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MEDGENOME

GeKNOWme

Internal Quarterly Newsletter

WORDS FROM THE MANAGEMENT

Dr Andrew Peterson

Chief Scientific Officer

Dear Colleagues,

I am tremendously excited and honored to be joining MedGenome as Chief Scientific Officer and to have the opportunity to join with all of you in driving our further growth and development. The company that all of you have contributed to building has changed the scientific and business landscape and the journey that we have ahead of us is full of possibility. I look forward to forming new relationships, strengthening already existing ones and working with all of you to continue and build on the excellent science that will drive our business growth in the years ahead.

Prior to joining MedGenome, I worked at Genentech for 13.5 years, most recently as Senior Director of Molecular Biology. As many of you know, while I was at Genentech I worked with MedGenome's research services business and had an extremely productive set of collaborations involving MedGenome and investigators all across India. Those experiences opened my eyes to the dynamic possibilities for genome science to contribute to a diverse and rapidly growing society and formed the basis of my decision to join MedGenome and commit myself fully to exploring how to drive our science forward together with all of you.

My role at MedGenome will be focused on increasing the scale and scope of our drug discovery efforts and where those efforts open up opportunities, contributing to the growth in the Company's diagnostic business. We as a company are poised for even stronger growth and development than we have already experienced and all of us will need to seek ways to continue to evolve and develop. Our growth opens up many possibilities and we all must continue to ask ourselves how to increase our productivity while maintaining high standards of scientific excellence. Let us all get involved because we care so much, that we want to make whatever we are doing the greatest it can possibly be.

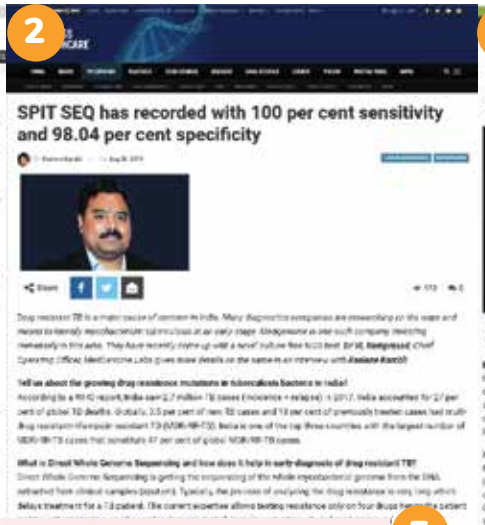
HIGHLIGHTS

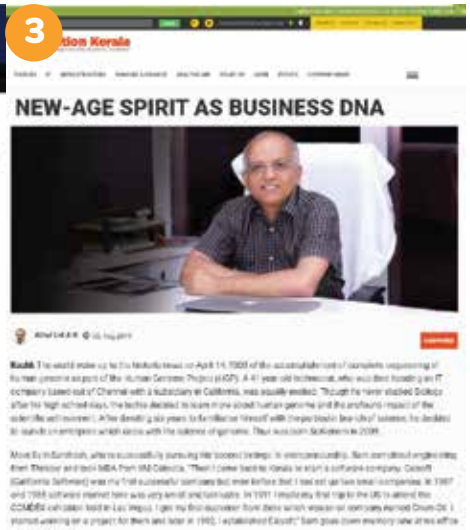
Most Talked About

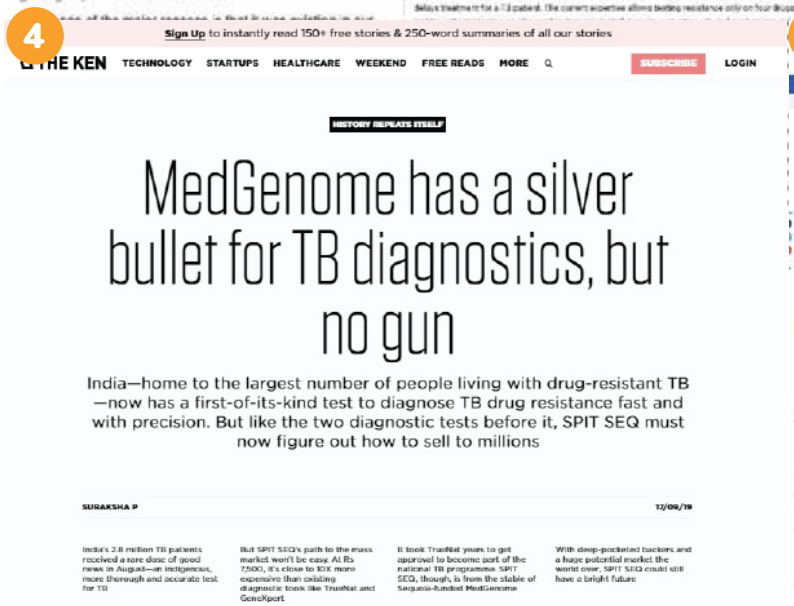
The News

EDGENOME NEWS | MAY To JULY 2019 | MEDGENOME NEWS

ACTIA • CLARIA • PRIMA • Business • Research • Awards • Genetic Counselling • Health Care







1. Autoimmunity is now gaining importance in India: Dr Aparna Jairam - ET Healthworld
   https://health.economictimes.indiatimes.com/news/industry/autoimmunity-is-now-gaining-importance-in-india-dr-aparna-jairam/71513387
2. SPIT SEQ has recorded with 100 per cent sensitivity and 98.04 per cent specificity - Express Healthcare
   https://www.expresshealthcare.in/lab-diagnostics/spit-seq-has-recorded-with-100-per-cent-sensitivity-and-98-04-per-cent-specificity/413805/
3. NEW-AGE SPIRIT AS BUSINESS DNA
   https://www.destination-kerala.com/new-age-spirit-business-dna
4. MedGenome has a silver bullet for TB diagnostics, but no gun - The Ken
   https://the-ken.com/story/medgenome-tb-diagnostics-spit-seq/
5. All about sickle cell disease- Dr Sheetal Sharda - Pioneer
   https://www.dailypioneer.com/2019/pioneer-health/all-about-sickle-cell-disease.html

MedGenome connect

Announcing the arrival of VeriSeq Version 2

Claria
Reproductive Genetics

MedGenome has been the market leader in NIPT segment, and has been setting high standards in prenatal genetic testing with the only SNP-based NIPT in India.

