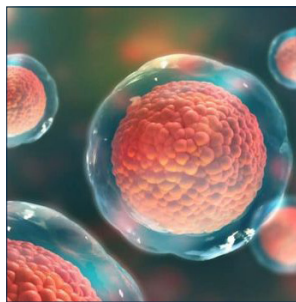# Workshop

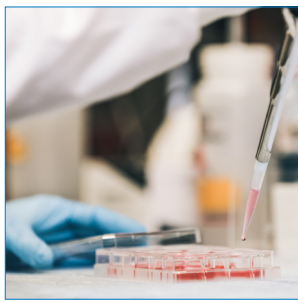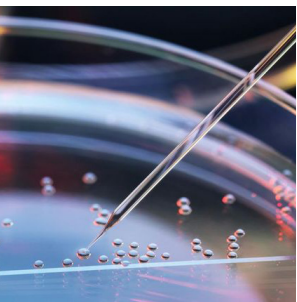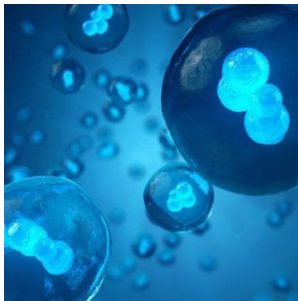## *Genetic Engineering 2019*

International Conference on

Molecular Biology and Genetic Engineering

November 07-08, 2019 | Melbourne, Australia

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Molecular Biology and Genetic Engineering

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M K Sarma

Assam Agricultural University, India

Biodiversity significance of therapeutically potential plant species indigenous to North East India

The North East region of India which occupies a total geographical area of 262, 179 square kilometer and located between 87o E to 97oE latitude and 21oN to 29oN longitude, comprises an important part of the Indo-Burma hot spot of biodiversity which is also known as the 'Cradle of Flowering Plants'. Northeast India characterizes the transition zone between the Indian, Indo-Malayan and Indo-Chinese bio geographic regions and a meeting place of the Himalayan Mountains and Peninsular India. Northeast India is, therefore, the geographical 'gateway' for much of India's flora and fauna, and as a consequence, the region is one of the richest areas in biological values harboring about 8000 of 15000 species of flowering plants available in India. It includes 40 out of 54 species of gymnosperms, 500 out of 1012 species of pteridophytes, 825 out of 1145 species of orchids, 80 out of 90 species of Rhododendrons, 60 out of 110 species of bamboos and 25 out of 56 species of canes. The region is affluent in medicinal and aromatic plants and many other rare and endangered taxa. Already 51, 95 & 18 number of species of medicinal plant in this region has been listed as Endangered, Rare & Vulnerable, respectively.

About 12.5% of the 4, 22,000 plant species documented throughout the world has been known to possess medicinal properties. More than 200 tribes of North East India possess great traditional knowledge of effective herbal medicine inhabit this region. A significantly large number of the population of this part of the country is still dependent on traditional health care systems and use different indigenous methods and materials to treat their own as well as livestock diseases. It has been reported that 152, 77, 81, 19 and 37 numbers of plants have been used by local people in the treatment of Malaria, Stomach trouble, Diabetes, gynecological disorder and disease related to childcare, respectively. This documentation, is however, not exhaustive

considering the great ethnic diversity, difficult terrains of the region and great eco geographical diversity. It has also been observed that people having access to modern allopathic systems of medicine still prefer herbal medicines for their easy access, lesser side effects and low cost. But very less information is available about diversity, uses and cultivation of these plants. Moreover, conservation and sustainable utilization of medicinal plants are important for better management of valuable resources. Several of these medicinal plant species have slow growth rates, low population densities, and narrow geographic ranges ; therefore, they are more prone to extinction. Conversely, because information on the use of plant species for therapeutic purpose has been passed on from generation to generation through oral tradition, this knowledge of therapeutic plants has started to decline and become obsolete through the lack of recognition by younger generations as a result of a shift in attitude and ongoing socioeconomic changes. Through the realization of the continuous erosion in the traditional knowledge of many valuable plants for medicine in the past and the renewal interest currently, the need arises to review the valuable knowledge with the expectation of developing the medicinal plants sector.

Keeping this in background, an attempt was made to focus on the important portion of this diversity that comprises a host of therapeutically important indigenous plant species of this region. So far, two years of our collection effort throughout the area resulted in a collection of medicinal plants which includes 179 shrubs, 177 herbs, 68 creepers and 115trees. The collected germplasm are being maintained in the field gene bank at BN College of Agriculture, Assam campus. The morphological and taxonomic characterizations of the genotypes are underway. It is believed that these valuable genetic stocks shall be of immense value for the research

on drug discovery, validation of traditional healing practices, micropropagation of commercial species and biotechnological studies including genomics, metabolomics & phenomics of medicinal plant. Although, a number of phytochemicals are known worldwide for their use as potential drugs for the treatment of various diseases including cancer, these traditional treasures of medicinal plants are yet to gain the attention of scientific community. They are not only considered as valuable economic resources to the country of India but also as the source of discovery of new drugs and treatments for the ailment of the entire human community of the globe.

