Vol 12 | January 2020

Geknowne Internal Quarterly Newsletter

www.medgenome.com



WORDS FROM THE MANAGEMENT

Mahesh Pratapneni

Co-founder, MedGenome

Dear Colleagues,

I am sure many of you have seen me around since the inception of MedGenome and wondered what I do!

Before associating with genomics and life sciences, I was focused on software and banking. I founded Emerge Ventures, a fund dedicated for applying scientific and technological advances to improve healthcare and education around the same time when Sam founded SciGenom. We brought our passion for creating world beating science-based companies together to form MedGenome. As Sam set about building the business, my role has been to develop our vision and strategy. As entrepreneurs we are often assessing what takes us ahead in the market. The toughest part for me is to often convince key partners like senior leadership and venture capitalists, to believe in our vision and support us in our plans and ventures.

As part of this initiative, I helped start GenomeAsia 100K in 2016 to amplify the scientific impact of our vision at a global scale. You must have read the recent Nature paper article "Genomes from Asia", that was an early outcome of this project. Bringing companies and large number of highly capable scientists, with competing priorities and diverse ideas from across the world, together to work for the common good is easily the toughest and more fulfilling venture I have ever worked upon!

We have accomplished a lot at MedGenome but have an opportunity to create a world leading organization for affordable genomics solutions. We have positively impacted lives of 100,000+ families so far. Let us together grow MedGenome to help a million families per year!

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Most Talked About

The News

EDGENOME NEWS

MAY To JULY 2019

MEDGENOME NEWS

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



MedGenome connect



Wish you all a happy and prosperous new year!

With the launch of VeriSeq NIPT, MedGenome got a shot in the arm, and enhanced MedGenome's foothold in prenatal genetic testing market.

With stronger enthusiasm and vigor, VeriSeq NIPT was introduced to more than 1000 Fetal Medicine Specialists, Gynecologists and IVF specialists.

More than 150 of such clinicians were from 5 different CMEs done in Claria for the 3rd quarter.

The business team has not left any stone unturned in the final lap of FY 2019-20 in maximizing the reach to new cities, new conversions, customer transitions



Briefing on MedGenome's offerings to prospective customers during CME at Mandi

from sporadic to intermittent & regular, and organized knowledge sharing programs in Tier 2 & 3 cities to end the year on a positive note.



We at Prima have conducted series of events and participated in good number of national oncology conferences and important CME's/stand-alone Meetings:

- Haematocon, Delhi
- AROICON, North East Chapter, Imphal
- Lung Cancer Year End Review Meeting, Mumbai
- MPAICON, Jaipur
- KMCH, 8th Annual Radiation Oncology Conference, Coimbatore

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



Prima Sales Team at Haematocon, Delhi

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

The major therapy areas touched through these engagement programs were Oncology, Haematology and Primary Immunodeficiency.

MedGenome connect



The last quarter as expected, was full of events, as we conducted 12 CMEs & RTMs, and participated in 9 conferences which included SIAMG – the biggest conference of the Indian clinical Geneticists at Hyderabad, ISPGHANCON – the premier conferences of Pediatric Gastroenterologists & Hepatologists at Chennai, and Local Pedicons at Odisha and Rajasthan. Overall, our reach was to more than 1800 clinicians across India.

8 out of 12 CMEs were conducted in Tier 2 & 3 cities, giving us access to nearly 250 clinicians.

The team is all the more geared up in closing this year on a high note, and maintain MedGenome's leadership status in genomics in India.



Dr. Ram addressing the gathering of Pediatric Neurologist during Child Neurology group CME at Mumbai

Mecra Infectious Disease Genetics

MedGenome Micra has conducted a good number of events and anchored various Infectious Disease Genetics CMEs:

- 1. Participated in World Congress on Lung Health (the Union) at Hyderabad
- 2. Organized an event at Guwahati to introduce molecular testing for infectious diseases in association with Ayursundra Group
- 3. Organized CMEs at various locations for more visibility and awareness on Micra

The major areas that were touched upon through these programs were CNS infections, Sepsis, Tuberculosis, etc. among others.



Well-attended Micra event at Guwahati in association with Ayursundra Group

Making a difference

Genetic testing provides hope for couple with family history of hearing loss

Vinay and Saroja (name changed), hailing from Vijayawada, Andhra Pradesh were a happy family until they discovered that their first born suffered from hearing and speech loss. They consulted various ENT specialists and as per their recommendation underwent a cochlear surgery for their son, whose hearing has been restored now. The couple experienced a lot of emotional trauma and were worried for their next unborn child.

