Confederation of Indian Industry

DECODING THE FUTURE

A COMPENDIUM OF CUTTING-EDGE GENOMIC TECHNOLOGIES

2024

Published by Confederation of Indian Industry (CII), The Mantosh Sondhi Centre; 23, Institutional Area, Lodi Road, New Delhi 110003, India,
Tel: +91 11 45771000; Email: info@cii.in; Web: www.cii.in

Confederation of Indian Industry

DECODING THE FUTURE

A COMPENDIUM OF CUTTING-EDGE GENOMIC TECHNOLOGIES

2024

Update

Table of Contents

Update

FOREWORD

Mr Kris Gopalakrishnan
Past President, CII
Chairman, Axilor Ventures & Co-Founder, Infosys
Chairman, CII National Task Force on Genomics

The world is witnessing a genomic revolution - a transformative era driven by deep tech innovations and an ever-expanding understanding of the human genome. With its unparalleled genetic diversity and rapidly advancing scientific community, India is uniquely poised to lead this groundbreaking transformation.

The Confederation of Indian Industry (CII) is steadfast in its commitment to positioning India as a global leader in genomics. This compendium highlights exemplary projects that range from pioneering research in rare diseases to other cutting-edge applications.

The present compendium showcases the exemplary projects covering groundbreaking research on application of genomics in rare diseases to other cutting-edge applications. By unlocking the power of genomics, we can revolutionize healthcare, improve agricultural productivity, and address pressing global challenges such as climate change and food security.

However, unlocking the full potential of genomics, requires addressing critical challenges such as challenges such as data privacy, ethical considerations, reducing cost of sequencing, infrastructure and workforce skilling.

Through this initiative, CII aims to foster innovation, advocate for supportive policies, strengthen industry-academia-government collaborations, and raise awareness about the transformative power of genomics. Together, these efforts are designed to accelerate genomic research and its application in India.

By working collectively, we can shape the future of genomics in India—driving scientific breakthroughs, improving human health, and securing a sustainable and prosperous future for generations to come.

Update

FOREWORD

Mr Chandrajit Banerjee
Director General, Confederation of Indian Industry

The global Genomics landscape is undergoing a rapid transformation, fuelled by unprecedented technological advancements and a growing recognition of its power to revolutionize healthcare, agriculture, and other industries. As a nation with a rich genetic diversity and a burgeoning pool of scientific talent, India is poised to emerge as a global leader in this field.

The Confederation of Indian Industry (CII) is helping drive India as a leader in Genomics and other emerging technologies. By actively advocating for policies that foster innovation and accelerate genomic research, CII is supporting India's rise as a global powerhouse in this critical sector.

To realize this ambitious vision, it is imperative to address key challenges such as data privacy, ethical considerations, and public private partnerships. Fostering collaboration among researchers, clinicians, industry leaders, policymakers, and the public is essential to unlock the full potential of Genomics in improving human health, agricultural productivity, and environmental sustainability.

The CII Compendium on Genomics Research and Technologies covers nearly 60 technologies on genetic research, next generation tools and technologies, and biotechnology applications. These range from precision medicine to climate-resilient crops, thereby showcasing the transformative impact of Genomics on improving quality of life, fostering economic growth, and ensuring environmental sustainability.

Through this Compendium, we aim to identify emerging opportunities and innovations in the Genomics field, explore policy advocacy areas where CII can provide valuable support, and foster a robust ecosystem for Genomics research and innovation. The Compendium of technologies will help to shape the future of Genomics in India, encourage scientific discovery, and advance healthcare for the country.

Update

Executive Summary

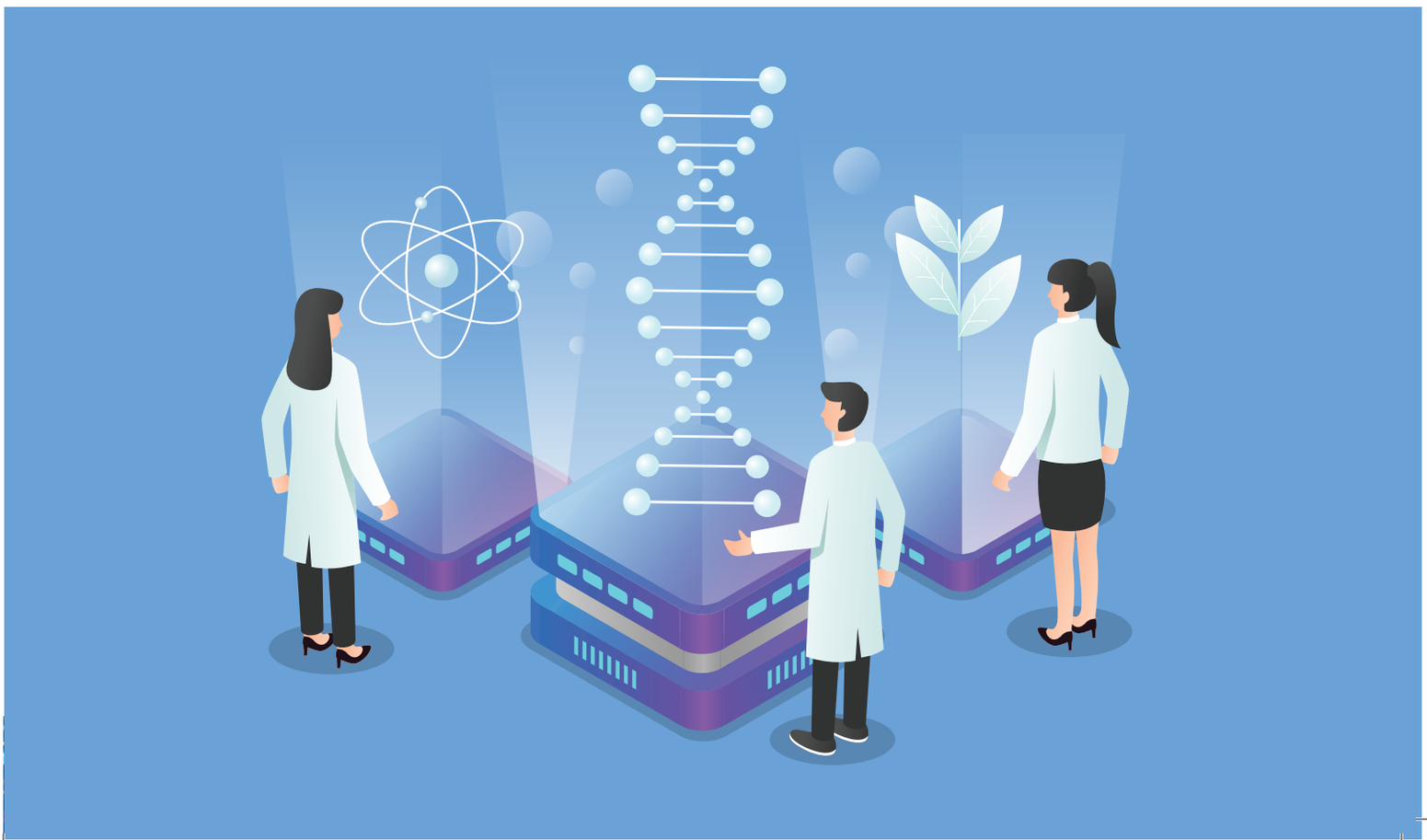
Genomics: A New Frontier in India's Tech Landscape

Genomics, the study of genes and their functions, is emerging as a powerful tool with the potential to revolutionize various sectors. From healthcare to agriculture, and from environmental science to personalized medicine, genomics is reshaping the world. India, with its rich genetic diversity and burgeoning scientific community, is poised to play a pivotal role in this global revolution.

The Confederation of Indian Industry (CII) recognizes the transformative power of genomics and is actively working to foster innovation and growth in this field. CII's National Mission on Technology, Innovation, and Research, an initiative dedicated to driving technological advancements, has identified genomics as a key area of focus. By promoting collaboration between industry, academia, and government, CII aims to create a thriving ecosystem for genomic research and development.

The present Compendium on Cutting-Edge Genomic Technologies is a testament to India's growing expertise in genomics. This comprehensive document showcases latest advancements in genomic research, applications, and technologies. It highlights the work of leading institutions and researchers and explores the potential of genomics to address pressing global challenges such as climate change, food security, and healthcare.

By investing in genomics research, developing skilled talent, and creating a supportive regulatory environment, India can unlock the full potential of this transformative field. CII National Task Force on Genomics through its initiatives and partnerships, is committed to making India a global leader in genomics and driving sustainable development for the future.



Update

CASE STUDIES FROM RESEARCH & ACADEMIC INSTITUTIONS

Multiplexed SNP panel assay for detection of single nucleotide polymorphisms SNPs for predicting genetic risk of preterm birth outcome

Name of the Institution

BRIC-National Institute of Biomedical Genomics
Kalyani, West Bengal – 741251

1. Brief Description of the Technology / Project

Preterm birth (PTB), or birth before 37 completed weeks of gestation is the leading cause of neonatal and infant mortality. Survivors of preterm birth suffer from delayed development and several health complications throughout their life. Hence, any reduction in the incidence of PTB, which has been elusive so far, is expected to significantly reduce the global health burden. The underlying causes of PTB are complex, with strong genetic contributions which remain to be identified (Ref 1). India is the leading contributor of preterm births and is currently among top five countries with highest rates of preterm birth. We conducted the first genome wide association study of preterm birth on 6,211 Indian women, from the GARBH-Ini pregnancy cohort (Ref 2) which is also the first reported maternal GWAS on preterm birth from South Asia (Ref 3) along with transethnic replication and meta-analysis with European women (Ref 4-6). We have identified a set of SNPs which are able to predict preterm birth in GARBH-Ini cohort with high confidence. The SNP panel assay uses genomic DNA from dried blood spot and saliva, using novel hybridization-based approaches and then the sequencing libraries can be pooled and sequenced a small bench top to high throughput production scale next generation sequencers.

2. Problem solved / addressed

The saturated draft assembly of the O. tenuiflorum (O. Sanctum) genome was about 386 Mb, along with the plastid genome of 142,245 bp, turning out to be the smallest in Lamiaceae. In addition to SSR markers, 136 proteins were identified as homologous to five important plant genomes. Biosynthetic pathway analysis revealed a high abundance of phenylpropanoids in O. sanctum. Phylogenetic analysis for chloroplast proteome indicated Salvia miltiorrhiza as the nearest neighbour. The comparison of the chemical compounds and genes availability in O. sanctum and S. miltiorrhiza suggests a significant potential for discovering new active molecules, highlighting the importance of Ocimum in future research.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Development stage

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

Provisional patent application is being filed prior to publication of the findings.

5. Suggestions on policy / regulatory interventions for the technology being described

Yes, policy intervention is required to implement this at scale. This genetic screening can impact at national level only if samples can be collected at health and pregnancy camps at preconception stage and early pregnancy and women triaged for risk of preterm birth. This will enable significant reduction in preterm birth rates at national and global levels. Policy regulations will be required for facilitating such screening.

6. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

On societal aspect, this panel can be used in antenatal clinics to triage women at high genetic risk of preterm birth, so that appropriate personalized antenatal medical care can be provided to them along with heads up for making appropriate neonatal care arrangements during delivery and post-natal follow up for reducing neonatal and post-natal mortality and complications. On business aspect, this panel can be implemented as a point of care in gynaecological consults at preconception stage and early pregnancy. The ease of collection and transport of samples along with cost effective assay which can be conducted at variable throughput will be particularly useful for implementation by the molecular diagnostic laboratories.

7. National or international collaborations associated with this technology or project?

This study was conducted in the GARBH-Ini cohort in Gurugram Civil Hospital in the Grand Challenge Program on Preterm Birth funded by the Department of Biotechnology, Govt. of India along with additional supports from multiple axillary projects funded in the Grand Challenge India program supported by Bill and Melinda Gates Foundation and BIRAC.

8. What is the market potential of the technology/project in both the near term and long term?

In short term, this diagnostic tool can be used to help in the diagnosis of preterm birth, and based on the presence of genetic variations appropriate clinical care can be provided to those women to reduce the risk of preterm deliveries and also to provide improved clinical support at delivery and follow up post-delivery and in early childhood to mitigate newborn mortality and health complications.

In the long term, if undertaken at scale and over time, this will contribute to significant reduction in preterm birth incidence (which escaped all present strategies so far in India and globally). It will lead to reduced neonatal mortality and health complications in early childhood and later life, thus positively affecting the global health burden.

Project related references:

1. Bhattacharjee E, Maitra A. Spontaneous preterm birth: the underpinnings in the maternal and fetal genomes. NPJ Genom Med. 2021;6(1):43.

2. Bhatnagar S, Majumder PP, Salunke DM, & Interdisciplinary Group for Advanced Research on Birth Outcomes—DBT India Initiative (GARBH-Ini). A Pregnancy Cohort to Study Multidimensional Correlates of Preterm Birth in India: Study Design, Implementation, and Baseline Characteristics of the Participants. Am J Epidemiol. 2019;188:621–31.

3. Bhattacharjee E, Thiruvengadam R, Ayushi, et al. Genetic variants associated with spontaneous preterm birth in women from India: a prospective cohort study. Lancet Reg Health Southeast Asia 2023;14:100190.

4. Zhang G, Feenstra B, Bacelis J, et al. Genetic Associations with Gestational Duration and Spontaneous Preterm Birth. N Engl J Med, 2017;377:1156–67.

5. Solé-Navais P, Flatley C, Steinthorsdottir V, et al. Genetic effects on the timing of parturition and links to fetal birth weight. Nat Genet 2023;55:559–67.

6. Pasanen A, Karjalainen MK, FinnGen, et al. (2023). Meta-analysis of genome-wide association studies of gestational duration and spontaneous preterm birth identifies new maternal risk loci. PLoS Genet 2023;19:e1010982.

Low-Cost Genome Profiling

Name of the Institution

BRIC-National Institute of Biomedical Genomics
Kalyani, West Bengal – 741251

1. Brief Description of the Technology / Project

Identification of genetic variants which might be associated with complex health phenotypes rely on profiling of genomes of large number of individuals. Approaches used for genomic profiling depend upon comprehensiveness versus cost. Whole genome genotyping arrays are the most commonly used workhorse of such studies as they provide reasonably comprehensive genome profiling at minimal cost. However, increasing efforts to profile non-European populations have resulted in the recognition of limitation of genotyping arrays.

For example, even with most recent genotyping arrays like the Infinium Global Screening Array (Illumina), which has genome-wide content selected for high imputation accuracy at minor allele frequencies of >1% across all 26 1000 Genomes Project populations, are unable to capture sufficient population specific variants, specially form South Asia and Indian subcontinent.

Our experience of using such profiling methods in Indian population has shown that 12.38% of the array markers have been found to be invariant and up to 40% of the same with low or no informative value in the samples from this subcontinent. While 30x whole genome sequencing remains the best solution to this problem, it is not feasible due to costs involved. As sequencing costs have dropped, low-pass sequencing (average coverage of the genome is equal to or lower than 1x), LPWGS have been found to address this lacuna in genome profiling without any substantial increase in cost. Recent studies have found that a human sample sequenced at 0.4x coverage is expected to have a single sequencing read covering each of around 28 million of the 84.7 million genetic variants identified in the 1000 Genomes Project, which is much more than what a genotyping array provides (typically 650,000 sites) (CONVERGE Consortium, Auton et al, Nature 2015). Additionally, LPWGS also provides additional information on novel and rare variants as well as the presence of pathogens. All these results in use of LPWGS an attractive and powerful method to extract enhanced information in health and disease genomics studies and for generating a genomic variant profile of an individual.

2. Problem solved / addressed

While the SNP microarrays are cost effective (about ₹4,500 per individual, 700,000 variants), they are able to achieve very limited capture of population specific variants and up to 40% of these markers can be of low or no informative utility in our populations. Whole Genome

sequencing at 30X depth profiles typically about 135 million variants and are able to capture all the population variants yet suffer from high costs (about ₹ 90,000 per individual). We have developed a low pass whole genome sequencing and analysis method which are of low cost, even lower than microarrays (₹ 3,500 per individual), yet profile about 125 million variants and are able to achieve a remarkably successful capture of population variants. In our ongoing study, we have generated low pass whole genome sequencing data on 4000 individuals for whom Illumina Infinium Global Screening array with multi disease drop in panel. Our genotype profiling was found to be accurate (99.28% concordance with microarray data) and were able to generate sequence data which resulted in autosomal, X and mitochondrial genome coverages of 1.783x, 1.758x and 100.275x respectively. The results obtained by using this method will further improve with the availability of the data generated in the Genome India Project.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Development stage

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

Not Commercialized. Validation and application in research studies ongoing.

5. Suggestions on policy / regulatory interventions for the technology being described

This innovation will enable ultra-low cost yet comprehensive profiling of genomic variants for health and discovery genomics projects. It will result in development of improved and population specific genetic marker panels for risk prediction, diagnostic and prognostic assessment of various diseases which can provide substantial support for targeted and efficient clinical management of patients.

6. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

The method was developed, and pilot data was generated in the GRBH-Ini cohort in an ongoing study of Multi Omics of Mothers and Infants (MOMI) funded by the Bill and Melinda Gates Foundation and BIRAC.

7. National or international collaborations associated with this technology or project?

This study was conducted in the GARBH-Ini cohort in Gurugram Civil Hospital in the Grand Challenge Program on Preterm Birth funded by the Department of Biotechnology, Govt. of India along with additional supports from multiple axillary projects funded in the Grand Challenge India program supported by Bill and Melinda Gates Foundation and BIRAC.

8. What is the market potential of the technology/project in both the near term and long term?

This innovative method has tremendous potential. In the short term, it will enable more effective and low-cost health and discovery genomics projects. In the long term, it will result in development of improved and population specific genetic marker panels for risk prediction, diagnostic and prognostic assessment of various diseases which can provide substantial support for targeted and efficient clinical management of patients. Further, the authorities can also consider using this method to generate genomic profile for individual based identification purposes like the UIADI.In the long term, if undertaken at scale and over time, this will contribute to significant reduction in preterm birth incidence (which escaped all present strategies so far in India and globally). It will lead to reduced neonatal mortality and health complications in early childhood and later life, thus positively affecting the global health burden.

Unravelling the Genome of Holy Basil: an "incomparable" "Elixir of Life" of traditional Indian medicine

Name of the Institution

***CSIR-Central institute of Medicinal and Aromatic Plants, Lucknow.**

***CSIR-Central Institute of Medicinal and Aromatic Plants, P.O-CIMAP, Near Kukrail Picnic Spot Lucknow-226015**

***Presently at: CSIR-National Botanical Research Institute, Lucknow**

1. Brief Description of the Technology / Project

Holy basil (Ocimum tenuiflorum, also, O. sanctum) is listed in ancient Ayurvedic scriptures as an "elixir of life" (lifesaving) herb and has been venerated for over 3000 years for its medicinal powers. Although utilized to treat a variety of diseases, validation of molecules for differential activity has yet to be completely investigated, as over 80% of patents on this plant are for extracts or plant parts, with a concentration on essential oil components. To better comprehend the plant's metabolic capacity, the whole nuclear and chloroplast genomes were sequenced for the first time, combining sequence data from four libraries and three NGS systems.