Here we would like to draw attention from the scientific community for intensive investigation of the therapeutic properties of the traditionally known species, their bio molecular characterization and screening of specific therapeutically important compounds based on biomolecular tools as well as attempt for conservation

Speaker Biography

M K Sarma is the Plant Breeding and Genetics Coordinator of the Advanced Level Biotech Hub, and also the Professor in the Assam Agricultural University. He has been performing research in the field of Plant breeding and Genetics for 23 years. He was also the visiting scientist to the Molecular Genetics and Genomics Laboratory, Chungnam National University, South Korea. He has published 65 Research Papers and 10 Chapters.

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Scientific Tracks & Sessions
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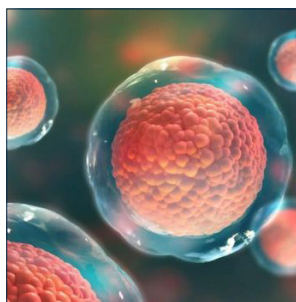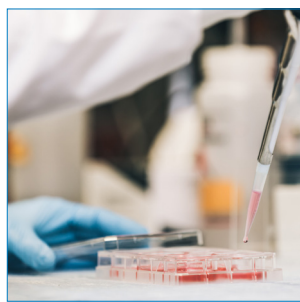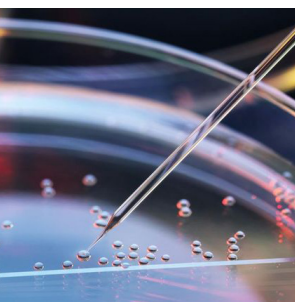
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Mitochondrial DNA structural variation sequencing from single cell (MitoSV-seq)

Elham Jaberi, Emilie Tresse, Joachim Weischenfeldt and **Shohreh Issazadeh-Navikas**
University of Copenhagen, Denmark

Mitochondrial DNA (mtDNA) point mutations and structural variations (SVs) have been reported to contribute to axonal and neuronal cell death and therefore diseases of the central nervous system. Both technical limitations and the heteroplasmic nature of mtDNA have made the identification of SVs in mtDNA challenging. We have developed a novel, high-resolution method, hereby called MitoSV-seq, to identify mtDNA-SVs and single nucleotide variations (SNVs) from single cells in this case in neurons by next generation sequencing, using a designed positive control. We isolated single neurons from brain of Ifnb–/–, a mouse developing a sever demyelinating experimental autoimmune encephalomyelitis and spontaneous neurodegeneration using Flow cytometry cell sorting. mtDNA was amplified exponentially at multiple sites using rolling circle amplification before sequencing. We found 15 SNVs and 39 SVs exclusively in 70% of Ifnb–/– neurons.

Compared with previous methods, MitoSV-seq is optimized to identify a higher proportion with better resolution of variations with low heteroplasmy in single cells. This could serve as an efficient way to identify mtDNA-SVs in a range of conditions that primarily affect mitochondrial functions in the brain.

Speaker Biography

Elham Jaberi has completed her Ph.D. in Cell and molecular biology. During her PhD thesis, she investigated the genetic and molecular basis of two neurodegenerative diseases, Parkinson's disease and ataxia. During her first postdoc experience, she found two novel genes associated with mental retardation, and Parkinson's disease. During her second postdoc at the BRIC, University of Copenhagen, she is working on a new animal model for Parkinson's disease like dementia; IFN-ß knockout mice (Ifnb–/–). She has 9 published and two submitted papers.

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Assessment of genetic diversity and inheritance studies for pre-harvest sprouting resistance in soybean (*Glycine max* L. Merr.)

M K Sarma, A A Sharma, N Ramchiary, Sangeeta Baruah and **P Bora**
Assam Agricultural University, India

A set of 43 diverse soybean genotypes consisting of improved varieties, breeding lines and some indigenous genotypes of North East India were subjected to analysis of genetic diversity along with screening and inheritance study of resistance to Pre-Harvest Sprouting (PHS).

Genetic diversity was studied based on eighteen morpho-physiological attributes and 28 polymorphic SSR markers. Variability parameters estimated for the eighteen traits displayed significant variation for all the traits. Per cent seed germination in pods (SGP) was considered as a measure of PHS tolerance. Both genotypic (GCV= 293.6) and phenotypic level (PCV= 45.08), the highest coefficient of variation was exhibited by SGP followed by seed germination and pods per plant. Character association studies revealed significant and positive association of PHS with seed germination per cent and number of branches. Highest positive direct effect on PHS was observed for number of clusters followed by seed germination (%) and pods per cluster.

