C) Immunoblot showing expression of SIRT2 in conditions of premature senecnece (doxorubicin mediated) and quiescence (0.1% serum starvation). Note increase in expression of p21 in both senescence and quiescence, while that of SIRT2 only in conditions of senescence.

ISCB sponsored Workshop

"Basic Molecular Machines in Cell Biology"

Patna University has successfully conducted three days workshop entitled as "Basic Molecular Machines in Cell Biology" at Department of Biotechnology sponsored by Indian Society for Cell Biology. After screening from several applications, 18 participants, which included various research scholars, faculties and students from different universities of Bihar were trained for several basic techniques of cell and molecular biology during this three days workshop (3rd -5th Nov, 2015). Apart from training in basic techniques, seminars were conducted about cutting edge technology of cell biology such as flow cytometry, fluorescent microscopy, stem cell etc.

Each day of the workshop was divided into three sessions: Lecture session, hands on training session and seminar session. On each day, participants were trained for two methods by hands on training and demonstration. Before experimental demonstration, lecture was presented about concepts, protocols and principles of these techniques. Every day after practical demonstration and hands on training session, there was a presentation about high cutting technology and model system used in cell biology for one hour.

On the 1st day all the participants were trained for plasmid transformation into bacterial cell via heat shock method. Also, protein electrophoresis (SDS-PAGE) was demonstrated simultaneously. The use of C. *elegans* as a model organism in biological sciences was explored during seminar session by Dr.Jitendra Kumar.

On the 2nd day participants were trained for plasmid extraction by alkali lysis method and analysis and detection of DNA by agarose gel electrophoresis. Simultaneously, a hand on training for polymerase chain reaction (PCR) was also given to the participants. Dr.Mahendra Seervi described fluorescence microscopy and flow cytometry and their application in cell biology during seminar session.

On the last day there was a lecture about animal cell culture and stem cells. After that, there was a demo about animal cell culture and C. *elegans* culture and maintenance. During seminar session the various cell death assays were explained by Dr.Mahendra Seervi.

On the closing session, Patna University Vice Chancellor Professor Y C Simhidri presented certificates to all the participants and appreciated the convener of this workshop Dr. Mahendra Seervi and Dr. Jitendra Kumar and Co-ordinator of PG Biotechnology Dr.Birendra Prasad for executing this quality workshop. Principal of Patna Science College and co-ordinator of DBT-PU-IPLS Programme Professor U. K. Sinha highlighted the benefits and insisted to conduct more of such workshop in future for training faculties and students with modern biology techniques and methods to upgrade the biological research standard in Bihar state.

Considering the importance and success of this workshop, it was highlighted as news in the many Hindi newspapers of Bihar such as Hindustan and DainikJagran.

(Mahendra Seervi)

ISCB sponsored Lectures in underprivileged colleges in rural areas.

Dr. Rolee Sharma, Associate Professor, Integral University, Lucknow delivered a Cell Biology Lecture to science students of a college located in Ataria, Sitapur, U.P.

A lecture on "*Defense against diseases: Immune system and vaccines*" was organized on 26th of October 2015 for the college students and college teachers of Sarvpalli Radha Krishnan College, Atariya, Sitapur, Uttar Pradesh. This lecture was sponsored by the Indian Society of Cell Biology (ISCB) and was held in a college in the rural area of Uttar Pradesh. The main objective of the lecture was to create awareness in young students in the area of Cell Biology of Immune cells in human body and about immunization in infants. The lecture was an attempt to impart scientific knowledge on immunity and vaccine biology, to develop interest in this area and motivate students to take up cell biology in their upcoming career and seek solutions to existing diseases for which no cure or vaccines are currently available. There were about 80 boys and girls of 11th and 12th standard, who showed great interest and enthusiasm during the entire duration of the lecture. There were some teachers as well. The welcome address was given by Mrs. Seema Mohan, Director, SRK College, Sitapur. The students were initially provided with a onepage handout which helped them to summarize the lecture. This was followed by the lecture by Dr. Rolee Sharma, Associate Professor, Department of Biosciences, Integral University, Lucknow and also the life member of ISCB. The lecture concluded with a brief question answer interactive session with the students. It was a pleasure to see the response and excitement in the sparkling eyes of the young boys and girls of the rural area.