Taking a leap further in aneuploidy testing, MedGenome launched VeriSeq NIPT Version 2, a noninvasive test that utilizes whole-genome sequencing of cfDNA fragments, derived from maternal peripheral whole blood samples from pregnant women of at least 10 weeks gestation, using counting based technology.

This a shot in the arm for MedGenome as it allows us to screen for a broader range of chromosomal and sub-chromosomal conditions associated with birth defects and adverse pregnancy outcomes than the standard NIPT offering.

VeriSeq NIPT Version 2 takes advantage of powerful Illumina NGS technology to bring a whole-genome sequencing (WGS) approach to NIPT, expanding test menu options to include common aneuploidies (chromosomes 21, 18, and 13), all rare autosomal aneuploidies (RAAs), sex chromosome aneuploidies (SCAs), and partial deletions and duplications, referred to as copy number variations (CNVs), ≥ 7 Mb in size. This enables clinicians to support expectant parents with informed, timely and personalized pregnancy management options better than ever before.

With the launch of VeriSeq Version 2, Claria NIPT is much more affordable, counters the competition, strengthen business relationship with key clients and doctors, and also cementing its leadership position in prenatal segment.

Huge turn-out at the prenatal CME at Safdarjung Hospital, New Delhi on 29th July

A momentum was already there with Claria conducting 10 CMEs and RTMs in Q2, and customer coverage reaching beyond 250. With various NIPT-centric CMEs & RTMs, and regular customer connect by both Business and Technical teams, one can expect the 3rd quarter to be the game-changer in FY 2019-20.

Prima
Cancer Genetics

Dr Vidya in discussion with KOL's at Raktavigyan, Patna

We at Prima have conducted series of events and participated in good number of National Oncology Conferences, we had quality and important scientific events for Team Prima.

We organized/participated in following important CME's/standalone Meetings

1. Indian Breast Cancer Conference, Jaipur
2. Raktavigyan, Patna
3. 5th Innovation in Oncology Conference, Faridabad
4. Surat Paediatric Association, Haematology Update

Our team of experts, Dr Ramprasad, and Dr Vidya, made our participation remarkable with their involvement.

The visibility and awareness on Prima and its offerings was boosted further by sales team across cities in India.

The major therapies touch-based through these engagement programs were Oncology, Haematology and Primary Immunodeficiency.

ACTIA
Inherited Genetics

Best wishes to you all for this festive season!

The 2nd quarter for financial year 2019-20 was significant, as we conducted 14 CMEs & RTMs, and participated in 4 conferences – 1 each at Hyderabad, Gurgaon, Chennai and Lucknow. With these, our reach was with nearly 600 clinicians pan India.

In addition to this, Actia also participated in Cure SMA Clinic, a patient awareness initiative of SGRH, Delhi wherein nearly 70 participants (Patients & Caregivers) attended the event. Actia also organized a patient camp on DMD at Ahmedabad wherein 25 patients came for screening.

The key agenda for Q3 is to further develop Tier 2 & 3 markets, and get as many new doctors in fold as possible.

Medgenome in the news - Gujarat samachar covered the DMD patient camp at ahmedabad on 7th September

MedGenome Scientific Symposium on 27th September 2019, Friday @ Narayana Nethralaya Auditorium

MedGenome recently organised a day-long symposium addressing various interesting facets that covered ongoing projects and developments in MedGenome.

The discussion involved key stake holders and some external participants. The event was attended by more than 100 scientific and key personnel from various departments of MedGenome.

The event started with Dr. Eric Stawiski's (VP Bioinformatics) opening remarks, who invited Mr. Sam Santhosh, Chairman & Global CEO to deliver the introductory speech.

Mr. Sam spoke about MedGenome in brief and he iterated how this kind of symposiums could be an inspiring event to understand the various dimensions MedGenome is exploring in both diagnostics and research space. He said he would look forward for many more such events to enable a continuous scientific interaction that can instil progressive outcomes.

This was followed by Dr. Ram's inspiring speech starting from his days of PhD till what is transpiring at MedGenome. He extensively spoke about how MedGenome is making a huge difference to the health sector in India owing to its rigorous quality and regulatory practices followed across the company. He also reiterated the fact that MedGenome's Reports are by far the best in market adhering to international norms much better while compared to other competitors in the industry.

Dr. Priya in her talk on "Expanding scope of non-invasive prenatal testing" stressed how the new technology of cell-free DNA testing is making an impact in prenatal diagnosis and treatment.

While Dr. Sakthivel Murugan in his talk on "Genetic Landscape of Neuromuscular Disorders – MedGenome Experience and Therapeutic Implications" touched upon the various tests on the offering covering critical ailments such as Neuro Muscular and Neuro Degenerative Disorders, and how our findings are helping doctors in their regular clinical practice.

Dr. Sheetal Sharda in her talk "Expanded Carrier Screening Testing: Are We There Yet" spoke about the need for awareness in regards to the "Carrier Screening Testing" in general population and particularly its impact on couple who are planning for a pregnancy specifically involving those whose marriage is of consanguineous nature.

