MEDGENOME

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Internal Quarterly Newsletter

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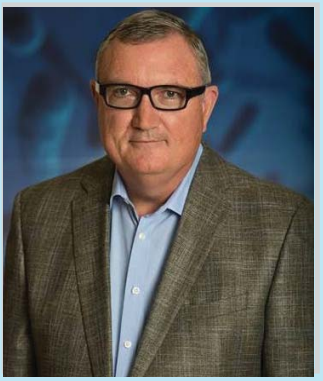
Management speaks



Michael Nemzek
Chief Commercial Officer

Dear MedGenome Colleagues,

Allow me to offer a warm greeting on behalf of the MedGenome team here in the US.

Moving into April, we are starting an exciting journey of high expectations into our new fiscal year following a very successful, record-setting year. Our impressive accomplishments come as a result of the outstanding work from all of us around the world. I would like to share how MedGenome's US business has grown significantly during the past year with valuable support from our fellow team members in India.

Trends in the US and European market are consistent with our expansion. There is a greater emphasis on more targeted clinical trials requiring genomics support, precision medicine initiatives to discover disease biomarkers are rapidly expanding, large-scale population genomics studies are increasing in number, and single-cell sequencing is sought after by researchers for an unprecedented level of resolution to find more in-depth insights. The use of sequencing in consumer genomics and disease risk prediction continues to grow in this market. We also see an increase in interest in our immuno-oncology genomics solutions as the immunotherapy drug development market is large and experiencing rapid growth.

As a result of ramping up commercial operations, our quarterly sales volume has grown significantly, requiring us to expand our laboratory capacity. We started with a lab with one each of MiSeq, HiSeq 2500, and HiSeq X instruments and have grown to add another HiSeq 2500, HiSeq X and the newest NovaSeq 6000 platform to significantly expand our capacity. In addition to seeing growth from new customers that we acquire, a significant portion of our business is now being made up of repeat customer business, a testament to the fact that customers are pleased with the work we are doing for them.

For the coming year, we are very excited about the prospects for further aggressive growth. We recently started to expand into the high growth single-cell sequencing market, where we have adopted the 10 X Genomics platform where we will now offer a range of new services including single-cell gene expression assays, T cell receptor assays and other long-read applications including *de novo* gene assembly. We have many exciting prospects to participate in large projects and expect that we will increasingly be in the consideration set for customers who are doing significant genomics research work. Further, we plan to considerably increase our field sales force in the coming year to continue to improve our market penetration. We are also very enthusiastic that we will be launching the Ophthatome Knowledgebase at the annual meeting of the Association for Research in Vision and Ophthalmology in Honolulu in May. The Ophthatome Knowledgebase will be the most significant repository of clinical phenotype information in Ophthalmology that can enable researchers to gain new insights into the diseases of the eye.

Through the people of MedGenome, we have built an extraordinary organization with many exciting opportunities and bright prospects. I feel fortunate to be a member of the team helping us achieve our goals and look forward to a great year ahead.

Highlights

Most talked about

MedGenome in news

1

THE HINDU BusinessLine

Who will finance innovation?

Ecosystem issues: While we achieved success with generic drugs in pharma sector, we aren't able to replicate the same in drug discovery, biomarkers and biosimilars. The countless procedures, lack of infrastructure, dependency on private sector and lack of an ecosystem to set up good institutes and centres of excellence have held up Indian innovation.

Finance constraint: Very few entrepreneurs and venture capitalists want to invest in any company/institute/product, which has a wait period of 8-10 years to be profitable, especially when policy is unpredictable. Government procedures make R&D difficult and time consuming. Lack of infrastructure and skilled people worsens the situation.

Capital risk: Innovation means capital risk. No success happens overnight, you have to make multiple attempts or even more than 10 times to achieve true innovation. This would mean for one success you would have to write off money for those nine failures. Banks rarely evaluate balance sheet intangibles such as intellectual property.

Beyond tax breaks: Though investment in R&D is increasing, it is insufficient to meet the needs of innovation. Besides the government can remove import taxes on equipment and consumables, reduce capital taxes for angel investors, allow easy visas for foreign personnel to visit and work.

Sam Santhosh is the Founder and Chairman, MedGenome, a genomics company that does

S&T research

2

TECHONOMY

EDITORIAL EVENTS VIDEO

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BIO & LIFE SCIENCES INNOVATION + EMAIL + PRINT

India: A Wellspring of Untapped Genetic Knowledge

By Sam Santhosh | January 10, 2018, 10:30 AM | Techonomy Exclusive

Courtesy of cosmin4000 / Getty Images

We have known for more than a decade that family history protects us from some diseases yet makes us vulnerable to others. Increasingly, scientists are recognizing that the citizens of one country provide unique insights into the relationship between genetics and disease. That country is India.

India has a long history of people from relatively few founder families who, in many cases, kept to themselves—much like the Amish in the United States or those who live on remote islands. Across this immense country and over many generations, people were separated by geographical barriers, religious restrictions, caste isolation and other societal constraints.

Endogamy, the practice of marrying only within a local group, hasn't turned out well in terms of health. Today, many of these isolated populations experience genetic diseases at rates higher than in more genetically mixed communities. Simply put, in these homogeneous groups there was more chance of two people who carried a mutated gene to marry and have kids. Sometimes the impact was visible right away; other times it took generations. In India, people in isolated communities have roughly twice the chance of developing an inherited disease than, for instance, the general population who live in the United States or Europe.

India is a wellspring of untapped genetic knowledge. Its people represent 20 percent of the world's population but only 0.2 percent of the sequenced population. The isolated groups there individually show tremendous similarity within their communities but are extremely distinct from each other. And there are some 4,000 to 5,000 of these groups, or population isolates. Genomic insights are, therefore, substantially easier to discover in India.

New insights await in disease-related biomarkers and drug-related biomarkers. Pharmacogenomic discoveries can be applied generally; in many instances, to those who suffer from a specific form of a disease. Others may be relevant down to the individual.