Vinay and Saroja opted for genetic counselling to understand if their second child will have the same issues as their first child and wanted to ensure their second child is healthy. They consulted Dr. Sunitha Tella, Head of the Clinical Genetics and Fetal Medicine Department at the Institute of Genetics and Hospital for Genetic Diseases, Hyderabad. She suggested the family to undergo genetic testing at MedGenome Labs, Bangalore, for the affected child. The first child, on being tested, was found to have two mutations (variants) in the GJB2 gene, which is associated with hearing loss. The parents were found to be carrying one mutation each, making them "carriers" for the disorder.

Carriers are those individuals who carry one defective copy of a gene (due to a mutation) but aren't affected with the disease. However, these carriers are at a high risk of having a child who is affected, especially when they are married to another carrier for the same gene. This was the case in their first child, who inherited two defective copies of the GJB2 Gene, one from each parent. The risk of having a similarly affected child in each pregnancy is 25%.

Based on these findings, doing genetic testing for these two mutations in the next child was essential. During Saroja's next pregnancy, the fetus was tested for these two variants. Fortunately, it was found that the fetus was only harboring one of the two mutations found in the first child. This meant that the child would be a carrier of the disease and wouldn't suffer from hearing loss.

This gave a huge relief to Vinay and Saroja who were anxious until now regarding the health of their unborn child with respect to hearing loss. Genetic testing helped the couple to know that their unborn child was not affected but just a carrier like them. Thus, genetic testing gave them hope and also allayed their anxiety.

This case also highlights the benefits for couples to undergo pre-conception counselling (i.e before planning for the next pregnancy) with a Genetic Counsellor; especially when there is positive family history for a disorder. Such counselling sessions help the couple to better understand the risk to the child as well as recommend a suitable Prenatal Genetic test.

Summary

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From our US office

This quarter we made our presence at the International Plant & Animal Genome XXVIII conference during January 11-15, 2020, San Diego, CA, USA. We presented our unique single cell genomics, genome assembly and annotation solutions at the event.

PAG brings together over 3,000 leading genetic scientists and researchers in plant and animal research, and over 130 exhibits, 150 workshops, 1100 posters and over 1800 abstracts.







We also attended the SLAS 2020 which had many interesting tracks encompassing cutting-edge science: Advances in Bioanalytics and Biomarkers, Assay Development and Screening, Automation and High-Throughput Technologies, Biologics Discovery, Cellular Technologies, Data Analysis and Informatics, Drug Target Strategies, Micro- and Nanotechnologies, Molecular Libraries and Precision Medicine Technologies. We were happy to present many of our unique solutions at the event.



MedGenome's Proud Moment

Genome Asia

The **GenomeAsia 100K** Project enables **genetic discoveries** across Asia

IRIT

GENOMES POOD AS A STATE Initial sequence data set from the GenomeAsia 100K project

GenomeAsia pilot project was featured in Nature journal's December 2019 issue

MedGenome is proud to be associated with this research. Thanks to teams who were part of this successful adventure

MedGenome's Proud Moment

The Indian Cobra genome has been decoded!!

nature genetics

Indian cobra genome

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The article featured on the cover of the January 2020 issue of Nature Genetics

MedGenome is proud to be associated with this project. Thanks to teams who were part of this successful adventure

MedGenome's Proud Moment

Accreditation by CAP for the second time Why is it so important to us?



Accreditation is the formal recognition by an authoritative body, in this case as you all know College of American Pathologists, of the competence to work to specified international norms or standards.

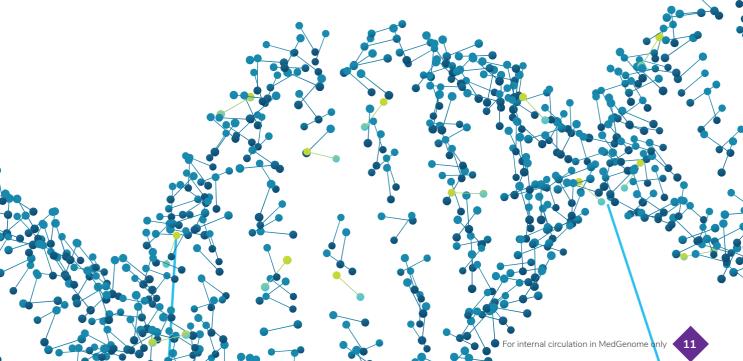
CAP guideline provides a clear roadmap for achieving accreditation and running a high-quality laboratory. College of American Pathologists (CAP) is the world's largest organization of board-certified pathologists and one of the oldest institutions, guiding excellence across the globe on best laboratory practices and standards.