Dr Sunil Verma, CCMB Hyderabad delivered a lecture at Ved International School in Modipuram, Merrut, UP under the banner of Indian Society of Cell Biology. He highlighted the scientific contributions of several Indian Scientists in different branches of science including biology. He also narrated the enjoyment of doing research particularly biological research and shared his own experiences of Oxford University and encouraged student to take science as their future career goal. Many senior faculties as well as the principal of the school attended this seminar.

Invitation of proposals for ISCB support to its outreach program

Indian Society of Cell Biology invites proposals for conducting workshops and for giving lectures in the colleges located in rural areas of the country. ISCB will fund Rs 20000=00 for conducting cell biology workshops and Rs 10000=00 for delivering lectures to science students in colleges located in rural areas. Details of this can be obtained from the society webpage www.iscb.org.in

Proposals should be sent to

Prof. H. S Misra
Secretary, Indian Society of Cell Biology
&
Head, Molecular Genetics Section
Molecular Biology Division
Bhabha Atomic Research Centre
Mumbai- 400085
Email: harimisra38@gmail.com

Last date for receiving proposals is **July 15, 2016**.

XL All India Cell Biology Conference
&
International Symposium on
Functional Genomics and Epigenomics
Jiwaji University, Gwalior
November 17-19, 2016

First Announcement

The Conference

The Indian Society of Cell Biology (ISCB) formally came into existence in 1976. The main objective of the society is to promote teaching and research in Cell Biology in Indian institutions and aims to bring Cell Biologists from various academic and research organizations in India on a common platform to share their knowledge. Since 1977, the society is organizing its annual meeting regularly in various research and academic institutions. The society joined the international federation of Cell Biology in 1978. The 40th all India Cell Biology conference is being organized by the School of Studies in Zoology in collaboration with Center for Genomics and School of Studies in Neuroscience, Jiwaji University Gwalior, during November 17-19 2016. The conference will cover almost all the areas of Cell Biology and its offshoots, with a special symposium on 'Functional Genomics and Epigenomics', considered as the future of translational research in human and environmental health. The scientific programs in the conference will broadly cover the following:

Scientific Theme

- ✓ Functional Genomics
- ✓ Epigenomics
- ✓ Development and Evolution
- ✓ Neurobiology, Aging and Behavior
- ✓ Cell Structure and Function
- ✓ Infection, Immunity and Diseases
- ✓ Plant Biology and Microbiology
- ✓ Molecular Toxicology, Environment and Conservation Biology.
- ✓ Cellular and Molecular Biology of Stress
- ✓ Cancer Biology and Drug Development
- ✓ Chromosome Biology, Cytogenetics and Clinical Diagnosis
- ✓ Stem Cell Biology and Therapeutics, etc.

Speakers

Agashe D, NCBS, Bangalore
Basu J, Bose Institute, Kolkata
Banerjee A, IISER, Pune
Barbhuiya M, JHUSM, Baltimore, USA
Burma P, DU, New Delhi
Das S, Bose Institute, Kolkata
Deobagkar D, Univ of Pune, Pune
Galande S, IISER, Pune
Jain V, BARC, Munbai
Kundu T, JNCASR, Bangalore
Mishra M, TIFR, Mumbai
Mishra SK, IISER, Mohali
Muniyappa K, IISc, Bangalore
Nair S, TIFR, Mumbai
Pasare C, UTSMC, Texas, USA
Prasad NG, IISER, Mohali
Pongubala J, UoH, Hyderabad
Ray P, ACTREC, Mumbai
Roa JC, Pontifical Catholic Univ of Chile, Chile
Sengupta S, CSIR-IGIB, New Delhi
Sivasubbu S, IGIB, New Delhi
Sarin R, ACTRECT, Mumbai
Sharma PR, UTSMC, Texas, USA
Singh BN, CDRI, Lucknow
Sinha S, NBRC, Manesar
Tapadia MG, BHU, Varanasi
Thakur MK, BHU, Varanasi
Tripathi AK, CIMAP, Lucknow
Tyagi AK, NIPGR, New Delhi
Varshney U, IISc, Bangalore
Wakeland E, UTSMC, Texas, USA and more

Pre-Conference Workshop on "Science Communication & Career Workshop Series" organized with Nature India and Nature jobs in partnership with WellCome Trust/DBT Indian Alliance, on 16th November 2016.