Building the database of Indian genomic data is one of the goals of GenomeAsia 100K, a not-for-profit consortium that MedGenome co-founded with Macrogen and Nanyang Technological University (NTU). Our goal is to sequence 100,000 people's genome to create a high-quality baseline against which more insights can be generated. More exciting pathways to drug discovery are within reach. More effective and efficient drug trials can be conducted. More people can be helped with more diseases if only the Indian genome is more fully studied.

For example, the *European Journal of Clinical Pharmacology* published a finding on genetic polymorphisms by studying the South Indian Tamilian population. Significant differences in how patients reacted to the antiplatelet drug Clopidogrel were described. Such work can lead to physicians more wisely using this drug to keep certain patients' blood flowing smoothly, avoiding clots and strokes.

Why has the Indian population been overlooked for so long given the rich information held in the isolated populations? Many of the genomics studies to date have been initiated and funded by U.S. and European organizations, and it follows that the vast majority of sequenced DNA hails from citizens of U.S. and European ancestry.

Now is a unique time in the history of world healthcare. We can sequence faster, and we can sequence at a lower cost. Indian genomic data will unlock more of life's source code to benefit everyone—people in India as well as Indianapolis and Innsbruck.

The near-term payoff will be seen in precision medicine. Large-scale genetic research studies in Indian patient cohorts increases the possibility of uncovering new insights into the biology of diseases, and enables better understanding of each type of cancer, heart disease, diabetes or any disease condition where genetics plays an underlying role. Over time, researchers and pharmaceutical companies hope to personalize medicine —personalized to a single individual's health and genomic heritage. The journey advances with discovering more disease and treatment-related biomarkers. India represents arguably the most promising genetic treasure trove in the world.

3

A 'game-changer' technology for cancer diagnosis

4

Business Standard MUMBAI | MONDAY, 26 MARCH 2018

Decoding genes to find solutions for diseases

MedGenome offers research and diagnostics in complex gene-related maladies; needs to expand reach, writes **Shameen Alauddin**

FACT BOX

1 **Mr. Sam Santhosh's views on Science and Innovation in India published in The Hindu Business Line**

https://www.thehindubusinessline.com/todays-paper/tp-indiafile/article22582457.ece

2 **Authored article in Techonomy by Mr. Sam Santhosh on why India is the most promising genetic treasure trove in the world**

https://techonomy.com/2018/01/india-wellspring-untapped-genetic-knowledge/

3 **Industry story on Liquid Biopsy in The Hindu Business Line**

http://www.thehindubusinessline.com/specials/pulse/a-game-changer-technology-for-cancer-diagnosis/article22637272.ece

3 **Mr. Sam Santhosh interview in Business Standard**

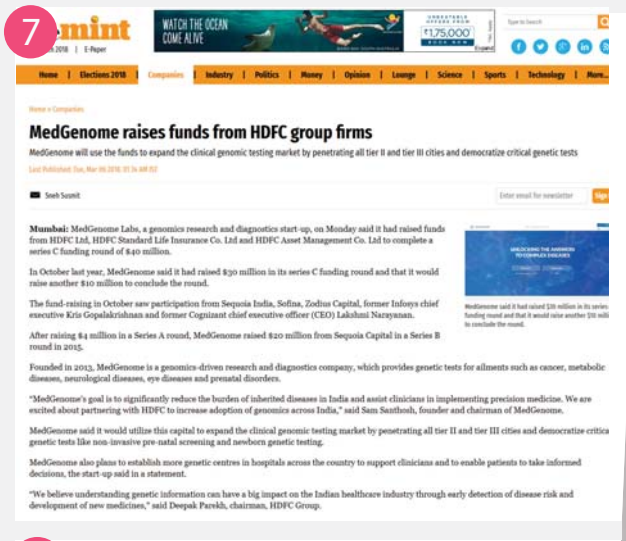
https://diagnostics.medgenome.com/pdf/2018/26thMarchBusinessStandard2018.pdf

5 **Authored Article by Dr. Sheetal on Sickle cell anaemia in Biospectrum**

https://www.biospectrumindia.com/features/17/10498/world-rare-disease-day-prevention-of-sickle-cell-disease-early-screening-and-awareness-a-must.html

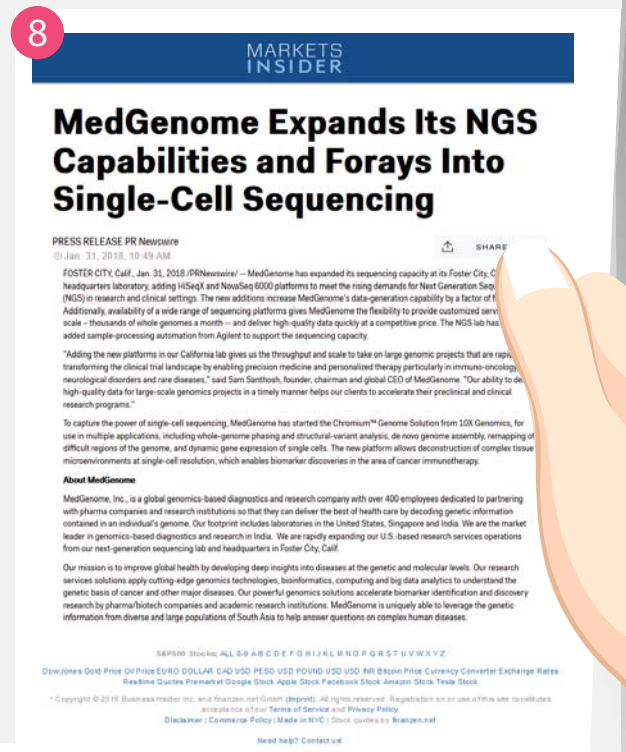
6 **MedGenome research on Maturity Onset Diabetes of the Young (MODY) published in Deccan Chronicle**

http://www.deccanchronicle.com/lifestyle/health-and-wellbeing/020318/mody-a-rare-diabetes-affecting-young-lean.html



7 **MedGenome Series C closing news with investment from HDFC in Mint**

http://www.livemint.com/Companies/VNkIG4Zkh20iZhoZjJfYwK/MedGenome-raises-funds-from-HDFC-group-firms.html



8 **MedGenome NGS Capabilities expansion news in Markets Insider**

http://markets.businessinsider.com/news/stocks/medgenome-expands-its-ngs-capabilities-and-forays-into-single-cell-sequencing-1014692524

Genomics centres launched in Chennai, Kolkata and Coimbatore

Sri Ramachandra Medical College and Research Institute (SRMC), Chennai

Kovai Medical Centre and Hospital (KMCH), Coimbatore

In the first quarter, MedGenome launched three genomic centres in association with Sri Ramachandra Medical College and Research Institute (SRMC), Chennai; Indian Institute of Liver and Digestive Sciences (IILDS), Kolkata and Kovai Medical Center and Hospital (KMCH), Coimbatore.