Dr. Sekar Seshagiri spoke extensively about India's uniqueness in terms of its diverse population groups. He highlighted how GenomeAsia is shedding new lights on the Indian Population how unique groups are being identified and studied upon. He further delved deeply on Familial Lung Cancer, Gall Bladder Cancer and Genomics enabled drug development.

Dr. Savita Jayaram provided an overview about "Single-Cell and TCR Pipeline Development and Applications".

Dr. Kushal Suryamohan stressed on our "De novo assembly" projects involving assembling genomes with different sequence lengths.

Dr. Eric Stawiski enumerated how Bioinformatics workflow is being organised in US Lab and provided an overview about MAnGo Design.

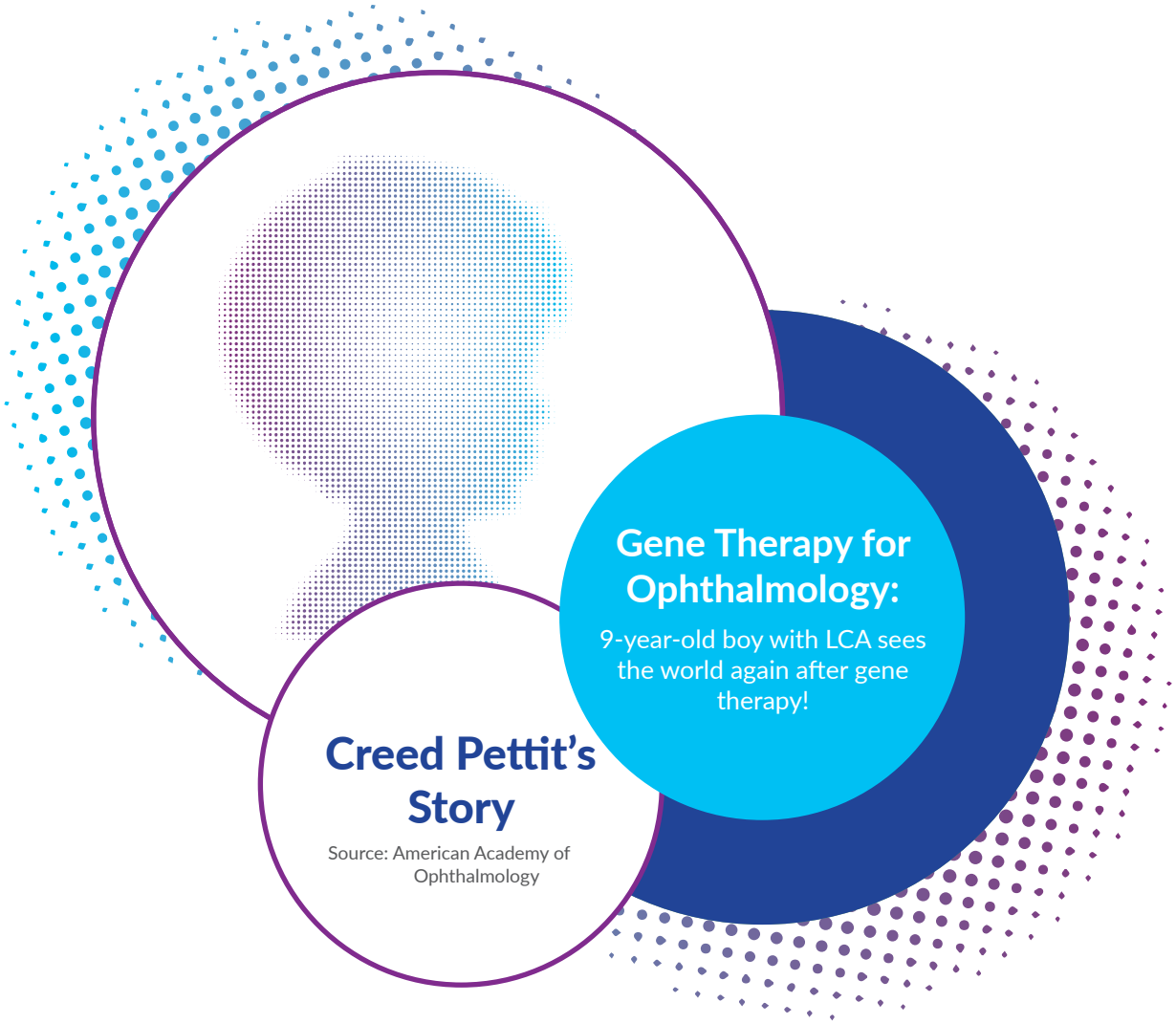
Dr. Ravi spoke extensively about the progress made in Bioinformatic tools at MedGenome and its utility in supporting diagnostics and ongoing R&D Projects. And, Dr. Ramesh Menon provided an overview on "Validation of a genome-wide polygenic risk score on South-Asian individuals for prediction of Coronary Artery disease". While, Dr. Soumittra N highlighted few aspects of our FGDS Program.

Dr. Andy Peterson spoke extensively about MedGenome's Infrastructure and Clinical Network to drive Drug Development. Dr. Jeff Wall provided deep insights derived out of GenomeAsia Project in his talk "The Genome Asia Project: What we learned and why its important for drug discovery".

The session ended with the External speaker Mr. Zoltan Takacs in his talk "The Snake Hunter" enthralled the audience with his experiences from adventures across the world. Who also spoke about the medicinal properties of various venoms and its importance in antivenom drug discovery.

Dr. Zoltan Takacs

Making a difference



Creed Pettit, a 9-year-old boy from Miami, Florida had been slowly going blind since the day he was born. After a series of tests and analysis his doctors advised genetic testing. The outcomes of the test indicated that he had a rare genetic condition called Leber congenital amaurosis (LCA).

The mutation was identified in *RPE65*, a gene associated with retinal dystrophy, which leads to vision loss and complete blindness in certain patients.