2. Problem solved / addressed

The saturated draft assembly of the O. tenuiflorum (O. Sanctum) genome was about 386 Mb, along with the plastid genome of 142,245 bp, turning out to be the smallest in Lamiaceae. In addition to SSR markers, 136 proteins were identified as homologous to five important plant genomes. Biosynthetic pathway analysis revealed a high abundance of phenylpropanoids in O. sanctum. Phylogenetic analysis for chloroplast proteome indicated Salvia miltiorrhiza as the nearest neighbour. The comparison of the chemical compounds and genes availability in O. sanctum and S. miltiorrhiza suggests a significant potential for discovering new active molecules, highlighting the importance of Ocimum in future research.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

- The draft genome of Ocimum obtained was published in BMC Genomics (https://doi.org/10.1186/s12864-015-1640-z) in 2015.
- Another publication {Genome-wide detection of terpene synthase genes in holy basil (Ocimum sanctum L.)} utilizing the obtained genome data of Ocimum was published in Plos One(https://doi.org/10.1371/journal.pone.0207097) in 2018.
- A CSIR project was obtained on the basis of Ocimum draft genome. The title of the project was "Utilization of Ocimum Genome for the Production of industrially important medicinal and aromatic compounds". The category of the project was "Focused Basic Research (FBR) under the Agriculture Nutrition Biotechnology theme of CSIR". The Project No was FC2020-23/MLP-02. Nodal Lab: CSIR- CSIR-Central Institute of Medicinal and Aromatic Plants, Lucknow.

4. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

Utilizing the Ocimum genome (CIM-Ayu), we successfully identified several terpene synthases as well as genes associated with phenylpropanoid and flavonoid biosynthesis. The genomic data, obtained from our in-house sequenced repository, enabled us to predict coding sequences for both known and unknown gene functions. By thoroughly characterizing these genes, we aim to uncover promising candidate genes that could facilitate the production of novel compounds, particularly flavonoids and terpenes. This research not only enhances our understanding of Ocimum's metabolic pathways but also paves the way for discovering new bioactive molecules, which could have significant applications in medicine and agriculture.

5. National or international collaborations associated with this technology or project?

- The draft genome of Ocimum obtained was published in BMC Genomics (https://doi.org/10.1186/s12864-015-1640-z) in 2015.
- Another publication {Genome-wide detection of terpene synthase genes in holy basil (Ocimum sanctum L.)} utilizing the obtained genome data of Ocimum was published in Plos One(https://doi.org/10.1371/journal.pone.0207097) in 2018.
- A CSIR project was obtained on the basis of Ocimum draft genome. The title of the project was "Utilization of Ocimum Genome for the production of industrially important medicinal and aromatic compounds". The category of the project was "Focused Basic Research (FBR) under Agriculture Nutrition Biotechnology theme of CSIR". The Project No was FC2020-23/MLP-02. Nodal Lab: CSIR- CSIR-Central Institute of Medicinal and Aromatic Plants, Lucknow.

6. What is the market potential of the technology/project in both the near term and long term?

Several terpene synthase and phenylpropanoid/flavonoid biosynthesis pathway genes were effectively identified using Ocimum draft genome variety CIM AYU. Our in-house genomic repository provided the sequences of these genes that allowed us to predict coding sequences for both known and unknown gene functions. Our aim is to characterize interesting candidate genes that may aid in the synthesis of new compounds, especially terpenes and flavonoids, by in-depth analysing these genes. Apart from improving our knowledge of metabolic pathways of Ocimum, this research opens the door to the discovery of new bioactive compounds that may have important uses in both agriculture and medicine.

Genetic Enhancement of Mulberry by Genomics Approaches: A multi-component Network Project" (Project code: PIC01003CN)

Name of the Institution

CSB-Central Sericultural Research and Training Institute
Mananthawadi Road, Srirampura, Mysuru-570008 Karnataka, India

1. Brief Description of the Technology / Project

The program envisages generation of large genomic resources (genes and genetic markers) and characterization of genetic resource available with the PIs leading to the discovery of novel QTLs and genes associated with the traits of interest. Donor lines for specific traits identified in the process will form the basis for the initiation of a focused molecular breeding and transgenic programs to introgress relevant traits for genetic enhancement of mulberry.

2. Problem solved / addressed

The sequencing and de novo assembly of the Morus indica (K2) nuclear genome has been completed. Generated large genomic resources related to different traits of interest. Phenotyping of large number of available germplasm resources was completed for the major traits of interest. Created the genomic basis for molecular breeding in mulberry through omics approach.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Development stage

4. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

- The sequencing and de novo assembly of the Morus indica (K2) nuclear genome has been completed.
- A set of 20 SSR molecular marker analysis against 172 diverse germplasm belonging to different Morus species has been studied for detecting genetic variation.
- A diverse set of 209 mulberry germplasm lines were screened for drought adaptive traits.
- A set of 232 panel of germplasm lines was screened with 29 genomic SSR markers and allelic diversity was identified.
- Based on seven crops data on growth and yield parameters, sixteen contrasting genotypes were identified for the higher leaf yield among 232 accessions.
- Phenotypic evaluation of 250 diverse mulberry germplasm accessions for nitrogen,

phosphorus, sulphur and zinc use efficiency for first trial was completed.

- Developed three mapping population and established in the field.
- Completed evaluation of root rot disease resistance mapping population consisting of 200 F1 progenies against Fusarium solani and Lasiodiplodia theobromae under glasshouse condition.
- SSR genotyping of the mapping population with six identified parental polymorphic markers was completed.
- A total of 36 putative mulberry transgenic lines were developed using three gene constructs.
- Drought-specific transcriptome data (12 condition-specific transcriptome libraries) have been generated and analyzed.
- Diverse types of the stress-responsive gene (i.e., genes with known functions, proteins of unknown functions PUFs, the domain of unknown functions, DUFs) have been identified and being validated by expression analysis and overexpression in model systems.
- A novel protocol for inducing rapid bud break has been developed and an India patent application on the invention has been filed.
- Comparative leaf transcriptomics of five mulberry accessions were conducted and a comparison has been made among the transcriptome of leaves of the two preferred cultivated varieties and three wild types of species.
- A few genes were selected for structural and functional validation. One of the selected genes, ARF, the auxin response factor (MiARF12709) was cloned from mulberry, and auxin inducibility was tested.
- Putative transgenic plants have been generated successfully and are being maintained for further functional validation.
- Primary metabolites (protein, carbohydrates, ascorbic acids, tocopherols and amino acids) were estimated in ten genotypes.
- Among ten genotypes, high primary metabolites were recorded in V1, Morus multicaulis, G4, S36 and G2.
- Secondary metabolites were extracted from these 3 varieties under different conditions and subjected to GC-MS analysis.
- TBME extracts under sonication showed better metabolite levels. TBME extract of methanol sonicated crude showed better levels of fatty acids derivatives.
- The nutritional indices traits are better in V1, G4 followed by S36, K2 and Morus multicaulis and nutritional conversion trait are better in G4, V1 followed by Morus multicaulis K2 and S36.
- RNA was isolated from silkworm, converted into cDNA, amplified and sequenced using specific primers of beta-fructofuranosidase gene from silkworm Bombyx mori.

- Total RNA was isolated from both Spilosoma oblique and Spodoptera lituraand converted into cDNA and amplified with specific primers of beta-fructofuranosidase gene from silkworm Bombyx mori.
- Comparative growth analysis of Spodoptera litura was done by feeding them on both mulberry and castor leaves.

5. National or international collaborations associated with this technology or project?

National collaboration with different universities and institutes as follows:

- Central Sericultural Research and Training Institute, Mysuru
- Central Sericultural Germplasm Resources Center, Hosur
- University of Agricultural Sciences, Bengaluru
- R. V. College of Engineering, Bengaluru
- National Chemical Laboratory, Pune
- University of Delhi, South Campus, New Delhi
- Jawaharlal Nehru University, New Delhi

6. What is the market potential of the technology/project in both the near term and long term?

- The genome assembly and annotation generated in the project will provide a blue-print and facilitate various large-scale and focused basic and applied genomics studies in Mulberry.
- The set of SSRs and DNA polymorphisms identified in this study can be used for large-scale genotyping applications for discovery of associated SNPs and/or candidate genes for various agronomic traits in mulberry.
- Identified SSRs will facilitate at practical use for mapping QTLs and for classical breeding.
- It needs to be saturated with more number of SSRs along with identified SSRs will be helpful to study co-segregation of polymorphic molecular markers for different traits of interest (Drought, Yield, NUE and root rot disease resistance) which will contribute to the development of a linkage / QTL map of mulberry.
- Selected SNPs will be useful for SNP chip development and SNP genotyping of mapping population and diverse germplasm for QTLs discovery.

Development of Hygrotolreant bivoltine breeds/ hybrids through molecular marker assisted selection (Pilot project approved by CSB) (August 2017-July 2018)

Name of the Institution

CSB-Central Sericultural Research and Training Institute
Mananthawadi Road, Srirampura, Mysuru-570008 Karnataka, India

1. Brief Description of the Technology / Project

The fluctuating environmental condition is detrimental to silkworm growth and developments. Especially variable humidity is inducing adverse effects on the silkworm. The combined effect of both temperature and humidity largely determines the satisfactory growth of the silkworms and production of quality cocoons. Expiration of carbon dioxide increases with rise in humidity. On the contrary, low humidity prolongs the length of the growing period of silkworm larva. In this regard, Bivoltine breeds which have been screened through MAS for temperature tolerance etc., was screened for the two different temperature and high humidity regimes and the highest survived Bivoltine breed was further considered for total RNa extraction and confirmation of genes presence through PCR amplification. Exposure of silkworm to high relative humidity results in the reduction in cocoon characters. The pyrexia gene can be used as potential candidate gene for identifying high humidity sensing in silkworm. The blast result of TRP Pyrexia showed 71% of identity with the water witch gene of Drosophila melanogaster which has been reported in sensing wet air i.e., high humidity. Based on the output of the present work, further breeding programmes can be initiated for development of hygrotolerant bivoltine breeds/hybrids through Molecular Assisted Selection (MAS) that can sustain fluctuating RH conditions throughout its life cycle which ultimately helps in production of quality silk.

2. Problem solved / addressed

The molecular basis of these hygroreceptors has been identified in the expression of specific transient receptor potential (TRP) cation channels that are involved in mechano- as well as temperature dependent transduction. Ionotropic Receptors play essential roles by regulating membrane potential, propagation of action potentials, neurotransmitter release, and intercellular communication. Though, there are reports which have contributed to the development of breeds for temperature tolerant there is a need of humidity tolerant breeding lines. Recent advances in molecular biology provide means to the scientists to identify RH sensing genes in insects. Interestingly, the molecular bases of these hygroreceptors have been identified in the expression of specific transient receptor potential (TRP) cation channels that are involved in mechano- as well as temperature dependent transduction (Liu et al., 2007). Ionotropic Receptors play essential roles by regulating membrane potential, propagation of action potentials, neurotransmitter release, and intercellular communication (Wallach et al., 2017). The gene (Pyrexia) responsible for high humidity sensing in silkworm was identified and used as marker in silkworm breeding.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The output of the project was utilized by the silkworm breeders working in different units of Central silk board in developing the silkworm which is tolerant to high humidity.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

The developed breeds/hybrids are under different levels of trails.

5. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

The impact of the project will be analysed based on the performance of the silkworm breeds/ double hybrids.

6. What is the market potential of the technology/project in both the near term and long term?

Based on the gene identified (pyrexia) as marker, the breeds/hybrids have been developed which helps the sericulturist to overcome the impact of high humidity.

AIT-01019-SI Screening of drugs to inhibit the PI3K-AKT pathway in Bombyx mori for controlling nuclear polyhedrosis virus infection.

Name of the Institution

CSB-Central Sericultural Research and Training Institute
Mananthawadi Road, Srirampura, Mysuru-570008 Karnataka, India

1. Brief Description of the Technology / Project

Among infectious microbes, viruses represent a particular threat because they offer few intrinsic targets for inhibition by antiviral molecules. This is because they consist in their simplest form in a nucleic acid encapsulated in a protein shell, and hijack molecular machineries from host cells to complete their replication cycle. The PI3K-Akt pathway is essential for the efficient replication of the baculoviruses. The PI3K-Akt signaling pathway plays important roles in cell survival, apoptosis, cell proliferation, and metabolic regulation, which can be activated by several viruses that modulate cellular events, and thereby augment viral replication. The earlier researchers have suggested working to enhance the inhibitory effect of drugs on viruses by targeting multiple host factors, such as PI3K-Akt, which are identified to be important for virus infection. The PI3K-Akt pathways play important roles in mediating multiple biological processes including development, cell surveillance, cell proliferation, autophagy, oncogenesis and inflammation. it plays important roles in controlling signals involved in mRNA translation. By targeting this pathway in the proposed project, the management of BmNPV will be done. In the proposed research project, elucidation of immune signaling pathways that could be activated by NPV infection to further delineate the cellular signaling pathways involved in baculovirus infection and finding novel therapeutic targets for NPV will be studied. It is proposed to evaluate the inhibitory ability of 91 oral drugs which target PI3K-Akt pathway in Bombyx mori nuclear polyhedrosis virus (BmNPV) infected silkworms to inhibit viral proliferation. The preliminary study conducted in silkworms for developing potential drugs for the management of grasserie disease in silkworm.

2. Problem solved / addressed

A total of 96 drugs/inhibitors were screened against the 8 PI3K-Akt proteins. 10 drugs/inhibitors were selected. Molecular docking and protein-drug interaction was studied. A standard concentration of 1mg/ml proved to have better survival in the silkworm larvae. DNA isolation was conducted, and PCR analysis has showed significant band changes in the Agarose gel electrophoresis. RNA isolation and RT-qPCR was conducted at SBRL, Kodathi. Results obtained from RT-qPCR showed significant changes in the viral genome in samples (Control, Drug-treated, NPV infected and NPV-Drug treated). Fold differences were calculated after the drug treatment and NPV-Drug treated samples compared to a standard Actin and GAPDH as a reference primer. Silkworm larvae were Orally fed with 1mg/ml of selected drug which was sprayed on the leaves. The survival of the treated larvae was noted, and the results showed 73.5% higher survival when compared to the NPV infected samples.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The present technology is under the field evaluation.

CRISPR/Cas9 based genome editing in mulberry silkworm

Name of the Institution

CSB-Central Sericultural Research and Training Institute
Central Sericultural Research & Training Institute, Central Silk Board, Ministry of Textiles, Govt. of India, Berhampore - 742 101, Murshidabad, West Bengal, India

1. Brief Description of the Technology / Project

This collaborative project with Tokyo Institute of Agriculture and Technology/Yamaguchi University funded by DST-JSPS and the Central Silk Board aims to develop genetically modified silkworm strains using genome-editing tools like CRISPR/Cas9, focusing on disease resistance. While India is the second-largest producer of raw silk, crop losses due to diseases like flacherie and environmental factors are significant, particularly in Eastern and Northeastern India. By leveraging expertise from Japan and advanced genetic manipulation techniques, the project seeks to create silkworm strains that are tolerant to complex diseases. This research holds the potential to improve silk production, enhance yields, and foster sustainable sericulture in India.

2. Problem solved / addressed

The project addresses the significant problem of crop losses in sericulture due to diseases like flacherie and environmental stressors, which result in major crop losses across various sericulture practicing regions of India. Current breeding methods have not effectively addressed these challenges. The introduction of genome-editing techniques, particularly CRISPR/Cas9, enables precise manipulation of silkworm genes responsible for disease resistance and climate adaptability. By developing disease-tolerant silkworms that can withstand biotic and abiotic stresses, this project aims to increase productivity, reduce losses, and promote sustainable sericulture, enhancing the economic viability of silk farming in India.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Development stage

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

Under Development Stage

5. During development and/ or implementation, have you encountered any regulatory or other challenges:

Permissions from Institutional Biosafety Committee (IBSC) & Review Committee on Genetic Manipulation (RCGM)were necessary

6. Suggestions on policy / regulatory interventions for the technology being described:

To support the adoption of genome-editing technologies in sericulture, policies should streamline the regulatory approval processes for genetic modifications, ensuring safety while fostering innovation. Clear guidelines for biosafety and environmental impact assessments, coupled with incentivizing research collaborations, will encourage the development and commercialization of resilient silkworm breeds.

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

The project aims to boost silk production by developing disease-tolerant silkworm breeds, enhancing both national productivity and global competitiveness.

8. National or international collaborations associated with this technology or project?

Dr. Katsuhiko Ito
Associate Professor
Department of Science of Biological Production
Graduate School of Agriculture
Tokyo University of Agriculture and Technology
3-5-8 Saiwai-cho, Fuchu, Tokyo, 183-8509, Japan

Dr. Jun Kobayashi
Graduate School of Sciences and Technology for Innovation
Faculty of Agriculture
Yamaguchi University

9. What is the market potential of the technology/project in both the near term and long term?

In the near term, the technology has the potential to reduce crop losses and increase productivity in the sericulture industry, while in the long term, it can establish India as a leader in high-quality, sustainable silk production, expanding global market share and driving innovation in agricultural biotechnology.

Genetic Characterization of Tropical Tasar Silkworm, Antheraea mylitta through Single Nucleotide Polymorphism Based Molecular Barcode

Name of the Institution

CSB-Central Tasar Research and Training Institute
Central Tasar Research and Training Institute, Piska Nagri, Ranchi-835303, Jharkhand, India

1. Brief Description of the Technology / Project

This project focuses on the genetic characterization of various ecoraces of Antheraea mylitta, including Raily, Barf, Korbi, and Bhopalpatnam from Chhattisgarh; Modal, Nalia, and Jata from Odisha; Sarihan, Modia, Munga, Laria, Wild Daba, and Semidomesticated Daba from Jharkhand; as well as Bhandara from Maharashtra, Mandla from Madhya Pradesh, Andhra Local from Telangana, and Jiribam from the Manipur-Assam border, alongside a new ecorace, Gajapati, also from Odisha. To preserve genetic diversity in the face of climate change, accurate ecorace identification is essential. This involves characterization of A. mylitta ecoraces using single nucleotide polymorphisms (SNPs) for molecular barcoding. Selected SNPs exhibiting interspecific variation were used to design Kompetitive Allele Specific PCR (KASP) primers, enabling precise identification of multiple ecoraces including Wild Daba, Raily, Modal, Barf, and Sarihan. The project employs ddRAD-seq analysis for SNP mapping, visualized through Integrative Genomics Viewer (IGV) to design effective KASP primers. Real-time PCR assays will be performed for genotyping based on fluorescent signals from KASP probes. This comprehensive approach aims to enhance the accuracy of ecorace identification across diverse populations in India.