D2 analysis followed by grouping of genotypes by Tocher's method resulted into grouping of the genotypes into seven distinct clusters. Highest contribution to diversity was exhibited by pod diameter (33%) followed by seed weight (22%) and pod length (15%).

The set of genotypes were also subjected to analysis of diversity with a set of 28 polymorphic Simple Sequence Repeat (SSR) markers. A total of 190 scorable bands in the 43 genotypes were studied. The number of alleles per primer varied from 2 to 12 with an average of 3.2 alleles per locus and the percentage of polymorphism varied from 14.29% to 100%. The PIC values ranged from 0.2688 (Sat_211) to 0.8562 (Sat_356) with an average of 0.6692. Most of the SSR markers had PIC value greater than 0.3 and hence these can be reported as the most informative markers. The diversity detected by the markers were evaluated by parameters Shanon -Weaver Diversity index and Gene Diversity.

Principal component analysis performed for the 43 soybean genotypes using 190 alleles of the twenty-eight SSR markers revealed clear diversity among the genotypes under study. The pairwise genetic similarity ranged from 0.21 to 0.81. Cluster analysis based on the SSR markers grouped 43 genotypes into eleven diverse clusters at 35% similarity level.

Pre-harvest sprouting is a major setback to soybean production under high rainfall condition of the North East Part of the country including Assam. This causes major yield loss to the crop and results in the degradation of seed quality. Inorder to expand soy cultivation in this nonconventional part of the country, it is very important to study the genetics and inheritance pattern of PHS. In the present investigation, soybean genotypes under study were screened for incidence of Pre-Harvest Sprouting (PHS) and scored on a scale of 0-9. Twenty-two entries showed significant susceptibility to PHS while the rest 21 entries were resistant to PHS sprouting under the same environmental conditions. This study revealed the presence of resistance to PHS paving the way for an attempt to study the inheritance pattern of PHS resistance in soybean. Nine cross combinations between highly resistant and susceptible exhibited complete resistance in F1 with score zero (0). The F2 populations exhibited segregation for PHS resistance in a definite 3 (Resistance): 1(Susceptible) ratio which was confirmed by Chi-square (χ 2) test. This confirmed that the resistance to PHS was governed by a single dominant gene.

Speaker Biography

M K Sarma is the Plant Breeding and Genetics Coordinator of the Advanced Level Biotech Hub, and also the Professor in the Assam Agricultural University. He has been performing research in the field of Plant Breeding and Genetics for 23 years. He was also the visiting scientist to the Molecular Genetics and Genomics Laboratory, Chungnam National University, South Korea. He has published 65 Research Papers and 10 Chapters.

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Significance of MicroRNA (miRNA) in prostate cancer hamstering by plant isolated compounds

Saritha Surapaneni

R R College of Pharmacy, India

Prostate cancer (PC) causes the highest mortality in men. Early diagnosis of prostate cancer involves in radiotherapy and many researchers have reported that MicroRNAs regulates the apoptosis by involving androgen receptor pathways. The gene expression can be controlled by the small non-coding RNAs. MicroRNAs regulate gene expression at the level of post-transcription involving innumerable pathological and physiological changes containing cancer cell invasion involves in progression and leads to metastasis with therapeutic resistance. Most of the research reported Isolated compounds to interact with most of the cellular signaling cascade and the process of the transcription factor repeatedly affecting the gene expression based on the in vitro and in vivo studies. These interesting experiments performed has reported MicroRNAs are the mediators in the regulation of isolated components that show enumerated biological effects. This review mainly focuses on the involvement of MicroRNAs in cell metabolism which includes glycolysis, glucose uptake and lipid metabolism by interactive with lactate secretion forming cell signaling pathway.

Speaker Biography

Saritha Surapaneni has completed her Ph.D. from Rajiv Gandhi University of health sciences Karnataka. Presently she is working as an Assistant professor in the Pharmacology Department of R.R. College of Pharmacy. She has published 7 papers and has participated recently in the 74th FIP World Congress of Pharmacy and Pharmaceutical Sciences.