His genetic diagnostic results allowed his ophthalmologists to treat him with Luxturna (voretigene neparvovec-rzyl), an FDA-approved gene therapy to treat children and adults with biallelic *RPE65* mutation. **TODAY CREED IS ABLE TO SEE THE WORLD AGAIN.**

Summary

- Genetic testing ensured identification of mutation in *RPE65* as the responsible gene for patient's blindness
- Subsequent gene therapy with Luxturna ensured restoration of sight
- More than 60% of cases of blindness among infants are caused by inherited eye diseases such as congenital cataracts, congenital glaucoma, retinal degeneration, optic atrophy and eye malformations

From our US office

Cell Symposia

Engineering Organoids and Organs

August 25-27, 2019 — Paradise Point, San Diego, CA, USA

This quarter we attended the "Cell Symposia: Engineering Organoids and Organs" conference.

Cell Symposium brings scientists studying organoids and organ engineering together with bioengineers to discuss the exciting opportunities and challenges for engineering complexity in higher-order organ-like systems and to foster collaborations and synergize efforts toward generating cellular platforms that can address a myriad of unmet needs.

Recently, we also organised a symposium on "Single-Cell Sequencing Solutions" where critical subjects in the area was touched upon by technical experts including MedGenome scientific fraternity. Present in the event were:

- **Dr Michael Bassik,** Principal Investigator, Bassik Lab,Stanford University, Department of Genetics
- **Dr Eric Chow,** Assistant Professor, Biochemistry and Biophysics, Director of the Center for Advanced Technology (CAT), UCSF
- **Dr Ankita Das,** MedGenome, Marketing Manager
- **Dr Jeff Granja,** Post Doc, Stanford University, Will Greenleaf Lab
- **Mr. Steven Hoffman,** Single-Cell Sequencing Marketing Manager, Illumina, Inc.
- **Dr Tarjei Mikkelsen,** 10X Genomics VP of Biology
- **Mr. Jose Jacob,** Mission Bio, Field Application Scientist

We participated at the ASHG 2019 event held between October 15th-19th, 2019, at Houston, Texas where over 6,000 professionals in human genetics attended to learn the very latest spanning the breadth of human genetics.

ASHG 2019 ANNUAL MEETING
HOUSTON • OCTOBER 15-19

Sneak peek into the world of science

FLT3

Dr Meeta Sunil
Bioinformatics Research

FLT3-ITD Finder: A new method to detect internal tandem duplications (ITD) from NGS samples in FLT3 gene implicated in cytogenetically normal AML

Leukaemia and Acute Myeloid Leukaemia (AML)

Leukaemia is one of the major forms of cancer that causes uncontrolled growth of anomalous blood cells, thereby disrupting all the key functions of the blood – oxygen transport (RBCs), immunity (WBCs) and clotting (platelets). As per the World Cancer Research Fund (American Institute for Cancer Research), leukaemia is the thirteenth most frequent cancer in the world with over 4.3 lakh new cases diagnosed in 2018 alone. The regional leukaemia rates across the globe are depicted in Figure 1, showing the rate being maximum in US, Australia and Europe.

Within MedGenome, the number of samples processed on HEME exome panel (that targets specific genes implicated in leukaemia) has increased rapidly from 30 samples (with an average of 3 samples per month) in 2016 to 781 samples (with an average of 78 samples per month) in 2019. Figure 2 shows the trend for the number of samples processed in MedGenome from 2016, indicating the increase in cases of leukaemia

Leukaemia originates in the bone marrow and can either affect the lymphoid stem cells (lymphocytic leukaemia) or the myeloid stem cells (myeloid leukaemia) (Figure 3). The cancer can progress quickly resulting in death within months (acute leukaemia) or slowly over a few years (chronic leukaemia). The, four major types of leukaemia are : -

1. Acute Lymphocytic/lymphoblastic Leukaemia (ALL),
2. Chronic Lymphocytic/lymphoblastic Leukaemia (CLL),
3. Acute Myeloid Leukaemia (AML),
4. Chronic Myeloid Leukaemia (CML). Leukaemia affect children (juvenile) and adults as well.

Figure 1: Estimated age-standardized incidence of leukaemia, 2012. It is based on data from the GLOBOCAN database of national estimates. Adapted from: https://www.mdedge.com/fedprac/article/160734/all/global-snapshot-leukemia-incidence

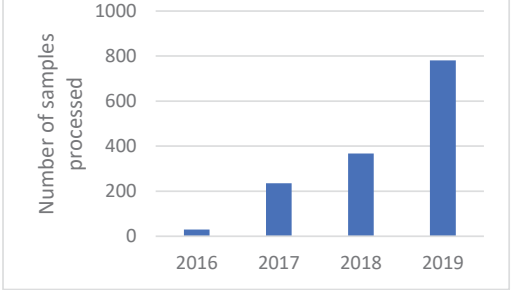


Figure 2: Number of samples processed in MedGenome on HEME exome panel from 2016 to 2019, taken from TrackPro

Among the leukaemia sub-types, AML is the most common in adults and has the least survival rate. It constitutes about 25% of all leukaemia cases worldwide. In adults, it has a late onset (average 65 years) while in children, it can happen at any age but is mostly seen in babies up to two years old or in the teens. AML is a heterogenous disease and 50% of its cases can be attributed to many different genetic aberrations as listed below:

- Chromosomal translocations (like PML-RARA, RUNX1-RUNX1T1, CBFB-MYH11, etc.) that can be seen in a cytogenetic analysis test like Karyotyping or FISH.
- Other somatic mutations in cytogenetically normal (CN-AML) cases in genes encoding/involved in signalling and kinase pathway (e.g. FLT3, RAS, PTPN11, etc.), epigenetic modifications (DNMT3A, IDH, TET2, etc.), nucleophosmin (NPM1), transcription factors (CEBPA, RUNX1 and GATA2), tumor suppressor (TP53), spliceosome complex, and, cohesion complex.