Jiwaji University

Jiwaji University was established in May, 1964 as a State University. The then President of India, Late Dr. Sarvapalli Radhakrishnan, laid the foundation of the University on 11th December 1964 at a sprawling campus of over 225 acres of land at Naulakha Parade ground. This was a generous contribution of Scindia family, in particular, Kailashwasi Maharaja Shrimant Jiwaji Rao Scindia and late Rajmata Shrimati Vijayaraje Scindia. The institution was christened after the name of Kailashwasi Shrimant Jiwajirao Scindia as a standing memorial to his persona. The organizing Departments (SOS Zoology, CFG, SOS NS) are among the most established departments of the University carrying out teaching & research in the areas of Animal sciences (Fish Biology, Entomology, Wild-life conservation, Environmental toxicology, Endocrinology, etc.), Human Genetics and Neurobiology.

Gwalior

Gwalior is a historical city in the heart of India, situated in Madhya Pradesh. The Ancient Indian Classical School of Music "Dhrupad" was fine-tuned here and spread to various parts of India to acquire local flavors. Gwalior is also known as "The City of Music" (perhaps the richest musical tradition in history), the legendary musician Tansen also belonged to Gwalior who was one of the nine jewels of Emperor Akbar's court. Gwalior has a beautiful large Fort Palace built during Tomar dynasty who were connoisseurs of Art & Music. Agra is about110 kms from Gwalior and is easily reachable to Tajmahal. Khajuraho group of temples depicting all facets of life is about 4 hours of journey by road. Orchha is 100 kms from Gwalior and is a treat for weekend trips as the village still carries old time feel with palaces, temples, cenotaphs and runs along the banks of Betwa river.

Registration & Accommodation

Registration fee includes conference kit, breakfast, lunch, high tea and dinner only, from 17-19 Nov, 2016. As Gwalior is a tourist city, accommodation will be very rush during these days. Accommodation is limited and will be provided to outstation delegates on first come first basis on request with reasonable payment (detail will be communicated soon). Participants who register after 15th September, 2016, shall not be considered for accommodation by the organizers. However, a list of budget hotels will be provided and participants are free to make their own arrangements. Please indicate your preferences clearly in the registration cum accommodation form.

Registration: Online from 1st June- 15th August 2016

Faculty	INR. 3500
Student/Post-doc	INR. 3000
Accompanying person	INR. 3000
Foreign delegates	$ 400
Accompanying person (Foreign)	$ 400
Late Registration Fee	INR. 500
(16th August- 15th September 2016)	$ 100
Spot Registration (Faculty)	INR. 4500
Spot Registration (Student/Post-doc)	INR 4000

Abstract Submission: 1st June- 15th September, 2016

Contact: xlaicbc2016@gmail.com

Organizing Secretary:
Prof. P. K. Tiwari
Phone:+91-751-2442772/865
Mob: +91-94-25712787,
-76-97311411, -94-52569750

Convener:
Prof. I. K. Patro
Phone: +91-751-2442789
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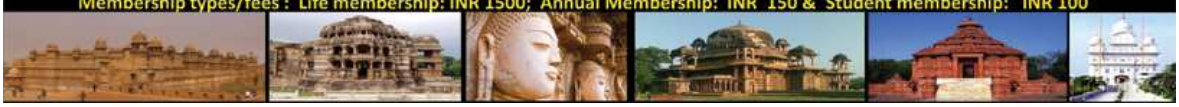
For more details, please visit : www.centreforgenomics.ac.in

Note: Participants, who are not member of Indian Society of Cell Biology, are encouraged to become member.
Membership types/fees : Life membership: INR 1500; Annual Membership: INR 150 & Student membership: INR 100