The focus of the facility at SRMC, Chennai and KMCH, Coimbatore will be to deliver the most up-to-date genomic based diagnostics for patients and also provide researchers a great opportunity to advance their understanding of the human biology. The new facility will enable researchers to find novel insights into the biology of diseases. The genomics centre will also empower clinicians with validated and actionable clinical information to make effective treatment decisions for their patients. Additionally, genetic counselling will be provided to patients on hereditary cancers, genetic disorders, pregnancy related issues and neurological disorders.

The IILDS-MedGenome centre is a state-of-the-art cell biology lab and also has a functional genomics platform to identify biomarkers and functionally characterize the biomarkers in liver cells. The centre would provide a deeper understanding of Non-Alcoholic Fatty Liver Disease (NAFLD) in the Indian subcontinent. NAFLD is the most common liver ailment that can lead to cirrhosis and hepatocellular carcinoma. There is a need for better understanding of the disease at a cellular level. The centre will aim for better understanding of the cellular mechanisms involved in the progression of NAFLD to fibrosis of liver.

Indian Institute of Liver and Digestive Sciences (IILDS), Kolkata

Highlights of the year 2017-18

Completed Series C funding

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You are here: Home » Business » HDFC invests in MedGenome

HDFC invests in MedGenome

DH News Service, Bengaluru Mar 6 2018, 0:26 IST

The company plans to establish more genetic centres in hospitals across the country.

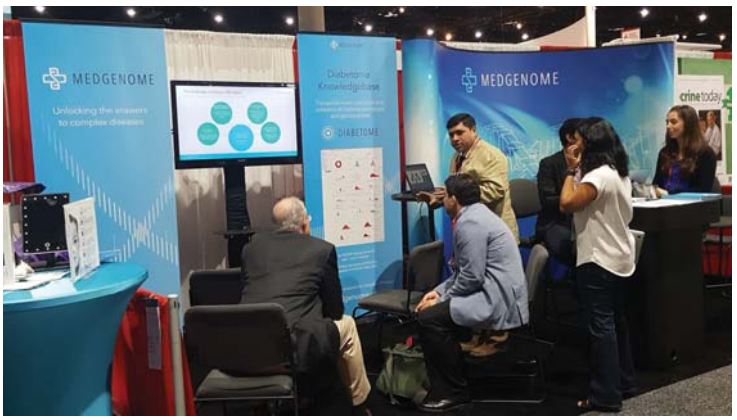
Genetic diagnostics company MedGenome Labs on Monday announced that it has received investments from HDFC Ltd, HDFC Life and HDFC Asset Management, to complete its Series C funding of $40 million.

MedGenome will utilise this capital to expand the clinical genomic testing market by penetrating all the Tier-II and Tier-III cities and democratice the critical genetic tests like noninvasive pre-natal screening (NIPT) and new born genetic testing, a company release said.

The company plans to establish more genetic centres in hospitals across the country.

Recognised by Business World

Launched Diabetome in USA



Received CAP Accreditation for the NGS lab in Bengaluru

CAP ACCREDITED
COLLEGE of AMERICAN PATHOLOGISTS

Research collaboration with MMM hospital Chennai

Launched Genomic centres in Chennai, Kolkata and Coimbatore

Received the award for Best Life Sciences Company (MODI award)

MedGenome connect

ACTIA

SIAMG Trivandrum

The period between Jan - Mar 2018 was quite exciting and full of events for Team Actia.

We participated in 8 important national and international conferences across India which includes SIAMG at Trivandrum, Kerala, PediGen 2018 at Pune, ISNSCCON 2018 at Hyderabad, PEDICON 2018 at Nagpur, DART conference at Bangalore, Neurology conference at Fortis, Chennai, Neurodevelopmental Conference at Manipal and GNE Myopathy conference at Delhi.

Our team of experts, i.e. Dr. Ramprasad, Dr. Sheetal, Dr. Sakthivel and Dr. Ravi Gupta made our participation remarkable with their involvement. The visibility and awareness on ACTIA and its offerings was boosted further by 12 RTMs and CMEs spanning across major cities in India. The major therapies touch-based through these engagement programs were Neurology, Nephrology and Ophthalmology. Thanks to Dr. Gaurav and Dr. Puneeth for collaborating and ensuring our successful participation in these meetings, that we could reach out to more than 1000 clinicians, thus allowing us to drive new conversions for our set of offerings.

PRIMA

The period between Jan - Mar was very eventful for team Prima. We participated in 10 important national events across India which includes the following:

1. Cochin ASH Update
2. Mumbai Bone Marrow transplant unit CME
3. Standalone CME at Indore on Lung Cancer CT DNA test
4. Pead Haematology CME at Surat
5. Lakshya Cancer Hospital CME on World Cancer Day at Pune
6. Tumour Board Meeting at INS Ashwini
7. Manipal Hospital CME on Next generation sequencing
8. Annual Review meeting on Gastric Cancers at Mumbai
9. CT DNA Standalone CME at Nagpur

Dr. Ram at Mumbai CME

Our team of experts, i.e. Dr. Ramprasad, Dr. Vidya, Dr. Sakthivel participated in these conferences and the major therapies touch-based through these engagement programs were Oncology and Haematology.