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Potentials of human umbilical cord-derived cells in clinical application

Hasan Mahmud Reza
North South University, Bangladesh

Extensive studies of the human umbilical cord, both basic and translational, over the last three decades have unveiled a plethora of information. The cord lining harbors at least two phenotypically different multipotent stem cells- mesenchymal stem cells (MSCs) and cord lining epithelial stem cells (CLECs). These cells exhibit mixed genetic profiling of both embryonic and adult stem cells, hence display broader stem features than cells from other sources. Importantly, umbilical cord-derived cells are immunologically privileged, non-tumorigenic, and ethically acceptable, thus provides a significant advantage over other stem cells. The high proliferative capacity, viability, differentiation potential and superior harvest of these cells have made them better candidates in comparison to contemporary adult stem cells. Following 30 replication cycles, these cells have been observed to retain their stemness, with their phenotype and karyotype intact. The striking features of low immunogenicity protecting self along with co-transplanted allografts from rejection largely define the transplantation potential of umbilical cord-derived stem cells. A good number of recent pre-clinical and clinical studies have established the amazing prospects of cord-derived stem cells in regenerative medicine. These cells have been successfully applied to many chronic conditions, using animal models, including type 1 diabetes, limbal stem cell deficiency, burn injuries, and wound healing, etc. with encouraging results. A substantial number of clinical trials using MSCs and CLECs are currently in progress, results of these studies are likely to delineate the potential use of these affordable and allograftable stem cells in various clinical applications.
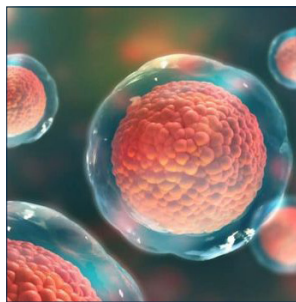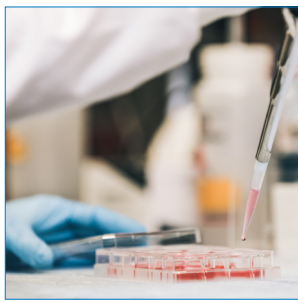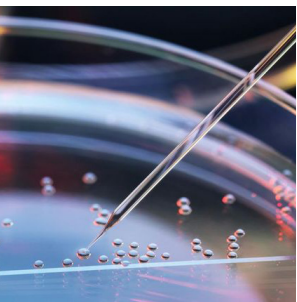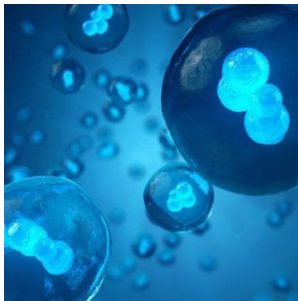
Speaker Biography

Hasan Mahmud Reza has a solid experience of research and teaching for more than 22 years in reputed universities and institute in Bangladesh, Japan and Singapore. He completed his B Pharm and M Pharm degrees from the University of Dhaka. He is currently leading several research teams dedicated to work on pharmaceutical dosage form development, behavioral neuroscience, natural products and lifestyle diseases like hypertension, in addition to stem cell research.

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Young Researchers Forum

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Signature pattern of gene expression and signaling pathway in premature diabetic patients uncover their correlation to early age coronary heart disease

Salma Ahmadloo[1], Ling King Hwa[2], Ahmad Fazli[3] and **Patimah Ismail[1]**
[1]Shahid Beheshti University, Iran
[2]Harvard Medical School, USA
[3]Serdang Hospital, Malaysia

Coronary Heart Disease (CHD) is still the number-one killer in the world. The number of people with premature CHD has more than tripled in the past 40 years and the figures are still growing. Notably, many of the patients with CHD have diabetes mellitus (DM). This study was carried out for the purpose of profiling expression of DM associated genes and identify related biological process and modulated signaling pathways of Malaysian male subjects with CHD from three ethnic groups, namely Malay, Chinese and Indian. In order to achieve the goal, four groups of subjects were divided into: 1) healthy subjects; 2) subjects with only DM; 3) subjects with only CHD, and 4) subjects with CHD + DM. The RNA was extracted from blood specimens by mean of commercial extraction kits. The RT2 Profiler™ PCR Array was utilized to determine gene profiling on group 1 and group 2, group 1 and group 3, group 1 and group 4. To validate the results of RT2 profiler™ PCR Array, significantly dysregulated genes were selected and validation was conducted through Q-RT-PCR in a larger and independent population. For this purpose, new subjects were divided into 1) healthy subjects. 2) Subjects with DM+CHD. 12 significantly dysregulated genes related to diabetes and Toll-Like receptor signaling pathway were identified which may be a culprit to susceptible diabetic patients to CHD development. In Silico experiments imply a role for inflammatory responses in the circulating leukocytes as a biomarker reflecting initiation of CHD in patients with DM. In conclusion, some differentially dysregulated genes and modulated pathways were identified which warrant further investigation in the setting of CHD and its risk factors. It is hoped that a greater understanding of genetic predisposition to CHD will unravel clues to its etiology and allow development of novel diagnostic and therapeutic tools to permit targeted interventions to reduce this global health burden.

Speaker Biography

Salma Ahmadloo has completed her Ph.D. in the field of Medical Genetics from Universiti Putra Malaysia. She is a Postdoc fellow in Shahid Beheshti University of Iran. She is an experienced Senior Researcher with a demonstrated history of working in the higher education industry.

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