Announcement and invitation of nomination for Indian Society of Cell Biology (ISCB) Awards for the year 2016

The Indian Society of Cell Biology is pleased to announce "**16th Prof. S P Ray-Chaudhuri 75th Birthday Endowment Lecture** and **1st Prof. Rita Mulherkar Award Lecture"** instituted as a mark of respect to Professor S.P. Ray-Chaudhuri and Prof. Rita Mulherkar for their contributions in Molecular and Cell Biology growth in India. The Executive Committee of Indian Society of Cell Biology is pleased to invite nominations for these lectures awards to be delivered during this year's annual meeting of the society and 40th All India Cell Biology Conference to be held at Jiwaji University between November 17-19, 2016.

Who can nominate- Life member or an ordinary member with minimum 3 years standing and has paid membership fees for the current year.

Who can be nominated- The person to be nominated should be an Indian citizen at the time of nomination/selection and should be an eminent scientist with outstanding original contributions in the area of molecular and cellular biology. The nominee need not be a member of the Society, but may be requested to become a member in due course of time. Further details about the award and the guidelines for the nominations can be learnt from the society webpage at www.iscb.org.in.

Nomination procedure: The nominating member is requested to obtain nominee's consent and send nomination form appended below along with his/her complete bio-data, complete list of publications and a 300 words summary highlighting nominee's seminal contributions. Please send

aforementioned documents of nomination as a single .pdf file through an email to harimisra38@gmail.com and also by registered post to Dr. H. S. Misra, Secretary, ISCB and Head, MGS, Mol. Biol. Division, Bhabha Atomic Research Centre, Mumbai- 400085.

Last date for receiving nominations is July 15, 2016.

NOMINATION FORM

Name & Address of the member making the nomination:

I wish to nominate ....

..... (address. .....

... ...)

for **PROFESSOR SP RAY-CHAUDHURI 75TH BIRTHDAY ENDOWMENT LECTURE / PROF. RITA MULHERKAR AWARD LECTURE** (please strike off one not applicable).

I have obtained consent of the nominee for the purpose. The biodata etc. including highlights of the significant contributions of the nominee are enclosed herewith for consideration.

Date Signature of the nominating member

Note: Upper age limit for Prof. Rita Mulherkar Award is 45 years.

Announcement of Executive Committee election for 2017-2019
&
appointment of a Returning Officer.

The tenure of present Executive Committee (EC) will get over in March 2017 and election of new EC for block year 2017-2019 is due. EC meeting held on December 6, 2015 in Thiruvananthapuram has appointed Prof. Rita Mulherkar, ex-President of the society and renowned cancer biologist, as Returning Officer for conducting election for the new EC for the period 2017-2019. As a preparatory note and as information to all the members of ISCB, I am pleased to share this with you and request to take active part in the process of electing new EC. As you all know the need and strength of voting in any democratic process, please come forward and take part. This involves a good amount of time and money, lets justify. When voting response is poor, the very purpose of election gets defeated. In past, it is felt that members do not come forward for voting in spite of sending well-equipped ballet paper along with stamped envelopes. I take active part in all the elections and do it without loosing my precious time.

We are about to announce the election of 2017-19's EC and its composition will be as below.

1.	President	One
2.	Vice Presidents	Two
3.	Secretary	One
4.	Jt. Secretary	One
5.	Treasurer	One
6.	Members	Twelve

Kind attention: Election for Secretary, Jt. Secretary and Treasurer is mandatory from same city/place. It means that if I vote for a secretary, I must vote for Jt. Secretary and Treasurer from same place, provided if there are people in the ballot paper. **It also goes to people proposing /nominating office bearers, to take care that all the three posts are nominated from same city.** Candidates should also make sure that all three individuals should have good resonance for proper and healthy functioning of secretariat.

Further communications on election will be sent from the Returning Officer, Prof. Mulherkar with detailed guidelines, proforma template and other requirements.

I shall be reminding you time to time for nominations as well as voting etc., so that we should achieve higher representations.

Please take active part in this process.

.....XXXXXX.....