2. Problem solved / addressed

Traditional methods of distinguishing A. mylitta ecoraces rely on morphological and biological traits, which can be inconsistent due to environmental influences. This project aims to provide a more reliable genetic framework for assessing diversity among ecoraces using SNPs, which are superior markers for population structure analysis compared to previous molecular techniques (e.g., RAPD, SSR). Initial phases identified 61,146 SNPs across 18 ecoraces, with 20 markers converted to KASP for five ecoraces. By expanding SNP screening and validation, the project seeks to establish a robust SNP-based DNA barcode for precise identification, facilitating effective conservation strategies and enhancing breeding programs for tasar production.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The project involves the SNP-based genetic characterization of A. mylitta ecoraces. This characterization has been completed, and selected SNPs are currently being optimized for the development of a SNP-based barcoding system for the identification of these ecoraces.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

Currently, the project is in the development stage and has not yet been commercialized. Once validated, the KASP-based SNP barcoding system aims for domestic implementation, particularly within India's silkworm breeding and conservation sectors, extending to other types of silkworms. Given the importance of silk in both traditional and modern textile industries, there is potential for broader global application. As the technology matures, partnerships with international silk production entities may facilitate global adoption, enhancing genetic resource management and boosting productivity in various countries engaged in sericulture.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

The development of KASP assays for 45 SNPs encountered challenges, with only 20 successfully converted. Issues arose from duplicate loci, suboptimal primer design near SNPs, and PCR condition optimization. Addressing these technical hurdles will be crucial for the successful development of assays that can effectively distinguish A. mylitta ecoraces.

6. Suggestions on policy / regulatory interventions for the technology being described

To effectively implement SNP-based molecular barcoding for A. mylitta, it is crucial to promote targeted funding for research on genetic tools in sericulture. Establishing robust regulatory frameworks that encourage the use of molecular markers in biodiversity conservation and breeding programs will elevate industry standards. Collaborations with agricultural departments and sericulture organizations can facilitate the development of comprehensive guidelines for the application of these genetic tools, ensuring sustainable practices and safeguarding genetic resources. Additionally, the creation of training programs for researchers and industry stakeholders in molecular genetics will bolster local expertise, fostering more effective adoption and implementation of advanced biotechnological methods in the field. These efforts will collectively enhance the productivity and sustainability of the sericulture sector.

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

The KASP-based SNP barcoding system is expected to revolutionize the identification and conservation of A. mylitta ecoraces, thereby impacting the sericulture industry significantly. This technology offers a molecular tool that aids in establishing efficient in-situ conservation strategies, reducing genetic erosion due to inter-crossing among ecoraces. Developed SNP based DNA barcode would be used as genomic signature for the identification of various A. mylitta ecoraces. Moreover, it will enhance marker-assisted selection (MAS) in breeding programs, potentially increasing tasar silk production and quality. The outcomes can contribute to sustainable livelihoods for silk farmers and boost the national economy, while also aligning with global biodiversity conservation efforts.

8. National or international collaborations associated with this technology or project?

The project has engaged with seven states specializing in Tasar sericulture and germplasm. Collaboration with the University of Hyderabad in India identified SNPs that can be utilized for the development of a KASP-based DNA barcoding system. International collaborations may also be explored with sericulture-focused organizations and universities globally to share knowledge and best practices in genetic characterization, enhancing the project's scope and potential impact on global silk production.

9. What is the market potential of the technology/project in both the near term and long term?

In the near term, the KASP-based SNP barcoding system offers significant market potential within India's silk industry, allowing for improved identification and breeding of A. mylitta ecoraces. This can enhance production efficiency and quality, meeting the rising demand for tasar silk. Long term, as the technology matures, it could extend to international markets, enabling countries engaged in sericulture to adopt similar genetic identification strategies.

Funding Agency: Department of Biotechnology, New Delhi

Transcriptome dynamics of Antheraea mylitta pertaining to heat stress response

Name of the Institution

CSB-Central Tasar Research and Training Institute
Central Tasar Research and Training Institute, Piska Nagri, Ranchi-835303, Jharkhand, India

1. Brief Description of the Technology / Project

This project represents the first comprehensive transcriptome sequencing of Antheraea mylitta, the tropical tasar silkworm, which is vital to India's silk industry. With climate change inducing heat stress, the project aimed to understand the molecular mechanisms behind the species' thermotolerance. A total of 80.8 gigabytes of data from 225.92 million raw reads were generated, leading to the identification of 1,349 differentially expressed genes (DEGs). Of these, 329 genes were up-regulated and 1,020 were down-regulated, with significant roles in heat shock proteins (HSPs) and chaperones, which are crucial for heat stress response. These insights offer valuable genetic targets for future interventions, such as gene editing, aimed at enhancing the species' resilience to thermal stress. By strengthening thermotolerance, the project could significantly improve the productivity and sustainability of tasar silk production.

2. Problem solved / addressed

The project addresses the significant impact of climate-induced heat stress on A. mylitta, which is responsible for the reduction in moth emergence, fecundity, and hatching success, thus negatively affecting silk production. Traditional breeding methods are insufficient to counteract these challenges in a rapidly changing climate. This project provides critical genetic insights into how A. mylitta responds to thermal stress, identifying key differentially expressed genes (DEGs) involved in thermotolerance, especially heat shock proteins (HSPs) and chaperones. These molecular findings offer new pathways for developing climate-resilient silkworm strains through gene editing, ensuring the sustainable production of tasar silk in the face of environmental stressors.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The project is in the development stage. Transcriptome sequencing has been completed, and key differentially expressed genes (DEGs) associated with heat stress have been identified. The next phase involves exploring gene-editing strategies targeting these DEGs to improve the thermotolerance of *A. mylitta*.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

Upon successful commercialization, this genetic technology will be implemented domestically within India's tasar silk industry, benefiting regions where A. mylitta is cultivated. The

enhancement of heat tolerance in these silkworms will stabilize and potentially increase silk production. As climate-induced heat stress affects silk production worldwide, this technology has potential for global application, particularly in countries that rely on sericulture. In the long term, the project could open doors for international collaboration and the adoption of similar strategies in other regions affected by climate change, providing a sustainable solution to global sericulture challenges.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

The primary challenges encountered during development are regulatory in nature, particularly surrounding the use of gene-editing techniques on A. mylitta. Regulatory bodies may require rigorous assessment of the environmental and ecological impacts of genetically modifying the species. Additionally, there are technical hurdles associated with optimizing the identified DEGs for effective gene editing, which must be addressed before the technology can be implemented on a commercial scale.

6. Suggestions on policy / regulatory interventions for the technology being described

To ensure the successful implementation of this technology, policy frameworks must encourage research and development in genetic tools for sericulture. Regulatory bodies should establish clear guidelines for the use of gene-editing technologies in agricultural species like A. mylitta, ensuring environmental safety and ethical considerations are prioritized. Targeted funding for molecular genetics research, especially for species crucial to local economies, would greatly enhance the pace of innovation. Additionally, there should be a collaborative effort between research institutions, government bodies, and sericulture industries to establish guidelines for field testing and commercialization, ensuring that any modified strains maintain ecological balance and improve industry sustainability.

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

This project will have profound implications for India's tasar silk industry, offering a solution to the challenges posed by climate-induced heat stress. By enhancing the thermotolerance of A. mylitta, silk production can be stabilized, securing the livelihoods of thousands of rural farmers dependent on sericulture. The genetic insights from this project will also strengthen conservation efforts by protecting the genetic integrity of the species. Economically, the project is expected to boost silk production, thereby increasing India's global competitiveness in the silk market. On a societal level, it will contribute to rural economic development and promote the sustainable use of biological resources in the face of climate change.

8. National or international collaborations associated with this technology or project?

Potential international collaborations with biotechnology firms and genomic research centres are being explored, particularly in the application of gene-editing technologies. International partnerships could help scale the findings globally, especially in regions facing similar environmental challenges in silk production.

9. What is the market potential of the technology/project in both the near term and long term?

In the near term, this technology has significant market potential in India, where the tasar silk industry is directly threatened by climate change. By enhancing the thermotolerance of A. mylitta, this project could lead to more consistent silk yields and improved silk quality, benefiting local economies and increasing productivity. In the long term, the potential for global expansion is considerable. As other sericulture-producing countries face similar climate challenges, this technology can be adapted to their unique environments. Furthermore, the genetic tools developed here could be extended to other agricultural sectors, offering wide-reaching applications in enhancing climate resilience across multiple species.

Funding Agency: Central Silk Board, Bengaluru

Whole Genome Sequencing of the Tropical Tasar Silkworm (*Antheraea mylitta*)

Name of the Institution

CSB-Central Tasar Research and Training Institute
Central Tasar Research and Training Institute, Piska Nagri, Ranchi-835303, Jharkhand, India

1. Brief Description of the Technology / Project

The whole genome sequencing of Antheraea mylitta, the tropical tasar silkworm, has been completed to identify the genetic basis for productive traits, such as high silk yield and fecundity. The comprehensive genomic data enables researchers to pinpoint specific genes responsible for these traits, opening up opportunities for future genetic interventions. This project lays the foundation for improving silk yield and enhancing reproductive capabilities in tasar silkworm populations. By leveraging gene induction and editing techniques, the identified genes can be manipulated to achieve targeted breeding programs or direct genomic improvements, ultimately leading to more productive silkworm populations for the silk industry.

2. Problem solved / addressed

The project addresses key challenges in the silk industry, particularly focusing on improving the productivity of the tropical tasar silkworm. Silk yield and fecundity are critical traits for the economic viability of silk production. Traditional breeding methods have limited effectiveness in enhancing these traits due to the complexity of their genetic makeup. By sequencing the entire genome of A. mylitta, this project provides precise genetic information that enables the identification and potential manipulation of genes related to these traits. The solution facilitates advancements in breeding, gene editing, and induction, offering a direct path to increased silk yield and reproductive success.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Development Stage: The whole genome sequencing of A. mylitta has been completed, and productive genes have been identified. However, the application of gene induction and editing for trait improvement is a future goal.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

If commercialized, the implementation of genome-based improvements for the tropical tasar silkworm would initially focus on domestic silk production in India, where A. mylitta is a key species for the tasar silk industry. The potential benefits, such as enhanced silk yield and fecundity, would lead to increased production efficiency and economic gains for local silk producers. Over time, these advancements could have global implications for the silk industry,

particularly in countries involved in silk production. The use of gene editing and induction to improve silk traits could also attract international collaborations, further broadening its impact on the global market.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

The project is likely to encounter regulatory challenges related to the use of genetic modification techniques, such as gene editing. Regulatory bodies may require thorough evaluations of the environmental and ethical implications of manipulating the genome of A. mylitta. Additionally, public perception of genetically modified organisms (GMOs) could present challenges in adopting these technologies on a commercial scale. Collaboration with regulatory authorities and addressing biosafety concerns would be essential to the successful implementation of gene-editing interventions.

6. Suggestions on policy / regulatory interventions for the technology being described

To facilitate the commercialization of genomics-based interventions in A. mylitta, regulatory policies should support responsible genetic research while ensuring biosafety. It is essential to establish clear guidelines for the use of gene-editing technologies in non-model organisms like silkworms. Policies should encourage innovation in agricultural biotechnology while addressing potential risks, including ecological impacts and ethical concerns. Collaboration between research institutions, industry stakeholders, and regulatory bodies is crucial for developing frameworks that balance scientific advancement with public safety. Special considerations may also be required to safeguard the indigenous knowledge and biodiversity associated with A. mylitta.

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

The whole genome sequencing of A. mylitta has the potential to revolutionize the tasar silk industry by directly influencing silk yield and fecundity, key factors in production. Economically, this could lead to significant growth for silk producers, particularly in India, where A. mylitta is a major source of natural silk. The national silk industry could benefit from increased output and improved quality, potentially enhancing its global competitiveness. Societally, the enhanced productivity would boost the livelihoods of silk farmers and contribute to rural economic development. Environmentally, gene-based interventions may reduce the need for extensive silkworm farming, thereby minimizing habitat disruption.

9. National or international collaborations associated with this technology or project?

The project involves national collaborations with the research institute National Institute of Animal Biotechnology, Hyderabad, for the intense analysis of Whole Genome Sequenced Data. International collaborations could arise with institutions specializing in genomics research and gene-editing technologies. Collaboration with international biotech companies or academic institutions would bring additional expertise and resources to the project, accelerating the development of gene-editing interventions for A. mylitta. This could also help to establish

India as a leader in silkworm genomics research, fostering future partnerships for broader applications in sericulture and other agricultural sectors.

10. What is the market potential of the technology/project in both the near term and long term?

In the near term, the market potential of this project lies in its ability to enhance silk yield and fecundity in A. mylitta, resulting in more efficient and cost-effective silk production. This would primarily benefit the domestic silk industry, particularly in regions where tasar silk is produced. In the long term, gene editing and induction technologies developed from this genomic information could have a broader global impact, improving silk production in other countries and potentially expanding to other sericulture species. The innovations could also lead to the development of new silk-based products or materials, opening up new market opportunities beyond traditional textiles.

Funding Agency: Department of Biotechnology, New Delhi

Integrating genomic and transcriptomics resources for functional insight into the biology of muga silkmoth Antheraea assamensis

Name of the Institution

CSB-Central Muga Eri Research and Training Institute
Central Silk Board, Ministry of Textiles, Lahdoigarh, Jorhat – 785700, Assam, India

1. Brief Description of the Technology / Project

The whole genome sequence and several transcriptomics sequence data of muga silkworm Antheraea assamensis is available as a part of the muga genome sequencing project. However, the detailed analysis must be performed to identify genes linked to silk traits and immune response so that such information can be used for screening muga populations with better immunity, and high silk yield and survival. The sequence data may be put to use for addressing some of the long-standing questions in muga culture such as disease tolerance, hibernation, yield quality improvement, etc. The genetic markers developed in this study may be employed in developing better breeds in muga. Gene information can be used in generating the gene disruptions in muga to develop better muga silkworm lines.

2. Problem solved / addressed

The genome of Antheraea assamensisis assembled and annotated. A database "Vanya Silkbase" containing genomes, transcriptomes and Gene expression in different tissues of the wild silkworms is developed which provides a centralized database and tools for scientists to access and analyse genetic information.Approximately 500,000 single nucleotide polymorphisms (SNPs), have been identified in both the wild type and cultivated varieties of the muga silkworm. These SNPs are important for understanding genetic diversity and can be used in breeding programs and genetic studies.A gene in the muga silkworm genome has been found that is homologous to a gene known to be involved in pupal hibernation in other species which could provide insights into the genetic mechanisms controlling hibernation in silkworms.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The project has been completed but the utilization of the data generated is still ongoing.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

'Vanya Silkbase' has been made available for access by the researchers working on silkmoths at global level.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

No regulatory challenges were faced by us during execution of the project.

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

The genome analysis revealed interesting information regarding the muga silkworm. Such information will be helpful in breeding program and also in studying the basic biology of not only muga but also other economically important wild silkmoths. The identified SNPs can be utilized in marker assisted selection. The 'Vanya Silkbase' has genomic and transcriptomic information of five wild silkmoths species, which can be utilized by researchers working on wild silkmoth breeding. For example, the work on identification of gene(s) linked to pupal hibernation would help in addressing the climate change issues in rearing of muga silkworms during unfavourable weather conditions, thereby leading efficient utilization of host plants and reducing the crop loss.

8. National or international collaborations associated with this technology or project?

The project was a joint effort between two institutes under the Central Silk Board: CMER&TI at Lahdoigarh and SBRL at Bangalore.

9. What is the market potential of the technology/project in both the near term and long term?

The data generated will help improve silk production in Northeastern part of India. Further research is required to apply the generated data to develop better breeds in muga silkworm.

Development and Evaluation of Bidensovirus resistant silkworm hybrids developed from marker assisted breeding lines -Phase II

Name of the Institution

CSB-Seri Biotech Research Laboratory
Seri Biotech Research Laboratory, Central Silk Board, Ministry of Textiles, Govt of India.
Carmelram post Kodathi Bangalore-560035, Karnataka, India

1. Brief Description of the Technology / Project

The Bombyx mori bidensovirus (BmBDV)/ Bombyx mori Densonucleosis virus-2 (BmDNV-2)/ BmBDV is one of the causative agents of Flacherie disease in silkworm Bombyx mori causing huge economic loss. A major gene, nsd-2 (non-susceptibility to densovirus-2), a putative BmBDV receptor involved in resistance under recessive mutation condition has previously been identified. The natural deletion occurring in the nsd-2 gene disrupting gene function has contributed to the evolution of BmDNV-2 resistant silkworm breeds.

The nsd-2 gene contains 14 exons and by comparing this locus in resistant and susceptible strains it was found that deletion of a 6kb region from exon 5-13 in resistant strain. The differences in nucleotide variation in nsd-2 gene in resistant and susceptible silkworm breeds can be exploited as a molecular marker for BmDNV-2 resistance silkworm breeding In this direction, the nsd-2 was used as a marker for screening silkworm breeds and identified breeds carrying resistance version of nsd-2 gene.

2. Problem solved / addressed

1. Developed FC1 and FC2 resistant to BmBDV (Viral Falcherie) infection. The on-station trials of the Double hybrids (FC1 X FC2) showed minimum of 3% and maximum of 12 % increase in the survivability as well as yield/100DFLs compared to control.
2. Out of 20 productive bivoltine breeds of CSRTI, Berhampore, 10 breeds were found to have nsd-2 resistant alleles in heterozygous condition, SK6, SK7, BHP8, BHP9 homozygous lines for BmBDV resistance were identified and maintained at CSRTI, Berhampore. A single hybrid SK6XSK7 resistant to BmBDV showed >90% survival in the bioassay experiments.
3. The Homozygous lines of the developed breeds showed > 90% survival during the bioassay experiments under laboratory conditions.
4. A modified multiplex PCR was developed for the identification of major pathogens in Bombyx mori

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The project output ie., BmBDV resistant FC1xFC2 (double hybrid) is under evaluation i.e., on Farm Trial in the farmers field in Southern India and SK6XSK7 (Single hybrid) are under evaluation under REC/RSRS stations in West Bengal regions.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

The project output i.e., BmBDV resistant FC1xFC2 (double hybrid) is under evaluation ie., on Farm Trial in the farmers field in Southern India and SK6XSK7 (Single hybrid) are under evaluation under REC/RSRS stations in West Bengal regions

5. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

1. Developed FC1 and FC2 resistant to BmBDV (Viral Flacherie) infection. The on-station trials of the Double hybrids (FC1 X FC2) showed minimum of 3% and maximum of 12 % increase in the survivability as well as yield/100DFLs compared to control.
2. Out of 20 productive bivoltine breeds of CSRTI, Berhampore, 10 breeds were found to have nsd-2 resistant alleles in heterozygous condition, SK6, SK7, BHP8, BHP9 homozygous lines for BmBDV resistance were identified and maintained at CSRTI, Berhampore.
3. A single hybrid SK6XSK7 resistant to BmBDV showed >90% survival in the bioassay experiments. The present on station trials showed 5-10% increase in survivability of resistant single hybrid and >10% increase in yield/100DFLs compared to control.
4. The Homozygous lines of the developed breeds showed > 90% survival during the bioassay experiments under laboratory conditions.