CLARIA

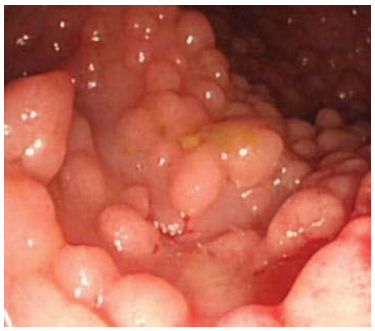
Dr. Priya giving lecture at Kolkata CME

December began for CLARIA with participation at the Life Conference in Bangalore followed by Fertivision in Delhi where Dr. Sam Balu presented on “The Benefits of PGS/PGD in IVF”. We had a joint stall with our colleagues from ACTIA at the Society for Indian Academy of Medical Genetics conference in Trivandrum. This was followed by a brief lull in the conference circuit on account of Christmas and New Year break. But then we kept our selves busy with CME's at Kolkata, two in Chandigarh and one in Bangalore. Our CME in Bangalore in association with Apollo CM Fertility also got some press coverage. February was relatively quiet with just one event in Delhi at the Maulana Azad Medical College. But March was busy with the conference season picking again and more CME's planned across the country.

The CLARIA webinar series chugged along with a webinar on the importance of Genetic Counseling in the Genetic Testing process. Our in-house genetic counsellor Dr. Madhvilatha presented and addressed questions from clinicians.

Making a difference

Six members of a family diagnosed with Familial Adenomatous Polyposis (FAP), an inherited disorder in Gujarat



In a strange turn of events, six members of a family have been diagnosed with Familial Adenomatous Polyposis (FAP) in the state of Gujarat. It came to light when a 52-year-old man went to Kailash cancer hospital and research centre (KCHRC), Goraj, Gujarat complaining of weight loss and changes in bowel movement. Colonoscopy testing confirmed the presence of multiple polyps (a small protruding growth) in his colon. These types of polyps are generally seen in a clinical condition known as Familial Adenomatous Polyposis (FAP).

Familial adenomatous polyposis (FAP) is an inherited disorder characterized by cancer of the large intestine (colon) and rectum. It is an adult-onset disease which is caused by a genetic mutation where in the body cells aren't able to supress the development of tumour. Typically 100-1000 polyps appear in the colon and rectum at an early age, which if left untreated, leads to aggressive colorectal cancer by the age of 40 years. There are currently no curative treatments for FAP and surgical removal of the polyps remains the mainstay.

On further investigation, it was found that a total of six family members (ages 35-60) had polyps and were diagnosed with FAP. All affected individuals were operated to remove multiple polyps in the colon and rectum. Surgical biopsy results showed that the polyps were pre-cancerous. Since this appeared to be a case of familial cancer predisposition, all twenty six family members were tested for genetic mutations which are known to underlie this type of cancer. Gene testing from the blood of these individuals revealed a mutation in the Adenomatous polyposis coli (APC) gene, not only in all six FAP-diagnosed family members, but also in four young individuals (ages 6-23 years) who have not yet been diagnosed with FAP. Of the ten members, four are young individuals who have a strong predisposition of getting polyps later in life, meaning they have more chances of having FAP disease. Hence, they were counselled and encouraged to undergo regular colonoscopies.

Generally familial colorectal cancers are rarely encountered and can have different genetic mutations associated with them. In the age of modern medicine, knowing the type of mutation associated with a particular cancer is becoming a very important factor in deciding the treatment. In this case of the FAP family, knowing that 4 family members have the APC gene mutation and will very likely develop polyps as they age, could eventually be a life saver through early diagnosis.

From our US office

MedGenome was invited to present a poster "*A Personalized Cancer Vaccine Approach to Treat Lynch Syndrome*" at the Molecular Medicine Tri-Conference, a premier conference in the bay area bringing together pharma, biotech and academic community. The summary of the poster presented is available in the press coverage on the event at https://www.medgenome.com/press/medgenome-presents-cancer-vaccine-approach-lynch-syndrome-patients/

MedGenome hosted Dr. Sekar Kathiresan at the Foster City lab for the January 2018 symposium on *genomics in cardiovascular diseases*. Dr. Kathiresan spoke on "*Genes, lifestyle, and risk for heart attack*."

The MedGenome Symposium in March featured talks by Dr. Kasthuri Kannan, New York School of Medicine on "*Genomics of Pineoblastoma*" and Dr. Rama Natarajan, City of Hope on "*Epigenetic mechanisms underlying Diabetic complications and Metabolic Memory*"

We have been focusing on developing brand awareness for MedGenome in the US market to enable business growth in the coming years. The podcast "*The Entrepreneur Way*', captures Sam's views and his entrepreneurial journey - http://theentrepreneurway.com/podcast/763-there-is-not-much-of-an-opportunity-for-you-to-rest-on-what-you-know-with-sam-santhosh-founder-and-owner-of-medgenome-labs-ltd/

Sneak peek into the world of science

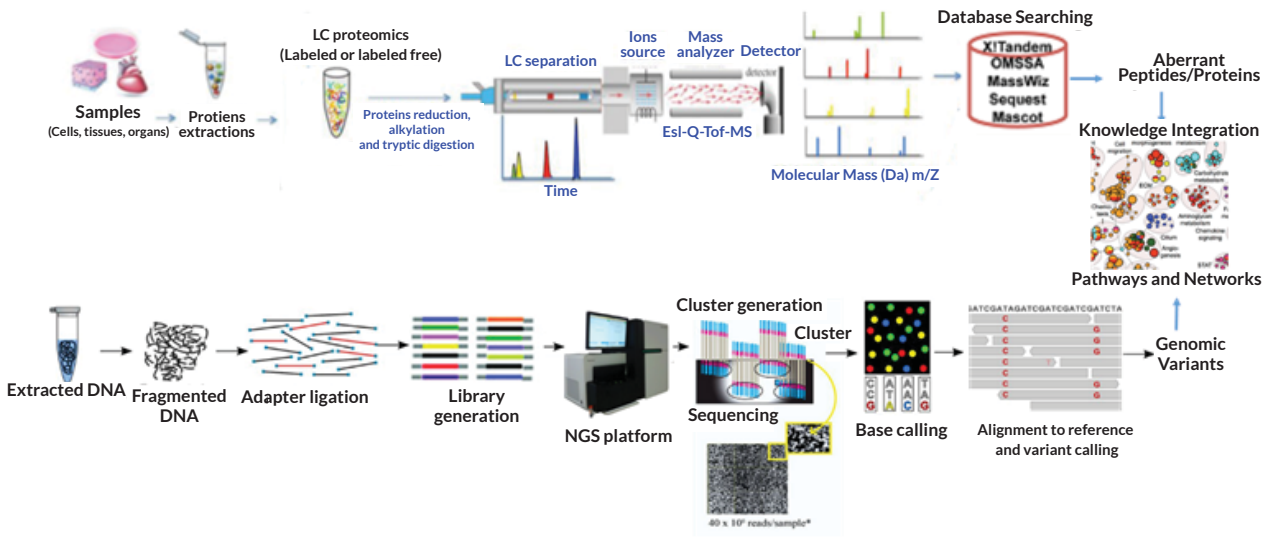
The emerging landscape of NGS and proteogenomics technologies in disease biology