A suggestion to become members of Indian Society of Cell Biology

I as a secretary of ISCB and as a members of several academic and professional societies, very confidently can say that Indian Society of Cell Biology is one of the finest scientific society having very high reputation not only in India but worldwide. Its growing exponentially in terms of its membership strength as well as quality of science its members do in India.
Therefore, ISCB request you all to reach out your colleagues and students to become member of the society.

Revision of membership fees was due for long time and therefore, last Executive Committee in its meeting held in Thiruvananthapuram discussed the possibility of increasing membership fees of the society. EC agreed to it and thereby membership fees of ISCB has been increased and will be implemented from 1st April 2017, after the approval of last EC minutes in EC meeting to be held in Gwalior.

New Membership slabs will be as below

Life membership	Rs. 3000=00	+ Rs 50=00 (admission fee)
Ordinary membership	Rs. 500=00	+ Rs. 50=00 (admission fee)
Student membership	Rs. 300=00	+ Rs. 50=00 (admission fee)

Membership form can be downloaded from ISCB website, www.iscb.org.in

Statement of accounts

[Due to delay in auditing of the accounts, which is underway, statement of account will be produced at later stage].

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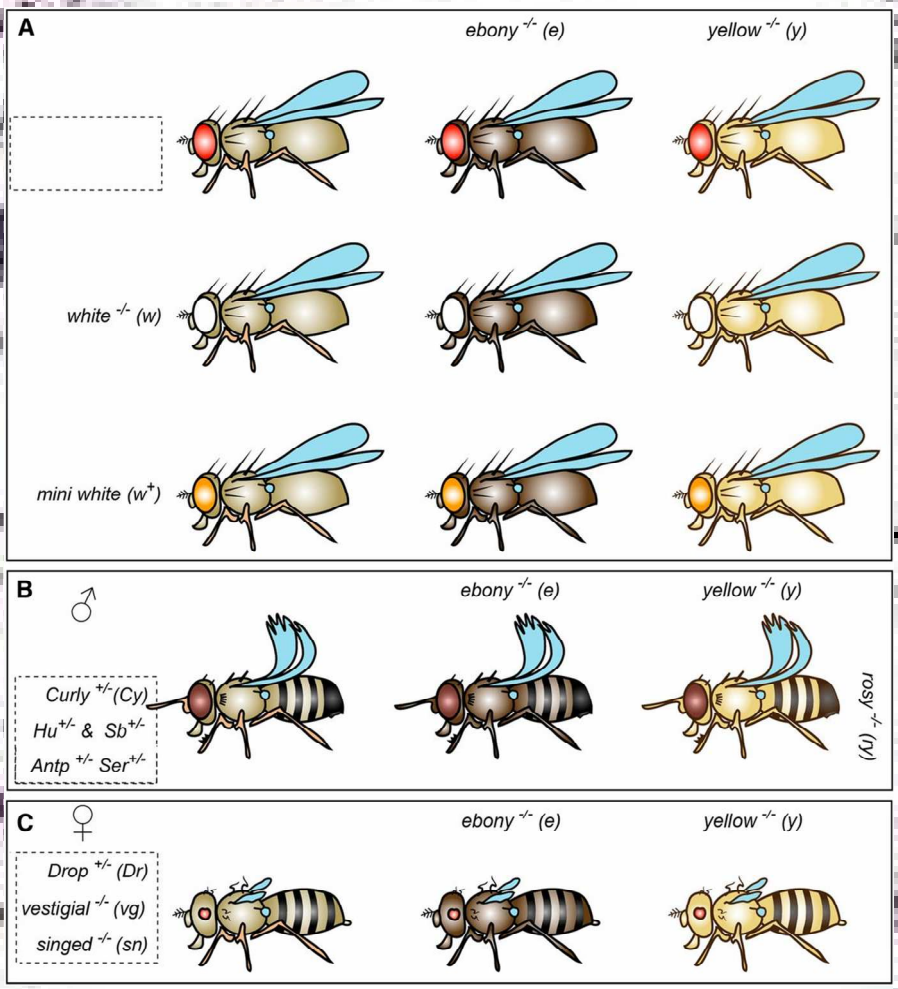
Cell Biology Newsletter



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