MedGenome has been able to get this accreditation for the second time as a result of our constant endeavour to maintain best standards and quality parameters – we follow the best methodologies, clean labs and thoroughly reliable process and procedures across India.

An accreditation is the validation of our hard work through consistent improvement – a commitment we adhere to year after year, month after month and every day. The accreditation is withdrawn if we fail in any manner at any point of time.

We have maintained it for the first two years (2017 to 2019) and hence we can continue with it for another two years (2019 to 2021) and I am looking forward for many more couplets like this 2021 to 2023 and so on.

It is a collective effort from all the sections of MedGenome and everyone's contribution through which we could get into this accreditation train. The journey is on as long as we follow the standards.



Sneak peek into the world of science







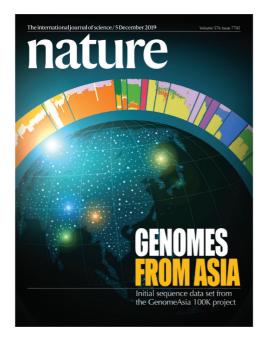
GenomeAsia pilot project was featured in Nature journal's December'2019 issue: How did we get there?

Ramesh Menon, Anjali Verma, Manjari Deshmukh, Akshi Bassi and Ravi Gupta Bioinformatics R&D division, MedGenome Labs Ltd, Bangalore.

It's a dream of any scientific researcher to be part of a study which gets published in journals such as Nature or Science. These two journals have published several landmark studies that has shaped science and technology all over the world.

Since it's inception in 1869, Nature journal gained its reputation by publishing several milestone discoveries in the human history, which includes : wave nature of particles (1927), the neutron (1932), nuclear fission (1939), the structure of DNA (1953), first cloning of a mammal - Dolly the sheep (1997), the human genome (2001) etc. However, there are several very important articles that gets a rejection from Nature journal and published elsewhere. Few examples are the rejection of paper on PCR - Polymerase chain reaction, Kerb's cycle etc.

For us, the journey started in early 2016, when MedGenome, as a start-up, making great progress in clinical diagnostics & services projects business in India, founded the GenomeAsia100K consortium along with Macrogen and Nanyang Technological University (NTU). The



objective was to generate high-coverage whole genome sequences from 100,000 individuals in Asia, predominantly from South Asia. This will help us to understand the genetic variability of the people in the region. In the past, two landmark studies have been published that discussed *peopling of Indian ethnic groups*. The first study made by David Reich's group (USA) and Thangaraj's group (India) was published in Nature Genetics, 2009. Their study showed that all Indians can be classified based on their genetic ancestry into two groups, namely: Ancestral North Indian – ANI, and Ancestral South Indian – ASI. Few years later, Analabha Basu and team further identified two more ancestries namely: Ancestral AustroAsiatic – AAA, and Ancestral Tibeto-Burman (ATB). The tribes from Andaman Nicobar island showed distinct genetic ancestry. Both these studies were based on the limited genomic markers as they have used genotyping arrays.

In its pilot study, the GenomeAsia100K project included 1,739 individuals of 219 population groups from 64 countries across Asia. The samples included 598 from India, 156 from Malaysia, 152 from South Korea, 113 from Pakistan, 100 from Mongolia, 70 from China, 70 from Papua New Guinea, 68 from Indonesia, 52 from the Philippines, 35 from Japan and 32 from Russia. The high-quality sequence data of Indian samples were generated from MedGenome's sequencing lab located at Narayana Netralaya hospital in Bangalore. We got access to the whole genome sequence data along with the relevant meta-data. We looked at the data in mainly four aspects:

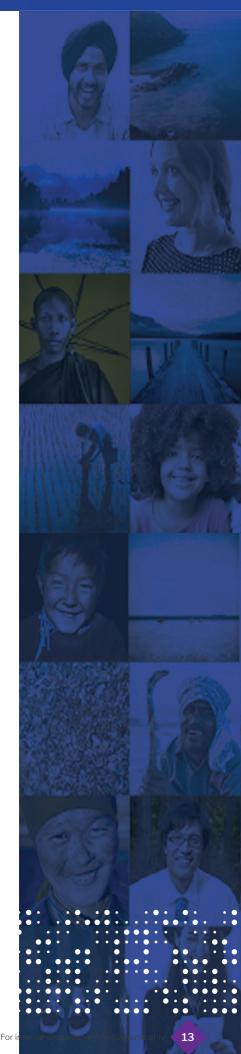
- (a) Ancestry analysis
- (b) Pharmacogenomic profiling
- (c) Creating a genotype imputation reference panel
- (d) Identity-by-descent analysis.