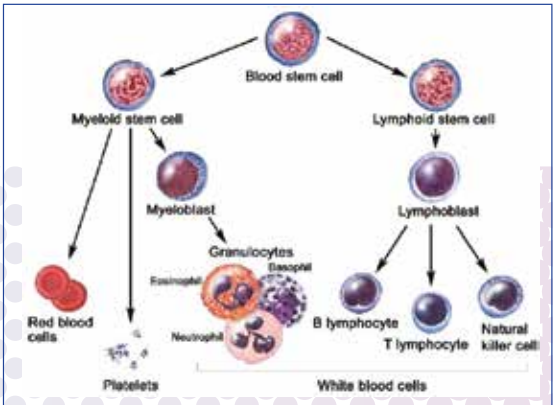


Figure 3: Types of haematopoietic/blood stem cells that are progenitors for RBCs, WBCs and platelets. Adapted from https://www.cancer.gov/types/leukemia/patient/child-aml-treatment-pdq

FLT3 gene and its implications in AML

The FLT3 gene encodes a 993 amino acids long FMS-like type III receptor tyrosine kinase. The translated protein consists of a signal peptide (SP) at the N-terminus in the extra-cellular region along with five Ig-like domains of similar sizes followed by a trans-membrane (TM) domain, a juxta membrane (JM) domain and a kinase domain (interrupted by a ~50 amino acids long kinase insert, KI) present intra-cellularly at the C-terminus (Figure 4).

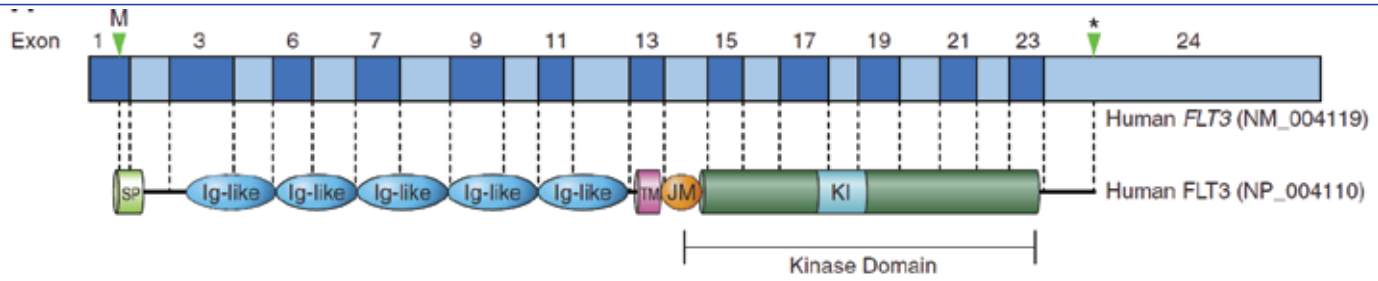


Figure 4: Domains in FLT3 protein. The figure is adapted from Kazi and Rönnstrand, 2019

FLT3 mutations are among the most recurrent ones in AML. Majorly, two types of mutations have been identified – Internal tandem duplication (ITD) in exons 14-15 within the JM domain (causing in-frame insertion of 1 to more than 133 amino acids and hence, elongation of the JM domain) and Tyrosine Kinase Domain point mutations (TKD). The FLT3-ITD causes the cancer in about 20-30% of adult AML cases and more than 35% of just the CN-AML cases while TKD mutations are responsible for 5-10% of the AML cases. The ITD is a gain-of-function mutation causing ligand-independent auto-phosphorylation and constitutive activation of the FLT3 receptor leading to uncontrolled proliferation, survival, and differentiation of aberrant myeloid cells, and thereby, inhibiting the growth of normal blood cells. The burden of ITDs in FLT3 has been strongly associated with prognosis, response to chemotherapy, leukocytosis, high blast counts, increased risk of relapse and a shorter overall survival.

Conventional method for detection of FLT3-ITD

Fragment analysis is the gold standard method to detect the presence or absence of ITD in AML patients. It is a PCR-based method where the region spanning exons 14-15 is amplified using fluorescent-labelled primers, separated by capillary electrophoresis and measured as peaks in terms of relative fluorescence units (Figure 5). The DNA is extracted from peripheral blood or bone marrow of CN-AML patient. The length of the ITD is calculated by subtracting the length of the wild type fragment from the length of the mutant fragment while the mutant allele fraction is measured as the ratio of area under the curves (AUCs) of the mutant fragment vs the wild type fragment peaks. Some mutants have a very low allelic burden and fall below the limit of detection by this method and get classified as false negatives.

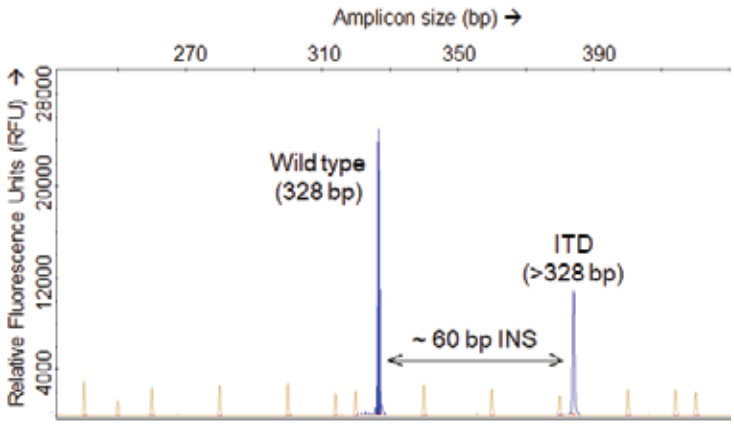


Figure 5: Fragment analysis of a FLT3-ITD +ve sample showing wild type (328 bp) and mutant (388 bp) fragments of FLT3 JM domain within the sample indicating an ITD of 60 bp.