6. National or international collaborations associated with this technology or project? If any, please share brief details:

The project is in collaboration with:

1. Central Sericultural Research and Training Institute, Mysore (CSB-CSRTI, Mysore)
2. Central Sericultural Research and Training Institute, Berhampore (CSB-CSRTI, Berhampore)

7. What is the market potential of the technology/project in both the near term and long term?

1. The developed BmBDV resistant hybrids (FC1xFC2, Double hybrid) has shown 3-12% increase in survivability against the control during autumn seasons when the flacherie incidences are high in southern regions contributing to 3-10% substantial increase in yield/100DFLs.
2. The performance of the BmBDV Single hybrid (SK6XSK7) in under evaluation at REC/RSRS stations of CSRTI, Berhampore, &the present data has shown 5-10% increase in survivability of resistant single hybrid and >10% increase in yield/100DFLs compared to control.

The overall performance of the developed hybrids has the potential to increase the farmers cocoon crop yield/profit by 5-10%. The major advantage for the farmers is that the improved hybrids quality and quantity parameters are at par with the existing hybrids & improved crop stability to maintain cocoon productivity at commercial rearing. The improved hybrids showed higher survivability (88.52%) and higher yield/100DFLs than existing hybrids particularly during monsoon and autumn seasons.

Identification of Mildew resistance Locus O (MLO) genes involved in powdery mildew disease susceptibilityin mulberry

Name of the Institution

CSB-Central Muga Eri Research and Training Institute
Central Silk Board, Ministry of Textiles, Lahdoigarh, Jorhat – 785700, Assam, India

1. Brief Description of the Technology / Project

To precisely identify specific Mildew resistance Locus O (MLO) genes involved in powdery mildew disease, the morus genome was scanned against MLO domain and reciprocal BLASTP search was performedwith one to one orthology of M. notabilis and Arabidopsis MLOs. Genome wide analysis identified 16 MLO genes in Morus spp. The deduced amino acid sequence of MLO proteinswere analysed by different prediction tools to identify transmembrane domains, protein localization and conserved protein motifsand Phylogenetic analysis. Coupled with different bioinformatics analysis and gene expression studies identified MLO2 and MLO6A as potential candidate genes involved in powdery mildew susceptibility in mulberry. Further, alternative splice variants of intron retention and exon skipping resulted in premature stop codon leading to the production of truncated MLO2 protein detected in powdery mildew tolerant mulberry accessions. The identified MLOs and alternative splice variants may be useful for mulberry breeding programs to develop powdery mildew resistant varieties

2. Problem solved / addressed

Powdery mildew disease is one of the major foliar diseases affecting mulberry, which is a sole food source for the production of silk from silkworm. Imparting genetic resistance to mulberry is the most desirable approach to manage diseases. Natural mutants/knockdown of Mildew resistance Locus O (MLO) genes have been utilized as a source of genetic resistance for development of powdery mildew resistant varieties in other agriculture crops. To utilize MLO genes in mulberry, information on these genes was lacking. In this project, we identified specific MLO genes involved in powdery mildew susceptibility using genome wide scanning together with various bioinformatics, gene expression and analysis of alternative splice variants.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented):

Developmental stage

4. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

This project identified MLO2 and MLO6A as candidate genes involved in powdery mildew susceptibility in mulberry. Further detected alternative splicing of MLO genes resulting in truncated proteins in powdery mildew tolerant germplasm of ME-0260, ME-0267, ME-0125 and

MI-0028. The identified MLO genes and alternative splice variants of accessions will be useful for mulberry breeding programs to develop powdery mildew resistant varieties. The outcome of this project will aid in imparting genetic resistance mechanism for powdery mildew in mulberry, as this approach is more desirable than chemical method of managing the disease for silkworm feed.

5. National or international collaborations associated with this technology or project?

CSB-Central Sericultural Research and Training Institute, Berhampore (CSB-CSR&TI, Berhampore)

6. What is the market potential of the technology/project in both the near term and long term?

The outcome of this project identified MLO2 and MLO6A as candidate genes involved in powdery mildew susceptibility in mulberry and alternative splicing of MLO genes associated with tolerant accessions. The MLO genes/accessions with alternative splice variants will be useful for mulberry breeding programs to develop powdery mildew resistant varieties.

Development of Lateral Flow Assay Kit for Diagnosis of Pebrine Disease in Silkworms.

Name of the Institution

CSB-Central Muga Eri Research and Training Institute
Central Silk Board, Ministry of Textiles, Lahdoigarh, Jorhat – 785700, Assam, India

1. Brief Description of the Technology / Project

The current invention relates to immuno diagnosis of Nosema infection in silkworms by utilizing lateral flow assay technology. Nosema (a genus of microsporidia) causes Pebrine disease in silkworms which has both horizontal and vertical mode of transmission. In the current study, we have cloned and expressed the Spore wall proteins (genes amplified from the Nosema assamensis) in heterologous bacterial expression system. The purified proteins were used to immunise rabbits to raise polyclonal antibodies against SWP1. The titres of which were determined later through ELISA. Further monoclonal antibodies were raised by employing hybridoma technology whose titres were also confirmed through ELISA. The sample kits were assembled and the confirmed positive samples (through microscopy and PCR) for Pebrine and the healthy samples were tested for its performance using the kit. The Kit has high potential to serve as “point of care (POC)” testing and will help in detection of the disease, thus helping in controlling the spread of the disease.

2. Problem solved / addressed

Mother moth examination by light microscopy is the only diagnosing method to detect Nosema infection followed across sericulture seed centres. However, this is cumbersome, highly error prone and often does not pick in case of mild infection. However, conventional microscopy will detect only mature spores and could not get any information on vegetative stages of the pathogen. Further, the specificity and sensitivity of the microscopy is substandard and prone to false positive results. In the recent, the development of molecular techniques for disease diagnosis has revolutionized the field of sericulture. Genomic DNA and RNA-based molecular techniques allow for the accurate detection of disease-causing pathogens in silkworms. But these techniques involve complex methodological procedures, time consuming and warrants expert manpower along with most expensive infrastructure felicities/equipment. Hence, it is proposed to develop a simple diagnostic test, which is accomplished through the use of transportable, portable, point of care diagnostic kit, known as lateral flow assay for the detection of Nosema sp. infecting the silkworms of India

3. Stage of the Technology / Project (Development stage / already commercialized and implemented):

Developmental stage

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

The lateral flow assay kit for detecting pebrine disease offers significant market potential, particularly in sericulture seed production centres located in our country.

5. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

The developed technology will be disseminated amongst the farmers and stakeholders involved in the mulberry and vanya sectors to increase silk production and, in turn, improve the socio-economic status of seri-farmers. The study has high potential in terms of commercialization since, sericulture being the primary employment for ~10 million farmers in India, the developed kit will not only be utilized by farmers but also suitable for seed production centers and CRCs. There is an ample opportunity to develop related diagnostic kits associated with other diseases in future where this study will provide the basic framework for generating efficient diagnostic kits.

6. National or international collaborations associated with this technology or project?

Yes. The project was a national collaboration between CSB-Seri-biotech Research Lab, Bhat Bio-Tech India (P) Ltd., (located in Veerasandra Industrial Area, Electronic City Phase II, Bengaluru-560100) and the Central Tasar Research and Training Institute, situated in Piska Nagri, Ranchi-835303, Jharkhand. It was funded by the DBT-Biotechnology Industry Research Assistance Council (BIRAC) with Proposal Reference No.: BT/AIR01106/PACE-20/20.

7. What is the market potential of the technology/project in both the near term and long term?

The lateral flow assay kit for detecting pebrine disease offers significant market potential, particularly in sericulture seed production centers. In the near term, this technology addresses an urgent need for early and accurate detection of pebrine disease, reducing economic losses and improving seed quality. As awareness grows, adoption across Indian sericulture units is expected to increase rapidly. In the long term, the technology could expand globally, particularly in countries with large-scale silk production, like China and Thailand. Its ease of use, cost-effectiveness, and ability to safeguard against widespread pebrine infection make it essential for sustainable sericulture growth

Figure 1. The developed LFA technology for detection of pebrine disease in silkworms

Whole Genome Sequencing of MTB Clinical Strains for Determining Drug Resistance and Strain lineage in India: A structured Nationwide approach

Name of the Institution

Department of Biotechnology
BRIC-National Institute of Immunology, Aruna Asaf Ali Marg, New Delhi, 110067

1. Brief Description of the Technology / Project

This project aims to create a comprehensive map of the genomic variation among Mycobacterium tuberculosis (Mtb) clinical isolates within India. The project envisages the sequencing of 32200 whole genomes of Mtb isolates from patients. The whole genome sequence data will be fully annotated, and mutations will be correlated with the anonymized clinical data of the patients. AI/ML-based tools will be developed to predict novel antimicrobial resistance (AMR) mutations. These data will be supplemented with high-depth transcriptomics data for a subset of samples, where the AMR prediction and the phenotypic drug sensitivity tests (DST)/treatment outcomes do not match. The entire data, along with newly developed tools will be made available on a web portal. Apart from this web portal and data a repository containing all the sequenced strains will be developed. The isolates' data will be available on the portal, and the isolates will be available from the repository. (http://intgs.nii.ac.in/InTGS/index.php)

2. Problem solved / addressed

Tuberculosis claims most mortality as an infectious disease, and the rate of emergence of multi-drug resistant and extreme drug-resistant strains has made it a global priority to make novel drugs and treatment strategies for tuberculosis. Continuous genome surveillance of Mtb is essential to identify the emergence of novel AMR mutations. Moreover, most of the R&D efforts to target Mtb rely on a handful of well-characterized reference strains such as H37Rv. However, these strains do not represent the diversity among the clinical isolates, hampering the development of effective therapy and diagnostic tools. This project aims to address these problems by continuously monitoring the genomes of Mtb isolates from all over India and also by creating novel tools for the prediction of novel AMR mutations. Availability of these isolates from the repository along with the whole genome sequence, clinical and phenotypic DST data, and high-depth RNAseq data is expected to solve these problems.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The sample collection at different sites from across India has started and is progressing. The development of the web portal and bio-repository is also ongoing.

4. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

In the short term, the project will enable us to understand the distribution and emergence of AMR mutations within the clinical isolates from India. In the long term, the genome data with the analysis tools will enable researchers from academia and industry to develop novel diagnostic tools for the detection of AMR in Mtb. The availability of well-characterized clinical isolates will be of use for researchers to test drugs and diagnostic tools.

5. National or international collaborations associated with this technology or project?

This project is a national collaboration between 10 institutes/hospitals. National Institute of Immunology (coordinating institute), JIPMER Puducherry (Clinical coordination), Hinduja Hospital Mumbai, BJGMC Pune, BMMRC Hyderabad, PGI Chandigarh, CCMB Hyderabad, NIBMG Kalyani, ICGEB New Delhi and ICMR- NIRT, Chennai.

6. Relevance of the project in terms of the market potential

The direct short-term market potential for the project is limited. Rather, it is expected to enhance the R&D activity aiming at development of novel therapeutics and diagnostic tools for tuberculosis.

Oral Cancer gene panel for cancer detection

Name of the Institution

BRIC-National Institute of Biomedical Genomics, Kalyani, West Bengal

1. Brief Description of the Technology / Project

A mutational signature in a set of genes that are markers of frank oral cancers has been identified.

2. Problem solved / addressed

Oral cancer is the topmost cancer among men in India. Detection of frank oral cancer is difficult. The gene panel would help in detection of oral cancers with molecular profiling at very early stages of disease thereby facilitating early detection and improved prognosis.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The technology is at development stage.

4. Challenge

Finding an industry partner for development of panels has been a challenge.

5. Suggestions on policy interventions

Development of capacities for production of interventions like gene panels as well as manufacturing of sequencing platforms and reagents and consumables in India can greatly reduce the cost of the interventions and technologies.

6. Anticipated project impact

The gene panel for oral cancer can result in early detection which can lead to improved prognosis.

7. National collaborations

Include national clinical partners like ACTREC, Mumbai, Dr. R. Ahmed Dental College and Hospital, Kolkata and TMC, Kolkata.

8. Market potential

The project has the potential to be used on samples collected in oral screening camps and clinics, and if used in conjunction with non-invasive methods of sample collection such as cytobrush and appropriate clinical interventions, will result in early detection of oral cancer, which will translate to improved prognosis and survival of patients.

Genomic surveillance for SARS-CoV-2 in India-Indian SARS-CoV-2 Genomic Consortium

Name of the Institution

Department of Biotechnology, Lodhi Road, New Delhi -110003

1. Brief Description of the Technology / Project

Indian SARS-Cov-2 Genomics Consortium (INSACOG) established in December 2020 has been conducting a national surveillance of SARS-CoV-2 genomic variants using next generation sequencing technologies to detect virus mutations and/or lineages that may pose a threat to public health. This country-wide genomic surveillance program has enabled rapid public health interventions to control the spread of SARS-CoV-2 virus. INSACOG facilitated the formation of a Pan India network of 67 laboratories to undertake genomic surveillance, thereby increasing the overall SARS- CoV-2 genome sequencing capacity in the country. This has resulted in the sequencing of SARS-Cov-2 virus samples across the country during the pandemic, along with centralised analysis pipelines for sequence and metadata at IBDC as well as real time reporting of VOCs in Integrated Health Information Platform (IHIP).

2. Problem solved / addressed

INSACOG has accelerated the translation of genomic data into clinical and public health research and interventions. By allowing a comprehensive and accurate detection of COVID-19 lineages from clinical and sewage surveillance samples using the genomic technologies and epidemiologic and bioinformatic tools, has resulted in:

a) Expansion of our knowledge of SARS-CoV-2 virus at the molecular and clinical level

b) Allowed tracking viral evolution by faster characterization of emerging lineages and assist with the surveillance of those evolved viruses

c) Accelerated the establishment and development of NGS technology in the country for future use in diagnostic assays and tracking transmission dynamics of COVID-19 and other viruses

3. Suggestions on policy interventions

Genomic surveillance of pathogens based on geo-temporal sampling as well as implementation of gene panel based screening of diseases can be greatly facilitated by involvement of multiple government agencies in DBT, health and family welfare, state health and civic administration as well as the industry for facilitating sample collection, correlation of sequencing data with epidemiologic information and development of innovative methods (both experimental and analytical) for improved efficiency and reduction of cost. Further, development of capacities for production of interventions like gene panels as well as manufacturing of sequencing platforms

and reagents and consumables in India can greatly reduce the cost of the interventions and technologies.

4. Project impact

Sustained efforts of the sentinel sites and sequencing labs led to rapid identification of viral variants emerging in the country during the course of the pandemic. These viral variants have been detected and tracked for any associated increase in transmission and disease severity, at the national as well as at the state level, during the outbreak.

5. National collaborations

INSACOG initially started with 10 laboratories across India, but it has since expanded. As of the latest updates, INSACOG comprises 67 laboratories spread across the country. These labs include a mix of national research institutes, regional labs, and specialized facilities that work together to conduct genomic sequencing of SARS-CoV-2 samples. These labs are coordinated by a central team, and their collective efforts allow for extensive surveillance of the virus, ensuring that new variants are quickly identified and monitored.

6. Potential of the project

Genomic surveillance of pathogens is going to be the need of the hour for prevention of large outbreaks of infections by various pathogens as the global focus now shifts from outbreak management to prevention. This approach is already being used successfully in some countries as early warning system for pathogen surveillance.

Mission Program on Pediatric Rare Genetic Disorders (Mission PRaGeD)

Name of the Institution

BRIC-Centre for DNA Fingerprinting and Diagnostics, Inner Ring Road, Uppal, Hyderabad, Telangana

1. Brief Description of the Technology / Project

Mission PRaGeD is a PAN-India initiative involving 16 centres across the country funded by the Department of Biotechnology (DBT), Government of India. Aim of the project is to develop an expanded program spanning diagnostics, research and counseling for "Pediatric rare genetic disorders". Patients with undiagnosed genetic diseases are recruited through telemedicine with a network of medical colleges (Pediatric Departments), DBT-UMMID centres, and collaborating centres across the country. Exome/genome based analysis of patients and/or parent-offspring trios is being performed using in-house bioinformatics pipelines. Novel variants identified from the genome analysis will be characterised for their functional roles using cell lines or model organisms such as mice, drosophila or zebrafish. Awareness programs are being conducted in the form of workshops, community awareness programs, visit to primary health centres, colleges, schools etc.

2. Problem solved / addressed

Rare diseases are progressive, chronically debilitating and/or life-threatening clinical conditions that have not received adequate attention in terms of diagnosis, research and treatment. The biggest challenge faced by the clinicians is error prone diagnosis often occurring due to limited testing procedures, limited knowledge on the pathophysiology of the disease condition and availability of affordable treatments. The yield of genetic testing is low using the conventional methods when compared to NGS based exome or genome sequencing which proves to be a powerful tool to identify variants in monogenic disorders. The technical facilities for functional studies in India are limited and there is an urgent need to connect these facilities and establish links of collaborating centres with these centralized facilities where the functional studies for novel sequence variations and novel genes can be carried out.

3. Project status

Project is in developmental stage. The project is designed for better understanding of genetics of rare diseases. There is no commercialisation potential at present however knowledge generated through work done under this project may lead to obtaining leads for commercialisation.

4. Suggestions on policy interventions

There is a need for development and implementation of guidelines for effective utilisation of next generation sequencing technologies in genetic diagnostics.

5. Anticipated project outcomes

Mission PRaGeDrecruits patients with rare genetic diseases from collaborating centres. Massive parallel sequencing followed by big data analysis leads to the establishment of the phenotype-genotype correlation of rare diseases specific to the Indian population. Unique mutation profiles identified will aid Indian clinicians accurate diagnosis. Further, the genome/exome data will add to the national databases of big data storage and access which eventually will lead to population specific comparative analysis. Rare disease conditions unexplained using exome sequencing will be routed for long read sequencing to enhance the yield of diagnostic testing in patients with rare genetic diseases.

6. National collaborations

Mission PRaGeD operates across the country by the joint effort of clinicians, scientists and patients. A total of 15 centres are collaborating in the project and actively recruiting patients with rare diseases for the study.

7. Market potential

There is no commercialisation potential at present however knowledge generated under this project may lead to identify technology for commercialisation.