by Savita Jayaram, Bioinformatics Scientist

Introduction

The last few decades have seen an unprecedented rise in genome scale data, that holds strong promise to uncover the molecular changes associated with disease processes. Next-generation sequencing (NGS) technologies are the primary source for this data surge. Due to their high speed and throughput, these technologies are being progressively applied across a wide spectrum of applications including epigenetics, chip-seq, genome-wide association studies (GWAS), small RNA, noncoding RNA, deciphering ancient DNA or environmentally derived samples, single-cell genomics and many others. Whole genome sequencing (WGS), whole exome sequencing (WES) and targeted sequencing strategies accord the opportunity to identify clinically actionable mutations (both somatic and germline) guiding precision medicine and clinical management of genetic disorders and chronic infectious diseases, like HIV and tuberculosis.Further, sequencing of the human leukocyte antigen (HLA) region by NGS is now being used to define an individual's immune response, inter-individual variations and predispositions to various infections, autoimmune diseases and efficacy to immunotherapy drugs. NGS and big data analytics have uncovered hidden patterns, correlations and insights that has greatly accelerated our understanding of the genome. For instance, earlier it was thought that Single Nucleotide Polymorphisms (SNPs) were the most prevalent and important form of genetic variation. However, copy number variations (CNVs) were found to comprise at least three times the total nucleotide content of SNPs. It was surprising to discover that nearly 12% of the human genome is copy number variable. Proteomics, on the other hand have contributed to the better understanding of the molecular basis of genetic variability. By and large, these approaches are dramatically accelerating the pace of human disease research and are already impacting patient treatment.

Schematic representation of genomic and proteomic technologies



The greatest challenge in bioinformatics has been to make meaningful sense of the deluge of data by integrating the knowledge originating from these diverse sources. Large scale projects by consortiums like the Cancer Genome Atlas (TCGA), launched in 2006, have generated multi-omics data including genomic, transcriptomic, proteomic, epigenomic and metabolomic information among others, from nearly 11,000 patient samples across 33 different cancers. The first draft maps of the human proteome saw a significant contribution from India, comprising the Human Proteome Map (HPM; http://www.humanproteomemap.org/), providing protein level evidence for 84% of the annotated genes.

Although these datasets have been made easily accessible to the research community, there was a shortage of available software tools to efficiently integrate this information and deliver a systems level insight, providing glimpses of how organisms behave as a whole. Genomics alone cannot provide information regarding the dynamics of downstream targets, protein-protein and protein-metabolite interactions. Proteomics is required to decode the genomic information to determine the effect of a given variation or post-translational modification on a protein sequence, or its higher order structure. Proteins thus fundamentally execute the activities dictated by the genes that influences their ability to bind, regulate or signal other proteins, creating a cascade and/or combined effect of genetic variations in a given pathway or functional network, providing the pathophysiological basis of disease.

Mass-spectrometry (MS) has emerged as the method of choice to profile proteins/metabolites albeit having much lesser throughput and an inability to multiplex a large number of samples in a single experiment, compared to other NGS technologies like DNA and RNA-Seq. MS-based methods, typically rely on standard protein database like RefSeq to infer the peptides and proteins, derived from the observed mass spectra. However, searches done in this way, mask the patient-specific or tumor-specific variations from being identified and also limit novel identifications resulting from splice site variations or gene fusions. In this context, proteogenomics techniques came to the rescue, as they utilized genomic or RNA-Seq data to generate six-frame translated customized protein databases that was then searched using MS-derived peptide mass spectra. Since searches were no longer confined to what was known, it accorded the ability to identify novel protein coding regions in the human genome, correct genome annotations, and estimate their relative abundance compared to normal. Particularly, protegenomics provided protein-level evidence for genomic variants in cancer cells, including, identification of novel splice variants and gene fusions.

The Clinical Proteomics Tumor Analysis Consortium (CPTAC), initiated in 2011, conducted MS analysis on 100 residual tumour tissues for 3 cancers from the TCGA cohorts, for which genomics data was already available and interrogated the data using proteogenomics approaches. The analysis revealed that while variants predicted by RNA-Seq data are in the order of 15-25,000, MS-analysis detected only about 50-100 aberrant peptides (about 1% of the total peptides detected were variant) indicating that, a large number of genomic variants do not express into proteins due to cellular control mechanisms or may not be detected due to limitations in the current MS technology. Hence, it is all the more essential to obtain protein level evidence for genomic variations for downstream clinical applications or biomarker discovery. Following the initial discovery phase of proteogenomics, one could then do targeted analysis in validation phase, using multiple reaction monitoring (MRM), focusing on a select few peptides of interest to get much more reliable quantitative information. Today, such strategies are being increasingly applied to study genome-derived, protein variations in disease biology.

MedGenome is slowly venturing into this space with recent projects using MS-based approaches to generate proteomic support to more efficiently predict 'neoepitopes'. Neoepitopes are peptides that are originate from somatic mutations and are recognized by different immune cells in the body, in the context of major histocompatibility complex (MHC) proteins. Neoepitopes presented by MHC class I molecules are recognized the cytotoxic CD8+ T cells, that get activated and specifically kill cancerous cells. This forms the basis of cancer immunotherapy and the making of cancer-specific tumor vaccines.

Consequently, the advent of NGS technologies has greatly enhanced our knowledge of disease and is being effectively applied to the clinic. There is now a greater awareness of how DNA sequencing-based tests can help gauge an individual's predispositions to particular diseases, based on his or her genetic blueprint allowing for targeted screening and subsequent pre-emptive intervention. For example, for doctors to prescribe the drug Zelboraf, Roche's treatment for Skin Cancer, they have to first ask patients to undergo a test for mutation (BRAFV600E), which is found in only half of such cases.