As the consortium is multi-centric several international groups were working on the data, looking at various aspects. These groups were located across the globe such as in: Genentech Inc. (USA), University of California (USA), NTU (Singpore), NIBMG (India) etc. Large amount of coordination and efforts were required for the data analysis, reviewing the results, especially when collaborators are working from different time zones.

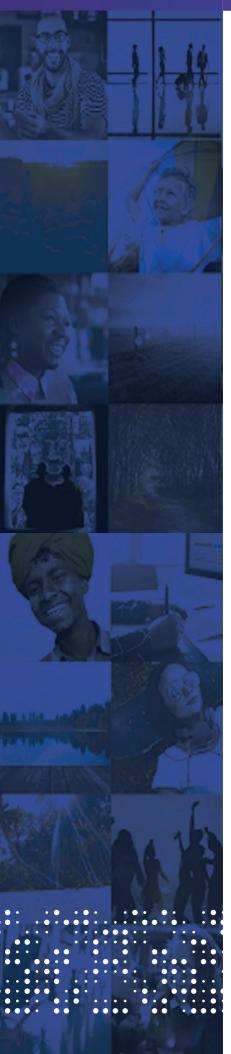
The study has given insights into previously unknown population genetic structure, as well as implications of sub-population/community specific genetic variations in diseases as well as drug reactions. This study provides a useful genomic resource which will be facilitating genetic studies in Asia including India. More than 20% of genetic variants identified in this study are not reported in previous studies like the Exome Aggregation Consortium (ExAC), 1000 Genomes project, gnomAD etc. In rare disease, genetic databases like ExAC, gnomAD, 1000G, dbSNP are used to filter variants based on allele frequency. Since, majority of the samples available in these databases are of European origin there are population-specific variants present with higher frequency which otherwise will be taken as rare variant. For example, when both the gnomAD and the data published in this study is used for filtering common variants (allele frequency > 0.1%), then we reduce the candidate variants roughly by two-fold as compared to when we use gnomAD alone. This study will improve the identification of a pathogenic variant for the rare diseases more accurately as it will help in filtering variants for South Asian ancestry more precisely.

The complex history of Asian populations and population structure has also been reported in this study. This study shows that people from India, Malaysia and Indonesia consists of multiple ancestral populations as well as multiple admixed groups. The rate of recessive diseases has increased because of strong founder effects. Our study found that the indigenous and the tribal population groups have higher *identity by descent* (IBD) as compared to other groups. Further, we found that the urban population from Chennai (size of 9 million) has an IBD score which is 1.3 times higher than the Finnish group. This suggests that our population group from Southern part of India have higher founder effect and also carry a higher chance of having recessive disorders.

Variation in certain regions in the genome that are ancestry related sometimes have implications to drug responses. In several clinics globally, the recommendations for dosing of certain drugs are guided by apparent or self-reported population identity. In this study, we assessed the allele frequencies of key pharmacogenomic variants in the



F



GenomeAsia pilot dataset to identify inter-population differences that have potential implications on drug testing and treatment. Interestingly, the study has identified drugs such as carbamezepine, clopidigrel, peginterferon and warfarin as the drugs with largest impact on genetic variation related to ethnicity and has predicted adverse drug responses in several population sub-groups. For example, a genetic variant in HLA-B gene is associated with risk for development of Steven Johnson syndrome in patients treated with carbamazepine was found to occur at an increased frequency in Austronesian group people (~400 million) from Indonesia, Malaysia and the Philippines. Also, the study assessed the allele frequencies of key pharmacogenomic variants in our dataset to identify inter-population differences that have potential implications on drug testing and treatment, and these novel findings can help the Pharma industry to reduce time and investment in their research while assessing the efficacy and toxicity of new drug development. The GenomeAsia has deeply catalogued population specific genetic variants in "very important pharmacogenes" (VIP genes) such as VKORC1, IFNL3, CYP2B6, CYP2D6 and CYP2C19, affecting dosage, efficacy and toxicity of associated FDA approved drugs.

Human genetic studies taking place across the world have minimum representation from Asian population groups. Most of these studies have been performed on people with European origin. Now, discoveries and genetic associations found from the European population may not necessarily be translated to non-European population group. This limits the researchers in understanding human diseases accurately for the non-European population including those from Asia (which represent 60% of the global population). Recently, there has been slight improvement in non-European studies but still it remains highly under-represented. This study has also published an imputation reference panel available at Michigan Imputation Server (MIS - https://imputationserver.sph.umich.edu/index.html). Our analysis revealed that our panel provides much superior imputation for South Asian ancestry as compared to the existing published reference panel. This will help the GWAS studies performed on the South Asian ancestry.