Garbh-Ini (Inter disciplinary Group for Advanced Research on BirtH outcomes -DBT India Initiative)

Name of the Institution

Department of Biotechnology, Lodhi Road, New Delhi -110003

1. Brief Description of the Technology / Project

The Garbh-Ini program of the Department of Biotechnology, Govt. of India is a large-scale research initiative that aims to improve understanding of the biological and environmental factors that influence preterm birth and guide interventions using multi-omics biomarkers and AI-driven tools. The program also seeks to understand the impact of maternal, postnatal, and environmental factors on the growth and development of children born to the cohort participants. One of the thrust areas under the programme is to understand the genomic associations of preterm birth through GWAS studies.

2. Problem solved / addressed

Preterm birth is the leading cause of neonatal mortality in India, accounting for 25% of the global burden. It is associated with increased risk of adverse health and developmental outcomes. Most genomic studies on spontaneous preterm birth (sPTB) have been conducted on European and African American ancestral populations. This is the first study from South Asia on the genome-wide identification of maternal SNPs associated with sPTB. These SNPs are known to alter the expression of genes associated with major pathways in sPTB viz. inflammation, apoptosis, cervical ripening, telomere maintenance, selenocysteine biosynthesis, myometrial contraction, and innate immunity. Efforts are being made to establish the preterm birth predictive ability of these SNPs and to develop an SNP panel for screening of mothers at risk of delivering preterm which will help administer appropriate interventions.

3. Anticipated project outcomes

From public health perspective, it would be interesting to evaluate the ability of these genomic markers to predict sPTB. If they are found predictive either by themselves, or in combination with other clinical and biological predictors, they will add value to a risk stratification algorithm to be used in clinical settings. Such a tool will enable early triaging of at-risk women to appropriate level of antenatal medical care.

4. National or international collaborations associated with this technology or project? If any, please share brief details

This is a multi-institutional programme being implemented by 4 institutes, THSTI, NIBMG, RCB and CDSA in association with Gurugram Civil Hospital and Safdarjung Hospital.

5. What is the market potential of the technology/project in both the near term and long term?

There is no commercialisation potential at present however knowledge generated under this project may be useful in developing and validation of an SNP array, which is likely to have commercialization potential.

National Genomics Core (NGC)

Name of the Institution

BRIC-National Institute of Biomedical Genomics, Kalyani, West Bengal and BRIC-Centre for DNA Fingerprinting and Diagnostics, Inner Ring Road, Uppal, Hyderabad, Telangana

1. Brief Description of the Technology / Project

Genome science is playing an increasingly important role to generate knowledge required to increase production of crops, understanding and management of diseases, etc. The demand for generation of genomic data, both in quantity and diversity, is expected to continue to increase. Since the equipment for genomic data-generation is expensive and expertise for handing this equipment is limited, it is not possible for funding agencies to enable efficient data-generation capacity in multiple institutions in India. The National Genomics Core is a platform that has been formed to provide genomics services – genome-scale DNA and RNA sequencing, genome-wide microarrays, gene-panel assays, etc. – to individuals, institutions and the industry throughout the country. The Core is a facilitator of genomics-driven discovery and application, and to accelerate the ushering in of a vibrant bioeconomy in our nation. The core is distributed into two centres housed within the National Institute of Biomedical Genomics, Kalyani and Centre for DNA Fingerprinting & Diagnostics (CDFD), Hyderabad.

2. Problem solved / addressed

The national genomics core has helped to create a distributed, high-throughput genomics facility of international standards for stimulating transformative research and development of genomics applications for national economic growth, social and health benefits, and cultural enrichment of communities. In addition, it also functions as a distributed facility for skill development in genomics for utilization of high-throughput technologies and for storage, retrieval, computation and statistical analysis of big data. Experimental methods for new services have been established like genome sequencing of SARS-CoV-2, Exosome isolation and exosomal RNA sequencing, telomere length reduction assay, single cell RNA sequencing, meta-transcriptome sequencing, B-cell and T-cell repertoire sequencing, whole genome bisulfite sequencing, FFPE whole genome and whole exome sequencing, ATAC Sequencing, ITS sequencing etc.

3. Commercial status of the project

The project has been commercialized and implemented for providing genomics services to private and government agencies. The services have been provided at national level. Jointly the core has provided services to more than 200 clients and generated revenues of more than 15 crores. NGC websites are: http://ngc.cdfd.org.in/, https://www.nibmg.ac.in/p/sop-for-access-1.

4. Challenges

Institutions have faced challenges regarding high cost of consumables and instruments since the same need to be imported

5. Suggestions on policy interventions

There is a need for development of guidelines for effective implementation of the genomic technologies in clinical studies, crop and agriculture management etc.

6. Project impact

The DBT National Genomics Core has been established at CDFD and NIBMG as a high-throughput genomics facility of international standards for stimulating transformative research and development of genomics applications. It also functions as a distributed facility for skill development in genomics for utilization of high-throughput technologies and for storage, retrieval, computation and statistical analysis of big data. The high-end genomic services and training imparted by the core has resulted in a large number of publications and has enabled researchers from grassroot level institutes to get updated about these technologies. The core has provided services to more than 200 agencies including government research institutes and private sector companies. In addition, the core has trained more than 500 students/faculty in genomic technologies through workshops.

7. Market potential

The genomics market is projected to have rapid growth expansion with the estimated CAGR of 18.7%, to reach USD 24.2 billion by 2026 from USD 10.3 billion in 2020.Next generation sequencing market for clinical applications segment accounted for USD 2 billion in 2020 and Clinical research is expected to be the fastest-growing end-use segment from 2021 to 2028.

Human microbiome initiative on selects endogamous populations of India

Name of the Institution

BRIC-National Centre for Cell Science, Pune Maharashtra

1. Brief Description of the Technology / Project

India is steadily moving from genomics to multiomics research and Human Microbiome Initiative is one such project with a target of sampling more than 3400 individuals across the country from 11 endogamous and 6 tribal communities. Comprehensive data on diet, demography, host genotype, Ayurvedic Prakriti phenotypes and correlation with bacterial, fungal, archaeal and micro eukaryotic diversity have helped to identify community-specific microbial signatures. To date, microbiome profiling for 3878 individuals has been completed. Tribal communities untouched by modern lifestyle and westernization harbour the higher microbial diversity which was found to confer health benefits. Hence biobanking this diversity is imperative to understand modern lifestyle-associated diseases. Microbes preserved from tribal communities may hold the key to the development of indigenous precision probiotics. This is the first reference human microbiome from healthy individuals which will pave the way for future research on different disease models and the development of precision probiotics for Indian populations.

2. Problem solved / addressed

Microbiome companies/start-ups rely heavily on the availability of healthy microbiome data for prediction of microbial dysbiosis in a patient sample. The microbiome profile of the patient is compared with the microbiome data available in public databases. Large amount of data is already available for western countries but for India this data is lacking. Comparison of microbiome profiles from Indian individuals with that of western has no meaning as their diet, geography, lifestyle are different. This is the first reference human microbiome from healthy individuals which will pave the way for future research on different disease models and the development of precision probiotics for Indian populations.

3. Project status

Sequencing of the data and data analysis is complete. Flagship paper on the work carried out is underway. Data will be made available first to domestic researchers followed by global researchers based on the data sharing policy.

4. Project outcomes

a) This is the first reference human microbiome from healthy individuals which will pave the way for future research on different disease models and the development of precision probiotics for Indian populations.

b) The first comprehensive study in the world to find an association of diet, demography, and Ayurvedic *Prakriti* phenotypes with 4 kingdoms (bacterial, fungal, archaeal and micro eukaryotic) diversity which has helped in the identification of community-specific microbial signatures.

c) Ayurvedic *Prakriti* phenotypes showed significant association with gut microbiome with Pitta Prakriti individuals having significantly different microbiome.

d) Biobanking of healthy gut samples will help in developing fecal microbial transplantation strategies after further characterization.

e) Preservation of more than 180 anaerobic bacteria will help in the development of indigenous precision probiotics.

5. National collaborations

National Centre for Cell Science, Pune; All India Institute of Medical Sciences, Delhi; Institute for Biodiversity and Sustainable Development, Imphal; KEM Hospital Research Centre, Pune; Savitribai Phule Pune University, Pune; Trans Disciplinary University, Bengaluru; and SRM Institute of Medical Sciences, Chennai.

6. Potential of the project

a) Healthy reference microbiome profiles generated will be immensely useful for microbiome-based companies for disease prediction

b) Stool samples bio banked can be screened for super donors for fecal microbial transplantation therapies

c) Bacterial isolates generated can be used as potential precision probiotics

ProBioPred: an online server for the prediction of potential probiotic candidate using machine learning approach

Name of the Institution

BRIC-National Centre for Cell Science, Pune Maharashtra

1. Brief Description of the Technology / Project

In this project NCCS developed a user-friendly web-accessible application "ProBioPred" that can predict the probiotic potential of a candidate strain based on its genome. The method uses trained Support Vector Machine (SVM) models based on manually curated features like genes encoding probiotic properties, presence/absence of virulence factors and antibiotic resistance. Currently, ProBioPred supports the prediction of probiotic strains belonging to genera, Bacillus, Bifidobacterium, Clostridium, Enterococcus, Lactobacillus, Lactococcus, Leuconostoc, Pediococcus, and Streptococcus due to their wide use as probiotics. The accuracy of trained models on test data for different genera ranged from 95.7% to 99.67% whereas the sensitivity and specificity range from 0.91 to 0.99 and 0.97 to 0.99 respectively.

2. Problem solved / addressed

Human microbiome studies over the last two decades underlined the importance of probiotic organisms which can sustain and compete with the commensal gut bacterial. Hence identifying indigenous probiotic bacteria has received considerable attention throughout the world. Next generation probiotics have additional capabilities to treat or cure certain diseases including psychobiotics. Developed web server will help screen thousands of bacteria in quick and efficient way to search for new possible probiotics. Selected strains can be then tested experimentally for their desired benefits.

3. Technology status

ProBioPred can be a first step for prediction of potential probiotic bacteria before moving to actual characterization of strains.CurrentlyProbioPred software is at the validation stage and would be made available for installation once it is patented.

4. Project impact

Once the technology be used on metagenomically assembled bins (MAGs) then large number of bacterial genomes can be screened for their potential use as probiotics.

Technology for efficient deletion of microRNAs using CRISPR/Cas9 with dual guide RNAs

Name of the Institution

Centre for Stem cell research (a unit of BRIC-inStem Bengaluru), Christian Medical college campus, Bagayam, Vellore

1. Brief Description of the Technology / Project

This study introduces a novel approach using CRISPR/Cas9 with dual guide RNAs (dgRNAs) to create short deletions in miRNA genomic regions. This method, utilizing single-copy lentiviral integration, achieves over 90% downregulation of targeted miRNAs within a week. It offers higher specificity and flexibility than sgRNA-based methods, enabling the deletion of individual miRNAs with similar seed sequences. Institute applied this approach in two human cell lines, showing its effectiveness in studying human erythropoiesis and iPSC biology. Deleting miR-451 and miR-144 blocked erythroid differentiation, while deleting miR-23a and miR-27a affected iPSC survival. The method also demonstrated efficient deletion of protein-coding genes, significantly impacting protein expression.

2. Problem solved / addressed

Efficient deletion of microRNAs by gene editing. 4. Technology status:

3. Technology status

In the process of generating CRISPR-Cas9 library to delete all the microRNAs.

4. Anticipated project impact

This technology can be transferred for the generation of pooled libraries to generate deletion of all the human miRNAs.

5. Market potential

This protocol has the potential to be extended to delete multiple miRNAs within miRNA clusters, allowing for future investigations into the cooperative effects of the cluster members on cellular functions. The protocol utilizing dgRNAs for miRNA deletion can be employed to generate efficient pooled libraries for high-throughput comprehensive analysis of miRNAs involved in different biological processes.

Erythroid lineage-specific lentiviral RNAi vectors suitable for molecular functional studies and therapeutic applications

Name of the Institution

Centre for Stem cell research (a unit of BRIC-in Stem Bengaluru), Christian Medical college campus, Bagayam, vellore-632002

1. Brief Description of the Technology / Project

Numerous genes exert multifaceted roles in hematopoiesis. Therefore, institute generated novel lineage-specific RNA interference (RNAi) lentiviral vectors, H23B-Ery-Lin-shRNA and H234B-Ery-Lin-shRNA, to probe the functions of these genes in erythroid cells without affecting other hematopoietic lineages. The lineage specificity of these vectors was confirmed by transducing multiple hematopoietic cells to express a fluorescent protein. Unlike the previously reported erythroid lineage RNAi vector, our vectors were designed for cloning the short hairpin RNAs (shRNAs) for any gene, and they also provide superior knockdown of the target gene expression with a single shRNA integration per cell. High-level lineage-specific downregulation of BCL11A and ZBTB7A, two well-characterized transcriptional repressors of HBG in adult erythroid cells, was achieved with substantial induction of fetalhemoglobin with a single-copy lentiviral vector integration. Transduction of primary healthy donor CD34+ cells with these vectors resulted in >80% reduction in the target protein levels and up to 40% elevation in the γ-chain levels in the differentiated erythroid cells. Xenotransplantation of the human CD34+ cells transduced with H23B-Ery-Lin-shBCL11A LV in immunocompromised mice showed ~ 60% reduction in BCL11A protein expression with ~ 40% elevation of γ-chain levels in the erythroid cells derived from the transduced CD34+ cells.

2. Problem solved / addressed

Overall, the novel erythroid lineage-specific lentiviral RNAi vectors described in this study provide a high-level knockdown of target gene expression in the erythroid cells, making them suitable for their use in gene therapy for hemoglobinopathies. Additionally, the design of these vectors also makes them ideal for high-throughput RNAi screening for studying normal and pathological erythropoiesis.

3. Technology status

Development stage- completed pre-clinical proof of concept and animal studies. Once commercialized, this may reach to global level as there are Sickle cell disease and β-thalassemia patients in almost all the countries. The technology has the potential for Functional cure for Sickle cell disease and β-thalassemia potential for a one-time treatment as alternative to regular blood transfusions.

4. Market potential of the technology

Lentiviral vectors for gene therapy for haemoglobin disorders are available as drug products. Therefore, this lentiviral vector also has market potential.

Gene editing mediated hematopoietic stem cell gene therapy for HIV

Name of the Institution

Centre for Stem cell research (a unit of BRIC-inStem Bengaluru), Christian Medical college campus, Bagayam, vellore-632002

1. Brief Description of the Technology / Project

Human immunodeficiency virus-1 (HIV-1) infection leads to acquired immunodeficiency syndrome (AIDS) and more than 30 million people are affected by it worldwide. CCR5 receptor present in human immune cells is an attractive target for HIV treatment owing to a naturally occurring CCR5 null variant (CCR5 delta32/delta32), which confers resistance to R5-tropic HIV-1. Hematopoietic stem and progenitor cells (HSPCs) from CCR5 null homozygous individuals have been shown to impart functional cure to AIDS patients on allogeneic transplantation. The limited availability of HLA matched CCR5 null donors poses major challenge to this approach as a regular therapy. As an alternative, institute developed CCR5 gene edited HSPCs for autologous stem cell transplantation. Investigators showed that the approach successfully produces immune cells that are resistant to HIV infection.

2. Problem solved / addressed

One-time treatment approach for HIV diseases.

3. Status of the Technology

Development stage- completed pre-clinical proof of concept and animal studies. The technology has the potential for a Functional Cure for HIV as a one-time treatment as alternative to regular anti-retroviral therapy.

4. Market potential

The market potential for HIV gene editing technology is robust, supported by the rapid growth of the gene editing market, advancements in CRISPR technology, promising research outcomes, and the ongoing need for innovative HIV treatments. The overall gene editing market is experiencing significant growth. An estimate suggests the market could surpass USD 29.93 billion by 2032, growing at a compound annual growth rate of 15.73% from 2023 to 2032.

CRISPR-Cas9 gene editing mediated hematopoietic stem cell gene therapy for β- Hemoglobinopathies

Name of the Institution

Centre for Stem cell research (a unit of BRIC-inStem Bengaluru), Christian Medical college campus, Bagayam, vellore-632002

1. Brief Description of the Technology / Project

Reactivation of fetalhemoglobin (HbF) is a commonly adapted strategy to ameliorate β-hemoglobinopathies. Here we developed a CRISPR-Cas9 mediated gene editing approach, which involves gene editing of patient's hematopoietic stem cells for autologous stem cell transplantation as a new treatment approach. We identified a novel regulatory region that on gene editing resulted in increased fetalhemoglobin and reduced the production of mutated adult hemoglobin. We demonstrate that the regulatory region gene-edited hematopoietic stem and progenitor cells (HSPCs) retained their genome integrity and their engraftment potential to repopulate for long-term hematopoiesis in immunocompromised mice producing HbF positive cells in vivo. Importantly, the editing induced therapeutically significant levels of HbF to reverse the phenotypes of both sickle cell disease and β-thalassemia major. In addition to this we have also developed HDR based gene editing of two other targets involved in disease reversal.

2. Problem solved / addressed

One-time treatment approach for β-hemoglobinopathies; Sickle cell disease and β-thalassemia.

3. Anticipated impact

The technology has the potential for a Functional Cure for Sickle cell disease and β-thalassemia as a one-time treatment as alternative to regular blood transfusions.

4. Market potential of the technology

The U.S. Food and Drug Administration (FDA) has approved two cell-based gene therapies, Casgevy and Lyfgenia, for treating sickle cell disease in patients 12 years and older. Casgevy, in particular, utilizes CRISPR-Cas9 technology, marking a significant milestone in gene therapy. Institute has a similar and functionally better pre-clinical product. The overall gene editing market is experiencing significant growth. An estimate suggests the market could surpass USD 29.93 billion by 2032, growing at a compound annual growth rate of 15.73% from 2023 to 2032.

Bio-inspired cationic lipid nanocarriers to deliver CRISPR/Cas9 system for efficient genome editing in mammalian cells

Name of the Institution

Centre for Stem cell research (a unit of BRIC-inStem Bengaluru), Christian Medical college campus, Bagayam, vellore-632002

1. Brief Description of the Technology / Project

Towards developing a safe and efficient lipid nanoparticle system for delivering CRISPR/Cas9 tools, we have developed a novel lipid nanoparticle system by screening library of steroidal sapogenins as a substitute for cholesterol in lipid nanoparticle formulations. We have identified that diosgenin doped liposomal formulations could efficiently deliver CRISPR tools, where Cas9 in pDNA, mRNA and protein forms than their respective commercial transfection reagents. The novel transfection reagent was filed for patent. Currently, we are exploring their applications in editing hematopoietic stem cells for treating beta-globinopathies.

2. Problem solved / addressed

No single transfection reagent was available for transfecting multiple nucleic acid. To this end, we developed novel liposomal transfection reagent for delivering CRISPR/Cas9 tools in pDNA, mRNA and RNP forms and demonstrated gene-editing efficiencies in multiple cultured cell lines. We designed and developed adenosine and cytosine base editing mRNA for efficient base editing Hematopoietic Stem and Progenitor Cells.