So it now crucial to recognise the molecular basis of cancer of every patient, before treatment. Based on the molecular profiles, drugs can then be repurposed for other diseases with similar aetiologies. Herceptin, a drug that was cleared by FDA to treat breast cancer was later found to be effective to treat gastric cancer as well. Another task posed by personalized medicine is identifying all the potential risk factors for a given disease.

Based on a study on 10,000 prospective cancer patients with matched normal, FDA has approved a 468-gene oncopanel for the first time as a targeted NGS-based diagnostic test/assay termed MSK-IMPACT (Memorial Sloan Kettering - Integrated Mutational Profiling of Actionable Cancer Targets), setting the stage in future for more such disease-panels. There is a dire need for more such panels covering a wider variety of disease phenotypes. The dawn of the immunotherapy era by initial set of FDA approved drugs such as Ipilimumab and Pembrolizumab, has shown considerable clinical benefit in several cancers, but may be contraindicated for patients with pre-existing autoimmune conditions, making it crucial to identify variants associated with autoimmune diseases to predict response to therapy. Taken together, an astounding potential exists for these technologies to bring enormous change in genetic and biological research, enhance our fundamental biological knowledge and influence disease management and patient care.

Sneak peek into the world of science

Advancing cancer vaccine research, the backstage story

Article by Papia Chakraborty, Sr Scientist and Head of Immuno-Oncology

Introduction

Cancer vaccines are an upcoming therapeutic modality which mobilizes the body's own immune system to eradicate advanced tumors and holds tremendous promise in the clinic.

The challenge, however, is that there is not one target for all cancers. Different cancers have different antigens and these antigens may vary from patient to patient. This calls for a truly personalized patient-wise target identification from the patient's tumor based on Next Generation Sequencing (NGS). These vaccine candidates not only need to be parsed out from the NGS information obtained from the patient's tumor and blood but also need to be validated in an immune cell culture system.

The Immuno-oncology research team in MedGenome's R&D lab is striving to tackle these challenges to make the cancer vaccine dream a reality. The team is led by Amitabha Chaudhuri, VP R&D and Papia Chakraborty, Head of Immuno-oncology at MedGenome, Foster City, California. Their goal has been to establish multiple cell-based and proteomics-based approaches for cancer vaccine identification and their validation.

Papia and her fellow scientist, Vasumathi Kode optimized an immune cell-based culture method to confirm the activity of predicted vaccine candidates using patient or normal donors' blood cells. Snigdha Majumdar from the Bengaluru team joined the duo in the Foster City lab to expedite the optimization of multiple experimental parameters and played a critical role in establishing the assay in the Bengaluru MedGenome lab. These assays are essential components for vaccine design to make sure that the vaccine will elicit an immune response in patients. The assay was used to identify vaccine candidates in a case study on Lynch Syndrome, a familial colorectal cancer wherein multiple members in a family get impacted by colon, endometrial, stomach and ovarian cancers due to mutations in DNA mismatch repair gene pathways. The study was chosen for an invited speaker presentation at the Molecular Medicine Tri Conference, 2018 in San Francisco, CA, USA and was very well received. The overall study was orchestrated by Arati Khanna Gupta, VP R&D India with patient samples obtained from the Goraj Hospital tie-up in Gujrat, India. Coral Miriam Magdalene and Jisha who are scientists at the Bengaluru lab and at the Goraj hospital site respectively also played an important role in the execution of this study.

In a complementary approach to identifying immunogenic vaccine candidates, Kayla Lee, an Associate Scientist in the lab has been using the 10X Genomic's single cell technology platform to identify and functionally characterize immune cells that respond to a vaccine. Looking at immune cells at a single cell resolution provides enormous details on how our immune system responds to a cancer antigen/vaccine. This information can be used to further train the immune system and develop novel cell therapy-based products to tackle cancer. This high-resolution immune profiling is also a powerful tool towards biomarker discovery and can be used to monitor patient response to immune checkpoint drugs in clinical settings.

Since patient blood may be limiting at times, there is an enormous need for an off-the-shelf cell-based product that would serve as a proxy for the patient's immune cells that could be used to screen a vaccine. Xiaoshan "Shirley" Shi, a post-doctoral fellow in the lab has been working to develop a synthetic vaccine screening platform. Such a platform is aimed to handle high volume vaccine screens at a very low cost. Shirley and Vasu have been able to validate gene constructs in immune cell assays that allow us to screen more than one vaccine candidate in a single assay. This is a significant first step in building this high throughput platform. Key to developing this platform is the ability to manipulate immune gene function using the Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) technology. Kayla has been working on integrating the CRISPR technology into our immune-oncology workflow. The team is very excited about the success of their initial CRISPR experiments.

The group has also optimized a proteomic-based mass-spectrometry screening method that aids identification of vaccine candidates directly from patient tumor samples. Though technically challenging, this is a very powerful method of vaccine candidate prioritization. The team is now working with Priyanka Shah, a bioinformatics scientist from the Bengaluru lab to set up a pipeline for high-throughput data analysis. Together, the team has been steadfast in their efforts in gathering knowledge and expertise in cancer vaccine candidate identification and has set up multiple experimental approaches that can be used not only to address disease areas like cancer but also be utilized towards auto-immune and infectious diseases.

From our Colleague

Safety of Women - India and Abroad

Article by Ramya Krishna, Communications Manager - PR

Women safety and empowerment is a widely debated topic across the world. With women excelling in all fields, travelling solo to unexplored places and most importantly living life on their own terms there are new challenges that have come up for the society to tackle. One of them is women safety and no country or a leader can ever claim that there is no abuse, violence or incidents involving with women.

Due to urbanization and rapidly penetrating social media, people have become more vocal about discussing the issues and narrating their experiences which previously weren't spoken about. If you glance through the daily news, there is always some or other news relating to assault, rape, acid attacks, abuse, trafficking, domestic violence, etc Yes, the nature and gravity of the crime differs basis the culture, society and customs. But the fact is that women safety is an important issue for the development of any country and society.