Further, identification of FLT3-ITD, bioinformatically, has also been challenging. There are few tools like lofreq and pindel that can detect such events from NGS data but their validation by visualization also becomes difficult in many cases owing to the anomalously mapped reads. Also, false positive as well as false negative cases have been observed with these methods. To overcome these limitations, an in-house pipeline has been developed that involves an accurate identification of the ITD from HEME exome panel data and allows easy visualization of the event.

FLT3-ITD Finder: A novel NGS-based assay for identification of FLT3-ITD

MedGenome's clinical NGS assay for prediction of FLT3-ITD called FLT3-ITD Finder has been designed for analyzing any DNA-seq data that covers the FLT3-ITD hotspot region (exons 14-15) and generating output files for summary and visualization of the predictions made on presence or absence of the ITD in the sample. It has been specifically tested on samples sequenced on the HEME panel that covers the FLT3 gene. The assay is based on the following logic:

- short reads from the sequenced DNA (sample) that come from a region bearing any structural variation (SV) will either not align to the reference genome or will align anomalously, i.e., with mismatches, and/or, gaps as insertions or deletions within the alignment.
- local *de novo* assembly of such reads will recreate the SV event, thus, yield a virtual sequence for the FLT3-ITD hotspot region along with the internal tandem duplication event.

FLT3-ITD Finde involves aligning adapter-trimmed reads to the reference genome for extraction of unmapped and anomalously mapped reads (reads that do not map with 100% identity) from the FLT3-ITD hotspot region spanning introns 13-15, their *de novo* assembly, global pairwise alignment of the resulting assembled sequences (contigs) to the reference genomic locus (FLT3-ITD hotspot region), parsing the alignment output for prediction of ITD events and reporting the predictions in a VCF file. The pipeline also outputs a custom alignment (BAM) and Fasta (reference) file that can be visualized in IGV, in addition to the VCF file, for validation of the ITD events. The different steps involved in the pipeline has been depicted in Figure 6.

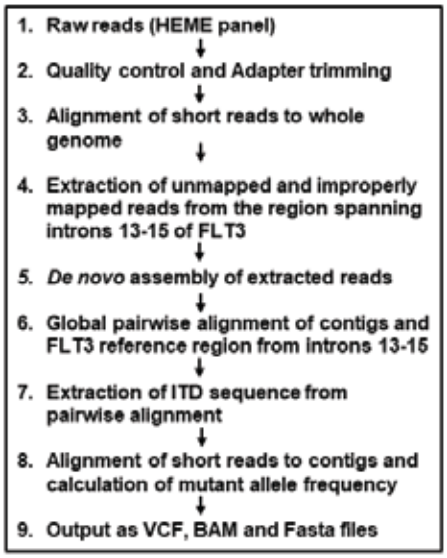


Figure 6: Steps involved in the NGS assay for prediction of presence or absence of ITD ion CN-AML cases

The pipeline has been validated on 15 clinical samples with 10 positive cases and 5 negative cases and was found to be 100 % concordant with Fragment analysis results. The longest ITD identified was 180 bp. The length of the ITDs, *in vivo*, can range from 3 to more than 400 bp. The length that can be identified by this method depends on whether it was captured by the sequencing parameters or not (longer insert size and longer read lengths favour capture of longer ITDs). The FLT3-ITD Finder is one of the CAP accepted tests in MedGenome

Conclusion

FLT3-ITD Finder addresses the many challenges faced earlier within MedGenome in identifying and reporting FLT3-ITD cases. These challenges include visualization of the event in IGV, false negative cases due to very low allelic frequency and false positive cases predicted by other bioinformatics tools. The method has been validated on clinical samples and with inter-lab comparison and has been found to be 100% accurate in predicting the presence or absence of one or more ITD fragments within a CN-AML patient. A shift from Fragment analysis to NGS assay has made the diagnosis more automated, economical and faster. In future, the assay could be further enhanced to include annotation of the predicted ITD events to further help clinicians select the treatment method.

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From our Colleagues

Art meets Science

"For most scientists, I think the justification of their work is to be found in the pure joy of its creativeness; the spirit which moves them is closely akin to the imaginative vision which inspires an artist. - By James B. Conant

Dr Hema Purandare - Consultant and Medical Director, MedGenome

Sukanya Sarkar - Genome Analyst

Dr Hema Purandare - Consultant and Medical Director, MedGenome

From our Colleagues

Our employee's little Picasso :)

By: Rutwik (9 years)
DNA of Amit D Parhar

By: Rutwik (9 years)
DNA of Amit D Parhar

By: Rutwik (9 years)
DNA of Amit D Parhar

By: Rishi P (3 years)
DNA of Roopa Shanmuga Kumar

By: Shivani Praveen (6 years)
DNA of Praveen Raj

9th Nextgen Genomics, Biology, Bioinformatics and Technologies Conference

Sep 30th - Oct 2nd, 2019, Taj Lands End, MUMBAI, INDIA

Genome is an organism's complete set of DNA and Genomic research concerns the sequencing and analysis of an organism's genome. The progressive research in this field has created a revolution in understanding complexities of living organism, diseases and various other factors that impact all living things – be it human, animal or plant. Genome/ genomic research has been applied to understand various diseases, precision medicine, drug discovery, snakebite cure, crop development, genetic diversity, etc. In 1975, a unique molecular marker, idiotype, was discovered on blood cancer cells which opened new avenues for cancer diagnosis and therapy- Cancer immunotherapy, truly a scientific breakthrough. The average life expectancy of a person with Down Syndrome is now 60 years compared to only 25 years in 1983 due to understanding of the genetic code of human chromosome 21. Advancement in technology has not only enabled scientists to dive deeper into genomics but it has remarkably reduced the cost associated towards the research as well as for the customers.