3. Status of the Technology

A patent filed - “Compact liposomal vehicle for delivery of large molecules, 2021, Indian Patent Application No. 202041010160” It is at proof-of-concept level.

4. Anticipated project impact

Currently, there are no transfection reagents available in India. More importantly, the developed transfection reagent could deliver multiple nucleic acids and proteins including genome editing reagents, this may serve as a potential alternative for electroporation and may help in reducing the cost of gene-manipulated ex vivo cell therapies such as CAR-T Cell Therapy.

5. Market potential

Popularizing the developed transfection reagent would help in reduce import dependence. As the market of Cell and Gene Therapies are growing at an exponential pace, the need for associated reagents also is increasing.

Cardiogenomics, stem cell and precision medicine

Name of the Institution

BRIC- Institute for Stem Cell and Regenerative Medicine, GKVK Post, Bangalore

1. Brief Description of the Technology / Project

Cardiomyopathies are a group of life-threatening heart muscle diseases that represent a significant proportion of heart failure and sudden cardiac death. Among cardiomyopathies, hypertrophic cardiomyopathy (HCM) is a hypertrophied heart without other cardiac and systemic diseases. Pathogenic gene variants encoding the sarcomere and signaling proteins cause the disease. However, for around 50% of cases, novel disease-associated genes remain to be discovered. In our gene discovery phase, applying exome sequencing of the Indian HCM cohort, we identified novel disease-associated variants in TTL and PRKCA genes. Institute performed functional characterization using iPSC-derived cardiomyocytes and a transgenic mouse model and confirmed its pathogenicity.

2. Problem solved / addressed

Institute analyzed the whole exome sequencing data from 300 unrelated idiopathic patients and identified variants in genes such as TTL and PRKCA. Replication analysis using exomes from UK Biobank, Estonia and Tommo Biobanks revealed additional variants in PRKCA. Functional characterization of variants using human iPSC derived cardiomyocytes done. Further, institute generated a representative transgenic mouse model expressing PRKCA-E207G showed increased heart-to-body weight ratio, hypertrophy, and fibrosis. MEK-inhibitor administration reversed these phenotypes.

3. Status of the Technology

Development Phase: Identification of novel genes and pre-clinical models for precision medicine. Identification of novel heart failure genes/ pre-clinical models including iPSCs and mice models will enhance the drug discovery.

4. National collaborations

20+ clinical collaborators across India for patient samples

5. Market potential

Identification of novel heart failure genes/ pre-clinical models including iPSCs and mice models will enhance the drug discovery.

Genomic insight-based therapy for eradicating gastric pathogen Helicobacter pylori

Name of the Institution

BRIC- Rajiv Gandhi Centre for Biotechnology, Thiruvananthapuram - 695 014, Kerala, India

1. Brief Description of the Technology / Project

Aim is to analyse the genomes of isolated H. pylori strains of Indian origin and find out the genes that are contributing to their antibiotic resistance, which is a serious health concern in the present scenario.

2. Problem solved / addressed

Based on the genome analysis of the Indian *H. pylori strains*, RGCB have been able to find the antibiotics that could be suitable for the treatment of *H. pylori* in India.

3. Status of the Technology

Development stage.

4. Anticipated project impact

Currently 4.4 billion people (over 50% of the population) in the world is infected with H. pylori and 1 million people in each year die with peptic ulcer and gastric cancer together. In India, the H. pylori infection prevalence varies. In some states it can be over 80%. So, the market size is huge.

Development of Pro-vitamin A Enriched Biofortified Banana

Name of the Institution

BRIC- National Agri-Food Biotechnology Institute (NABI), Knowledge City, S.A.S. Nagar, Mohali - 140306, Punjab, India

1. Brief Description of the Technology / Project

Micronutrient deficiencies, particularly Vitamin A, pose a significant public health challenge globally. India has the highest prevalence of Vitamin A deficiency (VAD) among South Asian nations. This deficiency is exacerbated by inadequate intake of pro-vitamin A (PVA) from vegetarian diets and poor nutrient absorption. To address this issue, the BIRAC-supported banana biofortification project was initiated in November 2012 in collaboration with the Queensland University of Technology (QUT), Australia. Prime Minister visit to QUT in 2014 underscored his support for developing nutritionally enhanced banana varieties to combat malnutrition in India. As part of this initiative, the research group at NABI has developed PVA (β-carotene) enriched banana (Grand Naine cultivar) to alleviate VAD. These genetically engineered (GE) banana lines are sterile (seedless) and propagated vegetatively, hence eliminating environmental safety concerns. Additionally, inserted genes are sourced exclusively from different banana varieties, ensuring no food safety concerns.

2. Problem solved / addressed

The introduction of pro-vitamin A biofortified banana addresses Vitamin A deficiency (VAD), a major health issue in India causing preventable blindness, growth retardation, and decreased immunity, particularly among women and children. Considering bananas as a staple crop and India is the world's largest producer, this GE banana approach offers a holistic solution to improve public health.

3. Status of the Technology

The biofortified banana lines are currently undergoing open field event selection trials (EST) across four agro-climatic regions in India (Tamil Nadu, Assam, Gujarat, and Punjab) following regulatory and biosafety procedures. The next steps involve selecting lead and backup events, conducting multilocation Biosafety Research Level (BRL) trials, performing detailed compositional analysis, and generating additional data as per regualtors for eventual commercial release.

4. Challenges encountered

Investigators encounter the following regulatory and developmental challenges during the process of development of GE banana lines:

a) **Transgene Copy Number**: Regulators prefer transgenic events with single-copy integration for subsequent developmental progress and characterization. Multi-copy transgenic events, despite their enhanced trait expression and no yield penalty, are less preferred.

b) **Crop Nature, Genome Complexity, and Transgene Copy Number**: Current guidelines for selecting transgenic events based on copy number do not differentiate between seed-propagated and vegetatively propagated crops, despite the stable genomes of the latter. Adjustments are needed to account for the ploidy level of target plant species.

c) **Molecular Characterization**: The requirement for molecular characterization data of multiple GE lines at early regulatory stages demands additional time and financial resources. Focusing detailed molecular analysis only on lead and backup events after assessing agronomical performance could be more beneficial.

5. Suggestions on policy / regulatory interventions

a) **Tailored Guidelines**: Apply specific guidelines for selecting transgenic events in vegetatively propagated polyploid crops, recognizing their stable genomes in subsequent generations, rather than using the criteria for seed-propagated crops.

b) **Multi-Copy Integration**: Allow selection of GE events with multi-copy integration, provided developers present adequate molecular data confirming clear events without major disruption of essential genes by T-DNA integration.

c) **Trait Stability Data**: Use generation-wise trait stability and yield data to address the complexity of multi-copy T-DNA integration and the potential for post-transcriptional RNA silencing and resulting trait expression.

d) **Institutional Support**: Encourage the association and cooperation of relevant institutes to assist developers in obtaining regulatory clearance, thereby speeding up the development process and reducing the regulatory policy burden.

6. Anticipated project impact/outcomes

The banana biofortification project, focused on enhancing PVA content through genetic engineering, holds significant potential across multiple dimensions:

a) **Business**: The commercialization of biofortified banana opens new market opportunities for health-conscious consumers and drives economic growth in the agricultural sector.

b) **Societal**: It addresses critical public health issues such as blindness and immune deficiencies related to VAD, especially in regions where bananas are a dietary staple.

c) **National**: The project's success positions the country at the forefront of agricultural biotechnology, demonstrating its capacity to address nutritional challenges through innovative solutions.

A single biofortified banana can fulfil the recommended daily allowance (RDA) of vitamin A, equivalent to the PVA content of 20 regulars Grand Naine bananas. Hence, it would be a valuable addition to government programs like mid-day meals for school children and nutrition initiatives for pregnant women.

7. National or international collaborations

The biofortification of PVA in banana is a multi-institutional initiative with national and international collaborations. National partners include DBT-National Agri-Food Biotechnology Institute (NABI), Punjab; ICAR-National Research Center for Banana (NRCB), Tamil Nadu; Navsari Agricultural University (NAU), Gujarat and Assam Agricultural University (AAU), Assam.

Biotech Consortium India Limited (BCIL), N. Delhi supports biosafety compliance, field trials, and data generation. International collaboration is with Queensland University of Technology, Australia. These partnerships leverage diverse expertise and resources to enhance the project's impact and success, addressing both national and global nutritional challenges.

8. Market potential

The market potential of the banana biofortification project is substantial. In the near term, PVA biofortified banana can address immediate public health needs by combating VAD in affected regions. In the long term, the technology could achieve global adoption in banana-growing areas, enhancing food security and nutrition. Furthermore, partnerships with agricultural companies and the food industry can drive economic growth and innovation in agricultural biotechnology.

Low Glycemic Wheat

Name of the Institution

BRIC- National Agri-Food Biotechnology Institute (NABI), Knowledge City, S.A.S. Nagar, Mohali - 140306, Punjab

1. Brief Description of the Technology / Project

Low glycemic wheat lines were developed through the EMS mutagenesis (non-transgenic approach) in the background of a good chapatti (unleavened flat bread) Indian bread wheat variety ('C306'). Starch is a major component (~70%) of grain and comprises two components - linear glucose polymer 'Amylose' (25%-30%) and highly branched polymer of glucose 'Amylopectin' (70%-75%). The larger proportion of amylopectin in wheat flour is highly digestible in the lower intestine releasing a large amount of glucose in the blood thus increasing the glycemic response. The glycemic index (GI) of chapatti made from the common wheat flour is high. Therefore, people with diabetes and obesity have to restrict the consumption of chapatti made from the same. The high GI response of chapatti can be reduced by replacing it with chapatti made from wheat flour consisting of high amylose content. The low glycemic wheat lines developed have shown improvement in agronomical traits and reduced glycemic index in comparison to the parent wheat variety. Experimental results from the studies using in vitro and in vivo mice models showed positive results suggesting the low GI response upon feeding the mice with chapatti made from the GI-improved wheat flour. Simultaneous, studies on chapatti quality characteristics done by using the low GI wheat flour confirm the consistency of the quality parameters similar to that of 'C 306'. Therefore, the low GI wheat developed at NABI will not only provide nutritional benefits but also good processing qualities such as softness, palatability, aroma, colour, puffiness, etc. making it a commodity for easy acceptance by society.

2. Problem solved / addressed

Low glycemic wheat has proven nutritional and health benefits. This also promote healthy gut bacteria and increase and aid in the production of small chain fatty acids (SCFA).

3. Stage of the Technology

The lines are ready for commercialization. BCIL, New Delhi advertised the expression of interest for its commercialization.

4. Market potential

Taking into consideration the market estimation and current players in the market, there are many companies manufacturing low glycemic wheat for diabetic, obese and lifestyle disease populations. Hence considering the other players in the market the market capture by NABI varieties is presumed to be 1% for two years and subsequently increasing to 1.5% and 2%.

Developing an Inventory of Iron Homeostasis-Related Genes in Hexaploid Wheat

Name of the Institution

BRIC- National Agri-Food Biotechnology Institute (NABI), Knowledge City, S.A.S. Nagar, Mohali - 140306, Punjab

1. Brief Description of the Technology / Project

Enhancing iron content and its bioavailability in crop plants is important to combat micronutrient deficiency including iron biofortification in humans. Although strategies could be designed for the biofortification of iron in wheat, limited progress has been made due to the lack of genetic information and molecular components involved. The genes contributing to iron uptake and mobilization were unknown in hexaploid wheat. Genomics approaches have contributed largely to enhancing our understanding of the molecular components involved in iron mobilisation in plants. Using transcriptomics (RNAsequencing - RNAseq)- based approach, a large inventory of genes expressed during iron deficiency responses was identified at different time points and tissues. The listed genes identified from this study serve as an important catalogue of candidate transporters and regulators of iron homeostasis response in crop plants. Currently, we are using forward and reverse genetics to explore the functionality of the candidate genes in hexaploid wheat.

2. Problem solved / addressed

The unknown candidate gene form hexaploid wheat is now reported, and the resource information has been now published as manuscripts as given with the reference Kaur, G. *et al. J Exp Bot* 70, 6141–6161 (2019) & Kaur, G. *et al.Environ Exp Bot* 208, (2023).

3. Stage of the Technology

The lines are ready for commercialization. BCIL, New Delhi advertised the expression of interest for its commercialization.

4. Project impact

The wider impact of this work contributes towards generating novel resources to develop wheat with enhanced in iron content as well as increased bioavailable mineral nutrients grains as a step towards solving the important problems in human health. Furthermore, understanding the pathways and candidate proteins by which Fe metals accumulate in plants will enable the development of crops with better content of nutrients and also create healthier food sources. New avenues for biofortification strategies will be developed that could be certainly expanded to other crop species. The information generated during this work will be expanded to the biology will be good for nutritional improvement for nutritional rich crops.

A Genomics-Assisted Synthetic Hexaploid Wheat (SHW) Gene Isolation and Pre-Breeding Platform for Improved Heat Tolerance and Sustainable Production

Name of the Institution

BRIC- National Agri-Food Biotechnology Institute (NABI), Knowledge City, S.A.S. Nagar, Mohali - 140306, Punjab

1. Brief Description of the Technology / Project

Through an international project (DBT-BBSRC) involving (NIAB, Cambridge, UK; PAU, Ludhiana, India and NABI, Mohali, India) genetic and genomic resources were developed and traits were identified that can help in better adaptation to the changing environment. 700 doubled haploid populations have been developed from BC1 of Synthetic X elite wheat crosses and evaluated for different traits related to heat stress tolerance.100 N-CSSLs have been developed Synthetics X Elite crosses and mapping of loci associated with heat stress tolerance was done. Potential material thus generated is being used in the crossing blocks at PAU for advanced cultivar generation.

2. Problem solved / addressed

Three synthetics developed from three different *Ae. tauschii* accessions *X T. durum* cultivar have been developed and identified as heat stress tolerant.

3. Stage of the Technology

Development stage. Heat stress tolerant QTL were mapped.

4. National or international collaborations

International project (DBT-BBSRC) involving (NIAB, UK, PAU, India and NABI, India)

5. Market potential of the technology/project in both the near term and long term?

This material can be utilized in current and future breeding programs to generate environmentally resilient varieties.

Indian Rice panArray (IndRA): A 90K Pan-genome SNP Genotyping Array for genomics-assisted crop improvement of rice

Name of the Institution

BRIC-National Institute of Plant Genome Research (NIPGR), Aruna Asaf Ali Marg (P.O. Box: 10531), New Delhi

1. Brief Description of the Technology / Project

Global rice germplasm with rich trait diversity harbours extensive genetic variation that cannot be optimally captured with conventional SNP arrays based on a single reference genome for their eventual utilization in genetic enhancement of rice. To overcome this bottleneck, "Indian Rice panArray (IndRA)" is a first-ever pan-genome-based SNP genotyping assay developed for crop plants. It enables researchers to target population-specific genomic variation by assaying SNP markers unique to different rice populations (indica, aromatic, aus and japonica, etc.), in addition to markers from the japonicaNipponbare reference genome. IndRA includes a total of 80,504 genome-wide informative SNPs, selected from > 50 millions of pan-genome based sequence variants, identified using > 4,000 diverse global rice accessions. Out of 80,504 markers, 60,026 SNPs correspond to 12 rice chromosomes from the Nipponbare reference genome and 20,478 SNPs specific to 12 different rice sub-populations. This makes IndRA as an ideal SNP genotyping solution for pan-genome based genetic studies including complex trait dissection and diverse molecular breeding applications to drive genetic improvement of rice.

2. Problem solved / addressed

IndRA enables researchers to target novel trait-associated genomic variations that are missing from the traditional reference genome. These arrays assay diverse cultivar-specific (pan-genome) genomic variations especially of Indian origin in addition to SNPs from reference genome. Therefore, this array provides higher genomic coverage and captures almost entire genomic variations existing within global germplasm accessions compared to other genotyping arrays available for rice. These arrays include more than 80,000 genome-wide informative SNPs, selected from millions of pan-genome based sequence variants, identified using thousands of diverse global rice accessions. This makes the arrays ideal SNP genotyping solution for pan-genome based genetic studies including complex trait dissection and diverse molecular breeding applications to drive genetic improvement of rice. These arrays have diverse applications in Indian trade and commerce, including DNA fingerprinting, genetic purity and hybridity testing. Besides, these arrays facilitate various genomics-assisted breeding applications, including trait association mapping, marker-assisted selection and genomic selection thus enabling genetic enhancement of rice.

3. Status of the Technology

This technology has been published and patent has been filed for large-scale SNP genotyping applications in rice. [Daware et al. (2022) The Plant Journal 113:26-46; INTERNATIONAL PATENT COOPERATION TREATY (PCT)-WIPO APPLICATION NO. PCT/IN2022/050901; INDIAN

PATENT APPLICATION NO. 202111045696]. A User-Friendly Web-Portal Rice Pan-Genome Genotyping Array Analysis Portal (RAP) (http://www.rpgaweb.com) developed for rapid RPGA SNP genotyping data analysis and to provide easy to use platform for imputation of RPGA-based genotyping data using 3K Rice Reference Panel and subsequent GWAS in order to drive genetic improvement of rice. SNP Arrays was released by Honorable Minister of Science & Technology Dr. Jitendra Singh Oct 8, 2021 for National Use.

4. Project impact

The developed IndRA array has been utilized for large-scale genotyping of about 15000 indigenous rice accessions conserved at National Gene bank in the Mission Mode Projects on "Germplasm Characterization for Trait Discovery" for accelerated crop improvement. Till date, this Array has been used extensively to genotype about 30,000 rice samples (~18 crores/1.8 million USD @60 USD per sample) at a global scale within one year of its release. It is expected to increase up to 50,000 samples per year (~30 crores) once this technology will be commercialized at a global and National level.

5. Market potential

Comprehensive genotypic characterization of large-scale germplasm resources conserved at Genebanks is essential to identify novel superior genes and natural alleles governing traits of agronomic importance for genetic improvement of rice. IndRA tags almost all dispensable genes from 3K rice pan-genome, therefore, provide an opportunity to perform pan-genome based genetic analysis and identify dispensable genes associated with important agronomic traits in rice. IndRA is an ideal genotyping solution for marker-assisted selection, genomic selection and bulk segregation analysis as well as highly proficient in genetic background recovery checking in marker-assisted breeding for fast-track development of climate-resilient, a/biotic stress-tolerant and superior rice varieties with enhanced yield and productivity. In this context, IndRA has huge market potential at a global level.