Instead of blaming the system, the laws, society, country or the company for your ordeal, it better you take charge of your own safety. Ignoring personal safety and security is a big mistake and poses a bigger risk for the individual than anyone else. Here are some safety tips which might help anyone:

General

- Get yourself trained in self-defence techniques or at least the basic self-defence moves
- When in a position to having to physically defend yourself, always target weak spots on your attackers body (neck, eyes, throat, nose, groin, instep etc)
- Do not give away too much details about yourself in social media
- Always save numbers of the following: ambulance, police station, fire station
- Have a safety app installed like: Safetipin, Shake2Safety, Stay secure, B safe, Raksha, Himmat etc
- Be part of women's support groups of your locality/ community so that you have a support system that encourages you to be open with issues/potential issues in your environment. This will also help youto be aware of trends or recent incidents in your locality/community.

From our Colleague

At Public places

- Keep your phone handy
- Avoid using headphones as you may not be aware of your surroundings

Some Quirky tips

- Use your heels, sandals, pen, scarf, shoes, umbrella etc as combat arms during testing times
- Always have police and ambulance ringtones handy and use when needed
- In any place observe the various exits which can be used in case of an emergency
- If you are asking for directions please check with more than 2 or more people
- When travelling alone in a cab and in doubt pretend to give out your location and cab details on a phone conversation

From our Colleague

An ode to GAs

by Sakina Aamir, Genome Analyst

Another day comes, and another day goes,
Far and wide the river of reports flows,
To the world, we are a bunch of pretty jolly folks,
Little do they know; our life is always giving us a stroke.

Our day starts with an array of dilemmas,
They come together to make our life a painful drama,
Should I do this recheck, or do I start with a proofread,
You're in the middle of 12923, but boss wants 12293 immediately!

We laugh, we joke, we work, and we strive,
But when CS mails us, we run for our lives,
To add to all that torturous anguish,
Our chairs always seem to mysteriously vanish.

Life in the GA room is full of cases and reports,
Patho, VUS and the dreadful NONE of course,
What do I say about the tricky, harrowing NONE,
We hate it, but there's no escaping from THAT ONE

We mix tea bags with TRFs while in the pantry,
We can't do more, coz time and space are scanty,
We take a quick view of the outside world,
And quickly return to get all the work done.

Some moments of joy surprisingly do exist,
Though its hard to find time to fit them in,
Some banter here, some musical sneezes there,
And exercise at 11 and 4 is always there.

Working as a GA all of the time,
Has messed with our vocabulary and our mind,
We do curse each other whenever we can,
"Wild-type" is for normal, "MR" is for daft.

It's a whole new world for us to see,
When we finally get to look away from our screens,
Some beauties to admire, all in colourful attire,
And we let our eyes and hearts to playfully wander …

We don't show our actual pain,
We tend to hide that we are in vain.
People think I am a recluse,
I wish I could tell them, I am just a GA on the loose….

Employee connect

The Map the Gap campaign

MedGenome is a proud supporter and founding member of GenomeAsia 100K, a non-profit organization dedicated to sequencing the DNA of 100,000 people from across 28 countries in Asia and making the data publicly available to scientists.

GenomeAsia has recently launched "Map the Gap" campaign to address the lack of genomic data from South Asians. The campaign was launched at the Festival of Genomics in London in January 2018.

While making up over 25% of the world's population South Asians, including Indians, account for only 1% of whole genome data. Map the Gap aims to sequence 100K South Asian genomes which will enable the development of carrier tests, faster diagnosis, and treatment for rare diseases. Addressing the critical lack of data and enabling researchers to undertake their life saving work for widespread disorders like cancer and diabetes.

The Map the Gap campaign seeks to increase awareness and raise $150,000. You can track our campaign progress at www.fundrazr.com/mapthegap and sign up for email updates at www.mapthegap.org. We hope you will help spread the word by following Map the Gap on Facebook @MaptheGap100K and Twitter@Map_The_Gap.

Buvanesh Kumar B facilitated by National HRD Network, Hosur Chapter

Buvanesh Kumar B, Assistant Manager HR, has been conferred the Rising Star Award -2017 by the National HRD Network, Hosur Chapter for his splendid services to the HR fraternity and the chapter. The Executive Committee of the chapter decides the recipients of the award annually. The criteria is driving the most number of unique initiatives in the year, contribution to the growth of the chapter, revenue generation and participation in the events conducted

Buvanesh had successfully spearheaded the "Young HR Leader" contest conducted by the NHRD Hosur chapter. A first of its kind programme done by a HR Association in the region. The contest was open for HR folks in the region below the age of 30, who had to portray the "Best HR Practices" put in by the contestants in their organisation. It was hugely successful in bringing new HR folks in the NHRD fold and an opportunity for other HR personnel to know the successful and best HR practices prevalent in other organisations.

Buvanesh was also instrumental in conducting the NHRD Corporate Cricket Tournament, which saw participation from 36 corporates from across South India. This was a hugely successful venture for the chapter, which took the visibility of the chapter brand beyond the regional boundaries and also resulted in revenue generation for the chapter. These two events played a clinching factor in winning this award.