With several organisations getting into genetic / genomic research and institutions providing talent pool to keep this industry growing, a constant knowledge exchange has become a need of the hour. Like its counterparts in US, UK and other countries, India is too moving fast in this segment and various organisations such as Scigenom Research Foundation (SGRF) doing its part to create platform for such knowledge exchange to take place. SGRF is a not-for-profit organization dedicated to promoting Science in India through research and education and organizes an annual conference since 2011, 'NextGen Genomics, Biology, Bioinformatics and Technologies (NGBT) Conference'.

100 Talks

700+ Delegates

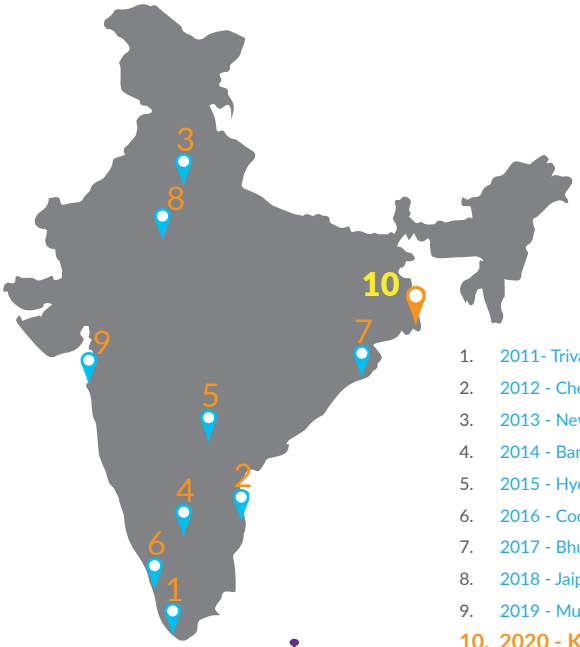
50+ International Delegates

25 Keynote Speakers

100+ Scholarship Awards

The 9th edition of NGBT was held in Mumbai at Taj Lands End from Sep 30th to Oct 2nd, 2019. The 2019 NGBT conference was jointly hosted in collaboration with Toronto Recombinant Antibody Centre (TRAC), Toronto, Canada, Tata Institute of Fundamental Research (TIFR), Mumbai, India, Advanced Centre for Treatment, Research and Education in Cancer (ACTREC), Mumbai, India, Indian Institute of Technology Madras (IITM), Chennai, India, and Maharaja Sayajirao University (MSU), Baroda, India.

The three-day conference showcased speakers from multiple areas of biology and biology-enabling technologies, both from India and abroad covering advances in genomics technologies for basic and translational science and includes talks focused on wide areas of biology including human genetics, drug discovery, clinical medicine, biomarkers, diagnostics, animal, plant, agricultural and conservation Sciences.



1. 2011- Trivandrum, Kerala
2. 2012 - Chennai, Tamil Nadu
3. 2013 - New Delhi
4. 2014 - Bangalore, Karnataka
5. 2015 - Hyderabad, Telangana
6. 2016 - Cochin, Kerala
7. 2017 - Bhubaneswar, Odissa
8. 2018 - Jaipur, Rajasthan
9. 2019 - Mumbai, Maharastra
10. 2020 - Kolkata, West Bengal

The inaugural ceremony was presided by the representatives from host and co host organisations- Dr Sekar Seshagiri, SGRF, Dr Prasanna Vekatraman, ACTREC and Dr Dev Sidhu, TRAC. Dr Steve Turner, Founder and Chief Technology Officer, Pacific Biosciences graced the ceremony as Chief Guest. The ceremony started with an introduction about SGRF, followed by welcome address by guests at dais and concluded with lamp lighting.

"Over the past nine years NGBT has evolved to create a forum for researchers, students, clinicians, plant and animal scientists, and technology/biology from India and across the globe to meet, share and gain knowledge on advances in science and technologies. The science of genomics is revolutionizing healthcare, drug discovery, plant and animal sciences. Our conference is intended to bring these cutting-edge advances accessible to scientist and aspiring students in India. The ultimate goal of Science is to help the well-being of all in society and our hope is for our conference to be a catalyst towards this goal"

Dr Sekar Seshagiri, NGBT Conference Chair and President, SGRF.

The conference featured scientific leaders from all around the world who shared their knowledge and expertise over the course of 3 days. The complete list is available on the conference website www.sgrfconferences.org

Dr Vishva Dixit
Genentech, USA

Dr Dev Sidhu,
Univ of Toronto, Canada

Dr HansJörg Schild,
Johannes Gutenberg-Universität Mainz, Germany

Dr Ivan Dikic
Goethe University, Germany

Dr Steve Turner
PacBio, USA

Dr Joe Beechem
Nanostring, USA

Mr James Brayer
Oxford Nanopore, USA

Dr Kanneganti Thirumala - Devi
St. Jude Children's Research Hospital, USA

> I am pleased that the NGBT initiative has enabled scholars, thinkers and thought leaders from around the world to meet and exchange ideas. Scientific developments in the genomics space is going to radically change many areas including agricultural sciences. It will positively impact our farmers and their well-being

Dr K. K. Narayanan, Founder and former CEO
Metahelix Lifesciences, India.

The conference was concluded with a stupendous talk by Dr Zoltan Takacs, who spoke about Deadliest Lifesavers - Therapeutic potential of animal venoms. The talk featured a breath-taking video on his rendezvous with various snakes, etc. and added with his sense of humour to the otherwise serious topic, made the session fun and engaging.