Targeted editing of rice genome for enhanced crop improvement

Name of the Institution

International Centre for Genetic Engineering and Biotechnology (ICGEB), Aruna Asaf Ali Marg, New Delhi

1. Brief Description of the Technology / Project

The pyramiding of widely dispersed useful genetic variability into commercially cultivated rice cultivars is very time consuming and also the availability these genetic variants to the plant breeding community becomes a bottleneck. With the targeted genome editing using CRISPR/Cas9 one could pyramid the required genetic variability into any established commercially cultivated rice cultivar directly without any requirement of actual rice mutants or without using the time-consuming plant breeding procedures. There are several gene loci in rice that negatively regulate the agronomic trait(s). We utilized the genome editing technology and selectively knockout the functioning of several rice gene loci that negatively regulate the agronomic performance by regulating the tiller number, plant height, panicle branching and spikelet number, grain length, width and weight.

2. Problem solved / addressed

Institute generated several loss of function mutation in MTU1010 mega rice cultivar Dense erect panicle *1(Os09g26999)* for its erect compact panicle with high spikelet number per unit panicle length, *OsTB1 (Os03g49880)* allele for high tiller number, the *OsCKX2 (Os08g0509600)* for increasing rice spike size and grain number and *OsGW2 (Os02g14720)* larger grain size. The established mutations were inherited stable for several generations with their predicted agronomic performance.

3. Status of the Technology

ICAR evaluated the agronomic performance of dep1 genome edited line and recommended for All India Co-ordinated trails to evaluate its performance before its release for commercial cultivation in India.

4. Scale of technology deployment

The MTU1010 rice cultivar is extensively grown in India, investigators anticipate that the improved version of this genome edited cultivar will be cultivated in much larger area.

5. Policy / regulatory interventions:

Government is already allowed genome edited SDN1 and SDN2 mutants for cultivation

6. Anticipated project impact

If it allowed for commercial cultivation the rice productivity can increase by 25-30%

7. National collaboration

Being developed in collaboration with ICAR system

Recombinant fungal enzymes for lignocellulosic biomass hydrolysis for biofuel application

Name of the Institution

International Centre for Genetic Engineering and Biotechnology (ICGEB), Aruna Asaf Ali Marg, New Delhi

1. Brief Description of the Technology / Project

Through extensive bioprospecting study, ICGEB scientists identified a fungal isolate that efficiently degrades the lignocellulosic biomass that has been pretreated to loosen or remove the lignin. The fungal isolate's genomics, transcriptomics and proteomics were performed to understand the nature of the cellulolytic enzymes secreted and their regulation. The fungus was further genetically engineered to derepress the enzyme secretion and overexpress key enzymes, which led to 8-9 -fold increase in titer and enhanced biomass hydrolyzing efficiency. The techno-economic analysis also indicated the cost-effectiveness of the process.

2. Problem solved / addressed

The natural host and enzymes available to hydrolyze the lignocellulosic biomass are inefficient and expensive. Because of the complexity of the problem, there are very few commercial companies in the market that can provide efficient enzymes. Therefore. it was important to identify a suitable platform that can produce efficient and cost-effective enzymes.

3. Status of the Technology

ICGEB enzyme technology has been scaled up in industry to a 15,000-liter scale, and the efficiency has been tested at multiple places, including ICT, Mumbai, and Praj Ltd.

4. Regulatory or other challenges:

ICGEB faced challenges in getting approvals from National Biodiversity Board (NBA) being an International Organization. Also, due to low return on profit and captive market, companies are hesitant to invest in the technology. There is only one multi-national company dominating the market.

5. Suggestions on policy / regulatory interventions

There should be relaxation in the policy guidelines of NBA for an international organization if they have a local seat and working under the Grant support of Government of India. In such scenario, the local seat of the international organization should be treated as National Organization. Additionally, a policy on the use of indigenous enzyme technology for 2G ethanol production would be needed.

6. Anticipated project impact

The major application of the technology is for producing second-generation biofuel. This technology can also be used by any biomass processing company that wants to hydrolyze the biomass into monomeric sugars and ferment them into useful industrial products. Another use of cellulase enzyme technology is in animal feed to increase the availability of digestible sugars.

7. Market potential

In India, the market potential for recombinant fungal enzymes for lignocellulosic biomass hydrolysis for biofuel application is influenced by several factors, both in the near term and long term:

Near Term:

- **Government Initiatives**: The Indian government has initiatives like the National Biofuel Policy and various subsidies that encourage the use of biofuels. This creates a supportive environment for technologies like recombinant enzymes that improve the efficiency of biomass-to-biofuel conversion.
- **Rising Energy Demand**: India's increasing energy demand, coupled with concerns over energy security and environmental sustainability, drives interest in alternative energy sources such as biofuels.

Long Term:

- **Scaling Up Production**: Over the long term, advancements in enzyme production technologies and economies of scale are expected to drive down costs, making biofuel production more economically viable in India.
- **Policy Support**: Continued support from government policies and incentives for biofuel production ensures a stable market environment for technologies like recombinant enzymes.
- **Environmental Regulations**: Strengthening environmental regulations and commitments to reduce greenhouse gas emissions could further bolster the demand for biofuels derived from lignocellulosic biomass.

Non-antibiotic-based selection-marker for selecting marker-safe plants in rice

Name of the Institution

International Centre for Genetic Engineering and Biotechnology (ICGEB), Aruna Asaf Ali Marg, New Delhi

1. Brief Description of the Technology / Project

In the present study, ICGEB initiated to develop a unique non-antibiotic-based selection system that offers a more natural and safe approach to select putative transgenic plants. The system is based on MG as the selection agent and plant glyoxalase pathway genes (GlyI + GlyII) as selectable markers. Like MG, the glyoxalase pathway is also ubiquitous and catalyzes the conversion of MG to D-lactate via GLYI and GLYII enzymes using glutathione (GSH) as a cofactor in the process. Therefore, considering the intrinsic nature of both MG and glyoxalases in plants, it is highly likely that MG can serve as a bio-safe selection agent to screen transgenic plants.

2. Problem solved / addressed

Markers are indispensable for the precise selection of transformed cells from a population of non-transformed cells. However, the possibility of horizontal flow of antibiotic-resistance genes to animals and vertical flow of herbicide-resistance genes to weedy plant relatives has raised a concern on the antibiotic or herbicide resistance genes-based selection markers for the plant transformation technology. Thus, considering the global biosafety and environmental issues, developing antibiotic or herbicide marker-free transgenic plants becomes essential.

3. Status of the Technology

The technology has been patented, and the know-how of the technology will be shared with the interested party after licensing of technology.

4. Challenges encountered

India has stringent biosafety regulations under the Environment Protection Act (1986) and the Rules for the Manufacture, Use, Import, Export, and Storage of Hazardous Microorganisms/ Genetically Engineered Organisms or Cells (1989). Compliance with these regulations, including obtaining approvals from regulatory bodies like the Genetic Engineering Appraisal Committee (GEAC), is crucial but can be time-consuming and complex.

5. Suggestions on policy / regulatory interventions

a) **Streamline Approval Process**: Simplify and expedite the regulatory approval process for non-antibiotic based selection markers while ensuring rigorous safety evaluations. This can encourage innovation and timely adoption of new technologies.

b) Harmonization of Standards: Collaborate with international regulatory bodies and scientific organizations to harmonize standards and guidelines for non-antibiotic based selection markers. This can facilitate smoother trade and adoption of technologies across borders.

6. Anticipated project impact

The modified vector has a multiple cloning site wherein any gene of interest can be inserted. The putative transformants can be selected using MG as the selection agent. MG-based selection system is bio-safe and can pave way towards better public acceptance of transgenic plants.

7. Market potential

The development of an efficient marker-freenon-antibiotic-based selection system holds immense commercial potential as it offers a safer approach devoid of the crucial biosafety concerns during the process of development of transgenic plants. Global biosafety and environmental concerns are major bottlenecks in promoting transgenics or GMOs to the public at large. Since this technology promises to overcome the two major challenges, there is an unlimited potential to propagate this technology commercially among the stakeholders and the various groups working in the area of crop biotechnology. This would lead more agri-biotech companies to invest and develop the technology increasing its market potential in both the near and long-term future. It holds value in both Business to Business (B2B) and Business to Consumer B2C sectors (B2C) of the industry.

Genomic exploration of microbial resources of Northeast India for potential applications in agricultural, industrial and therapeutics

Name of the Institution

BRIC-Institute of Bioresources and Sustainable Development (IBSD), Takyelpat, Imphal, Manipur

1. Brief Description of the Technology / Project

The rich bioresources of Northeast India remain unexplored. IBSD study focuses on the exploration, preservation and characterisation and genome sequencing of potential microbial resources from different unique ecological niches of NE India for potential applications in agricultural, industrial and healthcare products (enzymes, nutraceuticals, antibiotics), etc. Genomics and proteomics studies from these resources can relate to a new strategy and prospects to find active biometabolites and their biosynthetic pathways.

2. Problem solved / addressed

IBSD Imphal had carried out genome sequencing of microbes having therapeutic, agricultural, and industrial application potential.

a) **Therapeutic properties**: ***PaenibacilluspeoriaeIBSD35*** endophytic bacteria isolated from *Millettiapachycarpa* was sequenced with a genome size of 5,862,582 bp and ***Lactiplanti bacillus plantarum BRD3A*** isolated from traditional fermented rice-based beverage with a genome size of 3,3Mb which have antimicrobial potential. An antimicrobial peptide has been isolated from P. peoriae IBSD35 which have antimicrobial activity against the MDR pathogens.

b) **Agricultural application**: The genome sequence of ***Lysinibacillusxy lanilyticust 26*** rhizobacteria isolated from the C. chinense rhizosphere having the genome size 4.6 bp and Bacillus altitudinisLc5 endophytic bacteria were isolated from indigenous black rice with a genome size of 3.6-Mb produces major defensive enzymes and growth-promoting factors which can be an alternative strategy in plant and crop disease management to reduce the dependency on agrochemicals which have detrimental effects on the environment.

c) **Industrial application**: Genome sequence of ***Bacillus velezensisstrain*** **MRC 5958,** from Bakra Natural Hot Springs, a thermophilic cellulase-producing bacterium revealed genomic size of 4.4bp having potential thermostable cellulase-producing bacteria for converting the waste biomass into biofuel and other industrial enzymes.

3. Anticipated project outcome

a) From genome analysis, ***Paenibacilluspeoriael BSD35*** strain produced a potential novel antimicrobial peptide. It harbours type II polyketide biosynthesis pathway revealing terpenoids and secondary metabolites.

b) ***Lysinibacillusxylanilyticus*** t26 rhizobacteria genome harbored type III polyketides, non-ribosomal peptides, terpenes, and antibiotics and Bacillus altitudinisLc5produce major defensive enzymes and growth-promoting factors and antagonistic activity against the phytopathogens.

c) ***Bacillus velezensisstrain*** **MRC 5958** genome harbors putative cellulase biosynthetic gene

Genomics for conservation of indigenous cattle breeds and for enhancing milk yield

Name of the Institution

BRIC - National Institute of Animal Biotechnology, Opp. Journalist Colony, Near Gowlidoddy, Extended Q City Road, Gachibowli, Hyderabad, Telangana, India

1. Brief Description of the Technology / Project

India possesses a rich diversity of cattle breeds, with approximately 40 recognized at the project's start. Unlike Western breeds, indigenous cattle are renowned for their adaptability to challenging environments. However, many pure-line populations have dwindled due to factors such as crossbreeding and neglect. To conserve this valuable genetic heritage, the project utilized advanced technologies like Next Generation Sequencing (NGS) to develop a High Density (HD) SNP chip. This SNP chip was then employed to genotype 40 indigenous breeds, enabling a comprehensive analysis of their genetic makeup. Additionally, the project addressed a critical research gap by developing a reference genome for Indian cattle. This pioneering effort laid the groundwork for preserving the genetic diversity of indigenous breeds.

2. Problem solved / addressed

Historically, SNP (Single Nucleotide Polymorphism) chips available in the market were tailored primarily for exotic and Western cattle breeds, showing less than 50% polymorphic markers when applied to indigenous cattle populations. Addressing this limitation, the project successfully developed a high-density (HD) SNP chip named INDIAGU. This chip, containing 788K markers, is specifically designed for desi (indigenous) cattle and is now the world's largest cattle SNP chip. It boasts exceptional performance, with 97.4% high-resolution polymorphic markers in populations tested within desi dairy breeds. Using this HD SNP chip, pure lines were genotyped from 40 indigenous cattle breeds, cataloguing their genetic polymorphism and architecture. The resulting genotype data serves as a reference for identifying purebred and graded animals within these desi breeds. Another significant research gap was the absence of a reference genome for indigenous cattle. To address this, two platinum-standard genome assemblies were generated and both genomes are haplotype-resolved and exhibit remarkable contiguity, with an ungapped length exceeding 99.998%. These assemblies will serve as the definitive Reference Genomes for all future genomic research on indigenous cattle by the scientific community.

3. Status of the technology

SNP chip (INDIGAU), has been successfully developed, tested, and officially dedicated to the nation by the Minister of Science on August 13, 2021, for use by the scientific and breeding community. INDIAGU chip is now available to the scientific and breeding community and is already being utilized in various genomic projects. The markers from the INDIAGU chip have also been provided to the National Dairy Development Board (NDDB) for the development of a Low-Density (LD) chip, which will be used in the Department of Animal Husbandry and Dairying (DAHD) programs for mass-level genotyping of indigenous cattle. The reference genome, a critical resource for the scientific community, is publicly accessible.

4. Scale of commercialization

The SNP chip has been commercialized and is available through Thermo Fischer Scientific. Its primary application is within the research and breeding communities focused on Bos indicus species. The technology is currently being implemented at a domestic level, with availability for Indian researchers and breeders. However, its utility extends beyond India to neighbouring countries that have populations of Bos indicus species. The chip is being used for various genomic projects, including the development of a Low-Density (LD) chip by the National Dairy Development Board (NDDB) for mass-level genotyping of indigenous cattle in India. The scale of implementation is significant within these regions, contributing to advancements in cattle genomics and breeding programs.

5. Suggestions on policy / regulatory interventions

Simplify the process for obtaining permissions from state governments, agricultural universities, ICAR institutions, and private farms for collecting samples of purebred animals.

6. Project impact

a) **Genome Sequencing and SNP Discovery**: The genomes of 43 indigenous cattle breeds were sequenced, producing 24,241.3 Gb of data from 176 animals.

b) **IndiGau SNP Chip Development**: Featuring 788,496 SNPs, it is the world's largest cattle SNP chip, released on August 13, 2021, and represents NIAB's first publicly available product.

c) **Patent Filing**: A patent application for the high-density SNP chip was filed (Application No. 202241043917)

d) **Reference Genomes**: Two high-resolution genome assemblies for Sahiwal and Tharparkar were completed and are available on the NCBI portal, serving as definitive reference genomes for Indian cattle.

6. National or international collaborations

Dr. Curt Van Tassel's Group, USDA, USA has provided critical support in data analysis and marker identification, aiding in the development of the SNP chip.

7. Market potential

The SNP chip has substantial near-term potential for both the scientific community and breeders. It can be utilized for Genome-Wide Association Studies (GWAS), genomic selection programs, and genotyping tasks such as identifying purebred animals, sex determination, and parentage verification. This positions the chip as a valuable tool in research and service industries. Additionally, the development of a Low-Density (LD) chip from the high-density (HD) SNP chip presents a significant opportunity. The LD chip will be more affordable and feasible for large-scale genotyping, which can increase farmer accessibility for certifying animal purity and parentage. It offers a cost-effective solution for genomic selection programs in general herds, while the HD chip is suited for nucleus and well-characterized herds.

Indian Biological Data Centre

Name of the Institution

Regional Centre for Biotechnology, 3rd Milestone, Faridabad-Gurgaon Expressway. Faridabad 121001

1. Brief Description of the Technology / Project

The Indian Biological Data Centre (IBDC) (Website: https://ibdc.dbtindia.gov.in/) is the first national digital data repository dedicated to archiving all life science data generated from publicly funded research in India. Supported by the Government of India through the Department of Biotechnology, IBDC facilitates the implementation of the "Biotech-Pride Guidelines" (Promotion of Research and Innovation through Data Exchange). IBDC has developed portals and analysis pipelines that are widely used by the scientific community for data deposition, access, and analysis. It has been instrumental in creating data archival portals for nucleotide, metabolomics, proteomics, biological images, phenotyping data, and a data visualization repository for macromolecular structures.

2. Problem solved / addressed

The Indian Biological Data Centre (IBDC) has developed and deployed the Indian Nucleotide Data Archive (INDA) (Website: https://ibdc.dbtindia.gov.in/inda) and the Indian Nucleotide Data Archive-Controlled Access (INDA-CA) (Website: https://ibdc.dbtindia.gov.in/indasecure) to facilitate genomics data archival and sharing for the Indian scientific community. During the peak of the COVID-19 pandemic, IBDC quickly conceptualized and established a centralized repository for COVID-19 data sequenced in India by the INSACOG Consortium, which comprises 67 participating institutes (Website: https://ibdc.dbtindia.gov.in/insacog/statisticsinsacog). This repository has been crucial in providing uniform data analysis and enabling government agencies to track and respond to circulating variants in regions of concern. The portal features a real-time dashboard with detailed information on variants, including month-wise and week-wise distribution of variant frequencies. Additionally, it offers open-access data downloads for the research community, demonstrating IBDC's commitment to supporting scientific advancements and public health initiatives.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The Indian Biological Data Centre (IBDC) has developed comprehensive data archival, analysis, and sharing functionalities for various datasets. Specifically for genomics data, IBDC has created data portals such as the Indian Nucleotide Data Archive (INDA) and INDA-Controlled Access (INDA-CA). These portals include project-specific sections for initiatives like INSACOG, INSACOG-Sewage, GenomeIndia, and the Indian Human Microbiome Initiative. IBDC provides critical analysis services for INSACOG and INSACOG-Sewage, supporting the Government of India's COVID-19 surveillance activities. Through these advanced solutions, IBDC ensures efficient data management and facilitates significant research and public health advancements.

4. During development and/ or implementation, have you encountered any regulatory or other challenges?

A significant challenge faced by the Indian Biological Data Centre (IBDC) is the variability of uniformity in global data sharing policies and regulations. These policies vary widely depending on the data type, organism type, and data source, creating complexities in data management and sharing.

5. Suggestions on policy / regulatory interventions for the technology being described

To address the challenges of inconsistent data-sharing policies, there is a need for a dedicated policy that comprehensively covers all aspects of data-sharing and usage. This policy should provide clear guidelines tailored to different data types, organism types, and data sources, ensuring uniformity and facilitating efficient data management and sharing across all platforms.

6. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

IBDC has been part of important national-level projects like INSACOG, INSACOG-Sewage, GenomeIndia, Indian Human Microbiome Initiative and Mission program on Pediatric Rare Genetic Disorders (PRaGeD) projects and serving the community for the development of the genomics domain. IBDC has developed multiple analysis pipelines and data archival mechanisms for the real-time surveillance of variants of COVID-19 and acts as a central hub for data archival, analysis and sharing.