The GenomeAsia consortium is continuously collecting and analyzing several thousands of diverse genomes across Asia, which creates a unique platform for genetic studies, pharmacogenomic genomic research, which can pave way to the well-being of people in Asia. The pilot study genome browser is available freely and can accessed using the following link https://browser.genomeasia100k.org/.

References

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David Reich et. al. (2009). Reconstructing Indian population history. Nature Genetics

Analabha Basu et. al. (2016). Genomic reconstruction of the history of extant populations of India reveals five distinct ancestral components and a complex structure. PNAS.





MedGenome launched Direct to Consumer Test segment under the **ApnaGenome** brand. Following test will be covered under this new segment:

Basic Test



ApnaGenome was officially launched at the Kerala Literature Festival (KLF), Calicut held between 16th-19th Jan, 2020. The test was launched by famous Malayalam movie actress **Ms. Mamta Mohandas** at the KLF. At the launch she shared her tryst with cancer and how genetic testing can help in informative decision and precision treatment. She spoke passionately about the importance of genetic testing in India and the need for awareness about the latest test offerings being present in India.

Many event attendees took interest to know more about the product and bought the kits at the ApnaGenome stall. The positive response received during the event gave us the confidence to proceed further in our efforts to maximise our reach.

Optional Modules



Inherited Cancer Risk







15

For internal circulation in MedGenome only

From our Colleagues

Art meets Science

Art has a double face, of expression and illusion, just like science has a double face: the reality of error and the phantom of truth. — René Daumal









Bhushan Mahajan - Software Engineer

From our Colleagues

Our employee's little Picasso :)



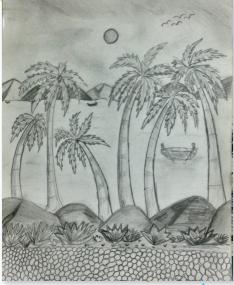
By: Aditri Gupta (7 years) •DNA of Ravi Gupta, Bioinformatics R&D



By: Gauri Phalke (13 years) DNA of Sameer Phalke, Senior Scientist



By: Aditri Gupta (7 years) DNA of Ravi Gupta, Bioinformatics R&D



By: Gauri Phalke (13 years) DNA of Sameer Phalke, Senior Scientist

Employee connect

WELCOV Our New-Joiners







M. Haniffur Rahman



Anguraj



M. Moquitul Haque





P Prasad

Sangeeta Mithailal



Tinchan Thangamma





Saswati Biswas



Venkateswaran



Anjali Mahesh Patil



Moni john



Pulluru Sai Sushma



Sathya Priya G



Victor Y





Namrata Vishwanath Pai







Vinisha Sharal



Nawaz P

Remya Koshy

Shewata Pandita

Vishnu Jayaraj



Jitendra Kumar Das



Nithyanandan T



Sandeep Kumar Singh



Sunanda Jha



Nalla Srividya











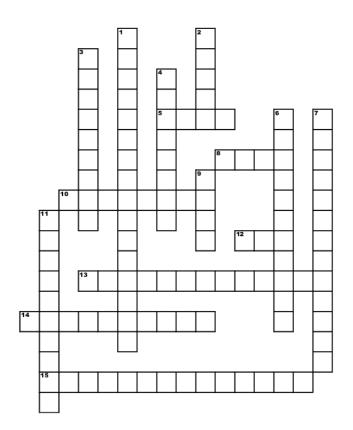






Employee connect

DNA Vocabulary

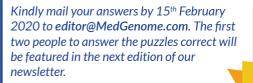


Across

- 5. Physical link between the mRNA and the amino acids sequence of proteins
- 8. Essential for protein synthesis in all living organisms
- 10. Organelle that produces proteins
- 12. Single stranded molecule found in Cytoplasm
- **13.** Process in which the DNA is copied into RNA by polymerase
- 14. Bonding of a large number of amino acids forming a chain
- 15. Process of producing two identical replicas of DNA

Down

- 1. Made up of adenine, thymine, guanine, and cytosine
- 2. Three nucleotides that form a genetic code
- 3. The monomer for Protein
- 4. A significant and bassic change
- 6. Process in which ribosomes create proteins.
- 7. Type of base that allows cells to copy information from one generation to another
- 9. The molecular unit of heredity
- 11. Monomer for nuclaeic acid





Solve the

Puzzle

&

Photo feature

Celebrations















MERRY CHRISTMAS. F BIRTH DAY WISHES FOR THE MONTH OF DEC - 2019...











The market leader in Genomics-based Diagnostics and Research



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			× X10		MiSeq		