SGRF awarded 100+ "scholarships" to support student participation at the NGBT meeting who were carefully selected by esteemed panel of abstract reviewers. The conference also awarded numerous prizes which were sponsored by prestigious and renowned journals. "We are grateful for the support from prestigious journals such as Nature, Cell and Science, EMBO for their support for student poster prizes" said Dr Krishna Rajalingam, Professor, University of Frankfurt and co-chair of the NGBT meeting.

EMBO Molecular Medicine EMBOpress | EMBO Molecular Medicine | molecular systems biology | SnapGene® Software for molecular biology | Science Signaling AAAS | nature

The conference also featured an author speaker talk by the 16th election commissioner of India, Mr. Navin Chawla. He spoke about his book – Every Vote Counts. Mr. Chawla's talk covered insights on democracy, voting system and experiences of people behind the scenes, which were thoroughly enjoyed by the audience.

SGRF also presented awards to honor scientific contributions made by distinguished researchers and scientists in various field of biological sciences

Excellence in Science Award

Dr Gagandeep Kang
CMC, India

Dr Vivek Malhotra,
CRG, Spain.

Lifetime Achievement Award

Dr John Kuriyan
UC Berkeley, USA

Dr Deepak Pental,
University of Delhi, India

Dr PK Gupta,
Meerut University, India

Dr Jon Pines,
Institute of Cancer Research: RCH, London

As stated by Ludwig van Beethoven "Only art and science make us suspect the existence of life to a higher level, and maybe also instil hope thereof". Acknowledging Art and Science as the source of creativity, NGBT also featured an art exhibition, known as Art Meet Science. Various talented artists exhibited their spectacular paintings and sketches. Added to this, was a special session by art restorer Ms. Rupika Chawla, who unravelled details on Raja Ravi Varma's paintings

On day 2, the conference session was followed by rocking performance by Dharavi Rocks- kids from the infamous Dharavi colony of Mumbai. The most amazing feature of the performance was the use of waste materials such as water jar, bottle, bottle caps, etc as musical instruments. Their beats and subliminal message on recycling made its way into the heart of the delegates.

The conference has grown exponentially over the last 8 editions and like each year, every top industry players such as Illumina, MedGenome, PacBio, MGI, Nanostring, Nanopore, Thermofisher, Twist Biosciences, AgriGenome, Premas, Fluidigm, etc supported and exhibited at the conference.

The successfully concluded conference was an amalgamation of the vintage and the beginners, who came forward to share knowledge and network for a better tomorrow. SGRF hopes to keep igniting the spirit of the great minds and enthusiastic future scientists for years to come.

Employee connect

WELCOME

Our New-Joiners


Neha Venkatesh


Vivek Ananth Murali


Lalit Chaudhari


Ankit Kumar Dubey


Manmit Kaur Bhatia


Soumyajit Dhar


Kiran Polavarapu


Roshan Nawab


Abhijith H S


Vishal Rajaram Sanap


Karumathil Sudeesh


Amit Dattatraya Parhar


Priyanka Ghosh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Tippeswamy R


Ravishankar Rai


Mahajan Swapnil Sanjeev


Jayashree Dey


Gundu Siddhartha


Mukesh Kannan


Vivek C M


Chethan BG


Amrita Mondal

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WELCOME

Our New-Joiners


Ashwini H


Priyanka R Bhargav


Urja Jayesh Asher


Rahul Kalra


Prakash Seenappa


Siva Guru Raja C


S Manjunath


Nanduri Ram Sai


Vinod Kumar Sharma


Ram Kumar


Parv Sachdeva


Shreya Sharma


Sravanthi Parchuru


Aswathy S L


Diksha Soni


Priti Priyadarsini Pati


Sourav Singla


Ashokkumar R


Pradeep Kumar P


Paridhy Vanniya S


Nithya H


Kalmesh Somappa


Sanjay Singh


Ruchit Patel

Employee connect

Find the 12 hidden words

Genetic Engineering

P Q A N D U W E F H A O K E B M X Q L E T D A R
I V Y F B I B Q V E B F T W T U J X Z P R R A O
X W T F T B N Y V A K O R R K T C P C E V A C P
A S G I U B G U X X G H W G X A L O O H B H C Y
F K E C X P X B D Z O P F O E T O X S S Z Y Z J
D Z N H K L S N D J L X Y B M I N T I I M J C S
W D E N S M S I N A G R O I O O I I I F Q F E A
V X S D N I E Y F X L V A E N N N C C O M H X H
D G P H X S I M L V Q V K A E G G X I L R K O P
N Y L S K Y P R D H G N D U G L C J T G M B D Q
A H I Z G K G J W S C A S T I A R T B O E A U S
M Z C Y B U G N O I T A C I F I D O M P T C N V
U Z I D W K Z B I W Z Q M D A E L Z Y Z A F T Z
H Y N Q G F V G W K Q F R C P K U A V Z L V X C
R O G L Q A V Z Y U X S N B D T R V C Y U T U B
E T D L T F U E I K D I M I D W O Z U Q P R O V
P N O I T A T N E M I R E P X E G N L W I A I T
U T V O E T V R A X L J Z K X Q H L C I N N F I
S T A S Z G E I Y J Y H U H L L L L O O A S V P
X G G I E M C L D W F U L G V H W J L G M G U T
J S D W G Z T I O I M F D C E F I O U I N E Z T
M V Y F E H O E P O H X G S E N E G W B A N U E
H S R R W C R W P T N W H G E N O M E S N I Y W
W K V T C R B W T E V B V O H N V F D E Z C P L

*Kindly mail your answers by 15th November 2019 to **editor@MedGenome.com**. The first two people to answer the puzzles correct will be featured in the next edition of our newsletter.*

Photo feature

Celebrations

Birthday

Photo feature

Onam Celebration

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