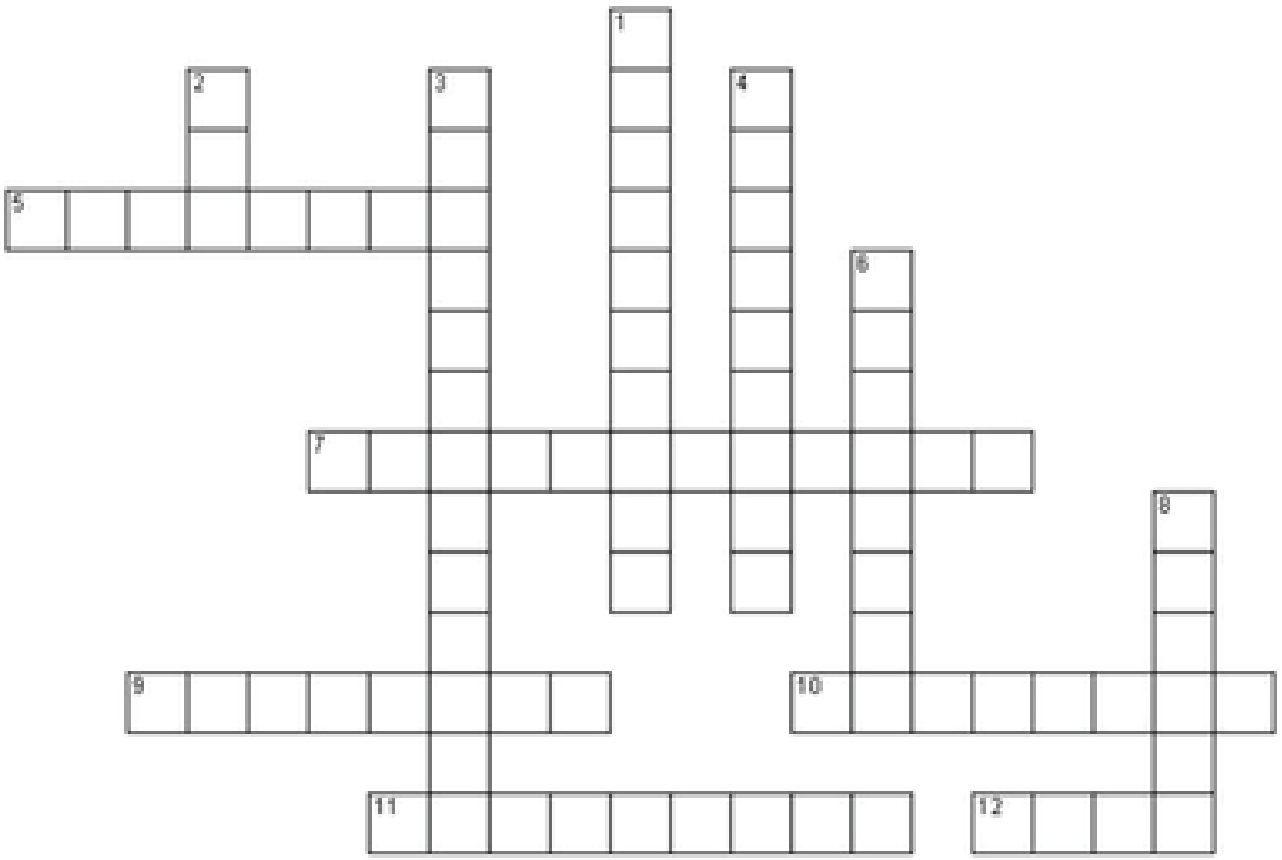
The National HRD Network is an association of HR professionals and has chapters across the country. The NHRD Hosur Chapter is one of the oldest and renowned chapters across the country winning the "Best Emerging Chapter National Award" 4 times in a span of 5 years, the most by any chapter. Buvanesh is a Life Member of NHRD.

Employee connect

Our New-Joiners

Employee connect

1. Cross word puzzle



Across

5 *A Change that occurs in our DNA sequence*
7 *A pair of alleles where one is dominant and one is recessive*
9 *A trait (allele) that is expressed regardless of the second allele*
10 *A Diagramshowing relationships between members of a family; used to track a specific trait*
11 *A trait that is only expressed when the second allele is the same*
12 *A portion of a DNA molecule that determines the traits of living things*

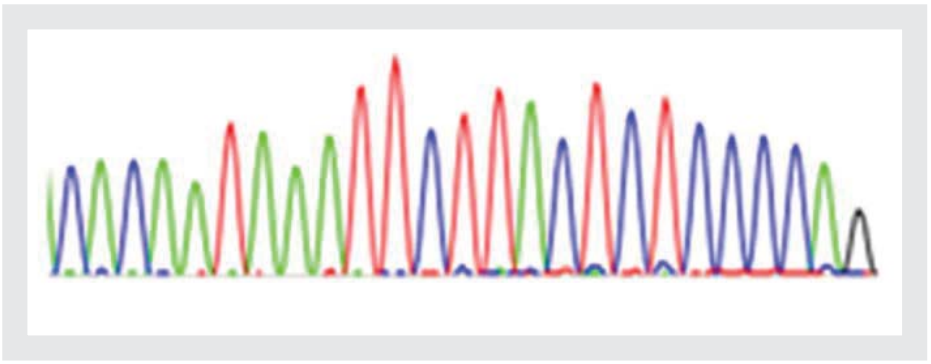
Down

1 *A pair of alleles where both are either dominanat or recessive*
2 *A molecule that carries genetic information in the cells of plants and animals*
3 *A chart showing all the possible outcomes of alleles that can result from a genetic cross*
4 *Physical or visible traits that can be seen*
6 *A particular combination of alleles for a particular gene*
8 *One of two or more alternative forms of a gene*

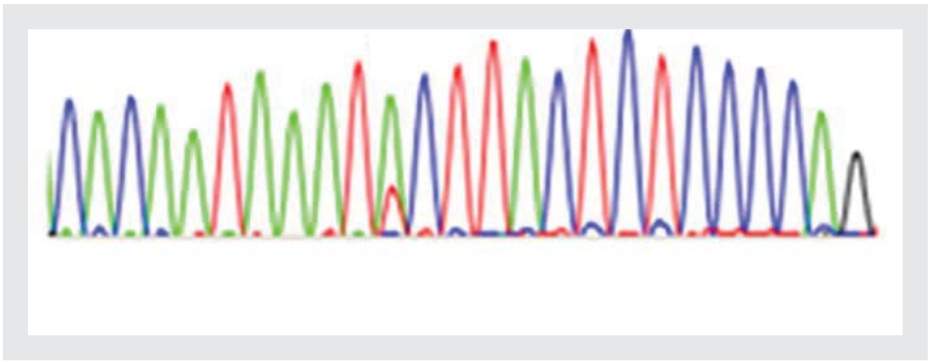
2. Spot the difference

(a) Probe CACAATAAATACTTACTCTCCCCAG

(b)



(c)



Note- A- Green, C-Blue, T- Red, G-Black

Last Puzzle winners:

Sneha.P
Genome Analyst

Lakshmi S,
Senior Research Associate.

Kindly mail your answers 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













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