7. National or international collaborations associated with this technology or project?

IBDC collaborates with national consortiums such as INSACOG, GenomeIndia, the Human Microbiome Initiative, and PRaGED to archive and analyze data. Internationally, IBDC has collaborated with the European Molecular Biology Laboratory- European Nucleotide Archive (EMBL-ENA) to get internationally acceptable INSDC accessions for genomics data submitted to IBDC's open-access site, INDA.

8. What is the market potential of the technology/project in both the near term and long term?

IBDC, with robust computational infrastructure and expertise in genomics data archival, sharing, and analysis, holds significant market potential. The growing demand for precision medicine, personalised healthcare, and advanced research in genomics drives the need for such specialised facilities. This data centre's pivotal role in national projects underscores its importance, positioning it as a central data analysis and archival hub. As the genomics sector expands, the demand for secure, efficient, and comprehensive data management solutions will continue to rise. Additionally, collaborations with research institutions, healthcare providers, and pharmaceutical companies can further enhance its market position, making it an indispensable resource in the evolving landscape of genomics and bioinformatics.

Development of Pro-vitamin A Enriched Biofortified Banana

Name of the Institution

National Agri-Food Biotechnology Institute (NABI), Department of Biotechnology, Ministry of Science and Technology (Government of India), Sector-81, Knowledge City, S.A.S. Nagar, Mohali - 140306, Punjab, India

1. Brief Description of the Technology / Project

Micronutrient deficiencies, particularly Vitamin A, pose a significant public health challenge globally. India has the highest prevalence of Vitamin A deficiency (VAD) among South Asian nations. This deficiency is exacerbated by inadequate intake of pro-vitamin A (PVA) from vegetarian diets and poor nutrient absorption. To address this issue, the BIRAC-supported banana biofortification project was initiated in November 2012 in collaboration with the Queensland University of Technology (QUT), Australia. Prime Minister Shri Narendra Modi's visit to QUT in 2014 underscored his support for developing nutritionally enhanced banana varieties to combat malnutrition in India. As part of this initiative, the research group led by Dr. Siddharth Tiwari at NABI has developed PVA (β-carotene) enriched banana (Grand Naine cultivar) to alleviate VAD. These genetically engineered (GE) banana lines are sterile (seedless) and propagated vegetatively, hence eliminating environmental safety concerns. Additionally, inserted genes are sourced exclusively from different banana varieties, ensuring no food safety concerns.

2. Problem solved / addressed

The introduction of pro-vitamin A biofortified banana addresses Vitamin A deficiency (VAD), a major health issue in India causing preventable blindness, growth retardation, and decreased immunity, particularly among women and children. Considering bananas as a staple crop and India is the world's largest producer, this GE banana approach offers a holistic solution to improve public health.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The biofortified banana lines are currently undergoing open field event selection trials (EST) across four agro-climatic regions in India (Tamil Nadu, Assam, Gujarat, and Punjab) following regulatory and biosafety procedures. The next steps involve selecting lead and backup events, conducting multilocation Biosafety Research Level (BRL) trials, performing detailed compositional analysis, and generating additional data as per regulators for eventual commercial release.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

The biofortified banana is yet to be commercialized in compliance with GMO regulations in India. Currently, it is at the stage of multi-location event selection trials to identify the most

promising events. Further, we would like to highlight that the World's first GE banana line resistant to fungal disease has recently been approved for commercial use in Australia, based on the research efforts in QUT (https://www.qut.edu.au/study/science-news-and-events?id=192796).

5. During development and/or implementation, have you encountered any regulatory or other challenges?

We encounter the following regulatory and developmental challenges during the process of development of GE banana lines:

- **Transgene Copy Number**: Regulators prefer transgenic events with single-copy integration for subsequent developmental progress and characterization. Multi-copy transgenic events, despite their enhanced trait expression and no yield penalty, are less preferred.
- **Crop Nature, Genome Complexity, and Transgene Copy Number**: Current guidelines for selecting transgenic events based on copy number do not differentiate between seed-propagated and vegetatively propagated crops, despite the stable genomes of the latter. Adjustments are needed to account for the ploidy level of target plant species.
- **Molecular Characterization**: The requirement for molecular characterization data of multiple GE lines at early regulatory stages demands additional time and financial resources. Focusing detailed molecular analysis only on lead and backup events after assessing agronomical performance could be more beneficial.

6. Suggestions on policy / regulatory interventions for the technology being described.

a) **Tailored Guidelines**: Apply specific guidelines for selecting transgenic events in vegetatively propagated polyploid crops, recognizing their stable genomes in subsequent generations, rather than using the criteria for seed-propagated crops.

b) **Multi-Copy Integration**: Allow selection of GE events with multi-copy integration, provided developers present adequate molecular data confirming clear events without major disruption of essential genes by T-DNA integration.

c) **Trait Stability Data**: Use generation-wise trait stability and yield data to address the complexity of multi-copy T-DNA integration and the potential for post-transcriptional RNA silencing and resulting trait expression.

d) **Institutional Support**: Encourage the association and cooperation of relevant institutes to assist developers in obtaining regulatory clearance, thereby speeding up the development process and reducing the regulatory policy burden.

7. Project impact/outcomes (business/ national/ societal/ commercial aspects) of the technology/project?

The banana biofortification project, focused on enhancing PVA content through genetic engineering, holds significant potential across multiple dimensions:

- **Business**: The commercialization of biofortified banana opens new market opportunities for health-conscious consumers and drives economic growth in the agricultural sector.

- **Societal**: It addresses critical public health issues such as blindness and immune deficiencies related to VAD, especially in regions where bananas are a dietary staple.
- **National**: The project's success positions the country at the forefront of agricultural biotechnology, demonstrating its capacity to address nutritional challenges through innovative solutions.

A single biofortified banana can fulfil the recommended daily allowance (RDA) of vitamin A, equivalent to the PVA content of 20 regulars Grand Naine bananas. Hence, it would be a valuable addition to government programs like mid-day meals for school children and nutrition initiatives for pregnant women.

8. National or international collaborations associated with this technology or project?

The biofortification of PVA in banana is a multi-institutional initiative with national and international collaborations. National partners include DBT-National Agri-Food Biotechnology Institute (NABI), Punjab; ICAR-National Research Centre for Banana (NRCB), Tamil Nadu; Navsari Agricultural University (NAU), Gujarat and Assam Agricultural University (AAU), Assam. Biotech Consortium India Limited (BCIL), N. Delhi supports biosafety compliance, field trials, and data generation. International collaboration is with Queensland University of Technology, Australia. These partnerships leverage diverse expertise and resources to enhance the project's impact and success, addressing both national and global nutritional challenges.

9. What is the market potential of the technology/project in both the near term and long term?

The market potential of the banana biofortification project is substantial. In the near term, PVA biofortified banana can address immediate public health needs by combating VAD in affected regions. In the long term, the technology could achieve global adoption in banana-growing areas, enhancing food security and nutrition. Furthermore, partnerships with agricultural companies and the food industry can drive economic growth and innovation in agricultural biotechnology.

References:

- BIRAC website for banana biofortification: https://birac.nic.in/desc_new.php?id=96#:~:text=An%20agreement%20was%20signed%20between,%E2%80%9D%20on%2024th%20August%2C%202012
- Indian Patent (application number 201911054228) filed entitled "Transformed Plants Having Increased Carotenoid Level and Methods of Producing Such" Link for patent details: https://patents.vakilsearch.com/transformed-plants-having-increased-carotenoid-level-and-methods-of-producing-such/201911054228
- https://www.banana21.org/projects/biofortification
- https://www.qut.edu.au/study/science-news-and-events?id=192796

Low Glycemic Wheat

Name of the Institution

National Agri-Food Biotechnology Institute (NABI), Department of Biotechnology, Ministry of Science and Technology (Government of India), Sector-81, Knowledge City, S.A.S. Nagar, Mohali - 140306, Punjab, India

1. Brief Description of the Technology / Project

Low glycemic wheat lines were developed through the EMS mutagenesis (non-transgenic approach) in the background of a good chapatti (unleavened flat bread) Indian bread wheat variety ('C306'). Starch is a major component (~70%) of grain and comprises two components - linear glucose polymer 'Amylose' (25%-30%) and highly branched polymer of glucose 'Amylopectin' (70%-75%). The larger proportion of amylopectin in wheat flour is highly digestible in the lower intestine releasing a large amount of glucose in the blood thus increasing the glycemic response. The glycemic index (GI) of chapatti made from the common wheat flour is high. Therefore, people with diabetes and obesity have to restrict the consumption of chapatti made from the same. The high GI response of chapatti can be reduced by replacing it with chapatti made from wheat flour consisting of high amylose content. The low glycemic wheat lines developed have shown improvement in agronomical traits and reduced glycemic index in comparison to the parent wheat variety. Experimental results from the studies using in vitro and in vivo mice models showed positive results suggesting the low GI response upon feeding the mice with chapatti made from the GI-improved wheat flour. Simultaneous, studies on chapatti quality characteristics done by using the low GI wheat flour confirm the consistency of the quality parameters similar to that of 'C 306'. Therefore, the low GI wheat developed at NABI will not only provide nutritional benefits but also good processing qualities such as softness, palatability, aroma, colour, puffiness, etc. making it a commodity for easy acceptance by society.

2. Problem solved / addressed

- Low glycemic wheat.
- Proven nutritional and health benefits.
- Promote healthy gut bacteria and increase and aid in the production of small chain fatty acids (SCFA).

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The lines are ready for commercialization. BCIL, New Delhi advertised the expression of interest for its commercialization.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

The biofortified banana is yet to be commercialized in compliance with GMO regulations in India. Currently, it is at the stage of multi-location event selection trials to identify the most

5. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

The current valuation exercise calls for forecasting the future value and determining the Net Present Value (NPV) that the low glycemic wheat seeds may generate for the licensee. The approach followed in the current valuation exercise is to create a standard financial model for the opportunity (size of the market, market share, projected growth over time, etc.), then discount the same based on the risk assessment of the size of the market, market growth rate, market share of the low glycemic wheat seeds, sale price of the low glycemic wheat seeds, escalation cost, taxes, inflation etc. The detailed market evaluation and sale price were calculated and are available with BCIL, New Delhi.

6. What is the market potential of the technology/project in both the near term and long term?

Taking into consideration the market estimation and current players in the market, there are many companies manufacturing low glycemic wheat for diabetic, obese and lifestyle disease populations. Hence considering the other players in the market the market capture by NABI varieties is presumed to be 1% for two years and subsequently increasing to 1.5% and 2%.

Developing an Inventory of Iron Homeostasis-Related Genes in Hexaploid Wheat

Name of the Institution

National Agri-Food Biotechnology Institute (NABI), Department of Biotechnology, Ministry of Science and Technology (Government of India), Sector-81, Knowledge City, S.A.S. Nagar, Mohali - 140306, Punjab, India

1. Brief Description of the Technology / Project

Enhancing iron content and its bioavailability in crop plants is important to combat micronutrient deficiency including iron biofortification in humans. Although strategies could be designed for the biofortification of iron in wheat, limited progress has been made due to the lack of genetic information and molecular components involved. The genes contributing to iron uptake and mobilization were unknown in hexaploid wheat. Using transcriptomics (RNA sequencing - RNAseq)- based approach, a large inventory of genes expressed during iron deficiency responses was identified at different time points and tissues. The listed genes identified from this study serve as an important catalogue of candidate transporters and regulators of iron homeostasis response in crop plants. Currently, we are using forward and reverse genetics to explore the functionality of the candidate genes in hexaploid wheat.

2. Problem solved / addressed

The unknown candidate gene form hexaploid wheat is now reported, and the resource information has been now published as manuscripts as given with the reference Kaur, G. *et al. J Exp Bot* 70, 6141–6161 (2019) & Kaur, G. *et al. Environ Exp Bot* 208, (2023).

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The knowledge generated from the above study has been disseminated through publications and data sharing at internal forums such as conferences and meetings.

4. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

The wider impact of this work contributes towards generating novel resources to develop wheat with enhanced in iron content as well as increased bioavailable mineral nutrients grains as a step towards solving the important problems in human health. Furthermore, understanding the pathways and candidate proteins by which Fe metals accumulate in plants will enable the development of crops with better content of nutrients and also create healthier food sources. New avenues for biofortification strategies will be developed that could be certainly expanded to other crop species.

5. National or international collaborations associated with this technology or project?

One publication was shared with an international lab (John Innes Centre, Norwich, UK). This will help in developing future collaboration for defining suitable approaches for crop biofortification.

References:

- Kaur, G. et al. J Exp Bot 70, 6141–6161 (2019)
- Kaur, G. et al. Environ Exp Bot 208, (2023)

A Genomics-Assisted Synthetic Hexaploid Wheat (SHW) Gene Isolation and Pre-Breeding Platform for Improved Heat Tolerance and Sustainable Production

Name of the Institution

National Agri-Food Biotechnology Institute (NABI), Department of Biotechnology, Ministry of Science and Technology (Government of India), Sector-81, Knowledge City, S.A.S. Nagar, Mohali - 140306, Punjab, India

1. Brief Description of the Technology / Project

Through an international project (DBT-BBSRC) involving (NIAB, UK, PAU, India and NABI, India) genetic and genomic resources were developed and traits were identified that can help in better adaptation to the changing environment. 700 doubled haploid populations have been developed from BC1 of Synthetic X elite wheat crosses and evaluated for different traits related to heat stress tolerance.100 N-CSSLs have been developed Synthetics X Elite crosses and mapping of loci associated with heat stress tolerance was done. Potential material thus generated is being used in the crossing blocks at PAU for advanced cultivar generation.

2. Problem solved / addressed

Three synthetics developed from three different *Ae. tauschii* accessions X *T. durum* cultivar have been developed and identified as heat stress tolerant.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Development stage

4. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

Heat stress tolerant QTL were mapped.

5. National or international collaborations associated with this technology or project?

linternational project (DBT-BBSRC) involving (NIAB, UK, PAU, India and NABI, India)

6. What is the market potential of the technology/project in both the near term and long term?

This material will be utilized in current and future breeding programs to generate environmentally resilient varieties.

Genomics for conservation of indigenous cattle breeds and for enhancing milk yield, Phase-I

Name of the Institution

National Institute of Animal Biotechnology, Hyderabad
National Institute of Animal Biotechnology (NIAB), Opp. Journalist Colony, Near Gowlidoddy, Extended Q City Road, Gachibowli, Hyderabad, Telangana, India - 500 032

1. Brief Description of the Technology / Project

India possesses a rich diversity of cattle breeds. Unlike Western breeds, indigenous cattle are known for their adaptability to challenging environments. However, many pure-line populations have dwindled due to factors such as crossbreeding and neglect. To conserve this valuable genetic heritage, the project utilized advanced technologies like Next Generation Sequencing (NGS) to develop a High Density (HD) SNP (Single Nucleotide Polymorphism) chip. This SNP chip was then employed to genotype 40 indigenous breeds, enabling a comprehensive analysis of their genetic makeup. Additionally, the project addressed a critical research gap by developing a reference genome for Indian cattle. This pioneering effort laid the groundwork for preserving the genetic diversity of indigenous breeds.

2. Problem solved / addressed

Historically, SNP chips available in the market were tailored primarily for exotic and Western cattle breeds, showing < 50% polymorphic markers when applied to indigenous cattle populations. Addressing this limitation, our project successfully developed a HD SNP chip named INDIAGU. This chip, containing 788K markers, is specifically designed for desi (indigenous) cattle and is now the world's largest cattle SNP chip. It boasts exceptional performance, with 97.4% high-resolution polymorphic markers in populations tested within desi dairy breeds. Using this HD SNP chip, we genotyped pure lines from 40 indigenous cattle breeds, cataloguing their genetic polymorphism and architecture. The resulting genotype data serves as a reference for identifying purebred and graded animals within these desi breeds. Another significant research gap was the absence of a reference genome for indigenous cattle. To address this, we developed two platinum-standard genome assemblies. Both genomes are haplotype-resolved and exhibit remarkable contiguity, with an ungapped length exceeding 99.998%. These assemblies will serve as the definitive REFERENCE GENOMES for all future genomic research on indigenous cattle by the scientific community.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

- The project is complete. The data has been thoroughly analyzed, and the targeted product, the SNP chip (INDIGAU), has been successfully developed, tested, and officially dedicated to the nation by the Minister of Science on August 13, 2021, for use by the scientific and breeding community.
- INDIAGU is now available to the scientific and breeding community and is already being utilized in various genomic projects by us. The markers from the INDIAGU chip have also

been provided to the National Dairy Development Board (NDDB) for the development of a Low-Density (LD) chip, which will be used in the Department of Animal Husbandry and Dairying (DAHD) programs for mass-level genotyping of indigenous cattle.

- The reference genome, a critical resource for the scientific community, is publicly accessible.
- A flagship paper detailing the work carried out is nearly complete and will be submitted for publication soon. Additionally, several related papers are being prepared or have already been communicated

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

The SNP chip developed through this project is available through ThermoFischer Scientific. Its primary application is within the research and breeding communities focused on *Bos indicus* species. The technology is currently being implemented at a domestic level, with availability for Indian researchers and breeders. However, its utility extends beyond India to neighbouring countries such as Pakistan, Bangladesh, Nepal, and other regions that have populations of Bos indicus species. The chip is being used for various genomic projects, including the development of a LD chip by NDDB for mass-level genotyping of indigenous cattle in India. The scale of implementation is significant within these regions, contributing to advancements in cattle genomics and breeding programs.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

During the development of the SNP chip, we did not face any regulatory challenges. However, identifying purebred animals of each breed posed significant difficulties. Many farms and herds maintained by state governments, agricultural universities, ICAR, and private entities, which are known for preserving purebred lines, either did not permit sampling or required extensive permissions that were challenging to secure. In some cases, permission was outright denied. Additionally, the task of exploring native tracts with experienced veterinarians to collect samples presented logistical challenges that required careful planning and coordination.

6. Suggestions on policy / regulatory interventions for the technology being described

a) **Streamlined Permissions for Sample Collection**: Simplify the process for obtaining permissions from state governments, agricultural universities, ICAR institutions, and private farms for collecting samples of purebred animals. A centralized approval mechanism could be established to expedite permissions, ensuring that research is not delayed due to bureaucratic hurdles.

b) **Support for Indigenous Breed Conservation**: Implement policies that support the conservation of indigenous breeds, recognizing their genetic value. This could include financial support for conservation programs and the integration of genomic tools, such as the SNP chip, into breeding strategies aimed at preserving genetic diversity.

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

The project achieved several significant outputs:

a) **Genome Sequencing and SNP Discovery**: The genomes of 43 indigenous cattle breeds were sequenced, producing 24,241. 3 Gb of data from 176 animals. This resulted in the identification of 48.1 million SNPs across breeds using Freebayes SNP discovery.

b) **SNP Chip Development**: DBT-NIAB SNP Chip Version 1: Created with 1.29 million markers, split into two plates (DBT-NIAB Cattle-SNPchip-Ver1-A and Ver1-B) with 652,084 and 651,925 probes, respectively.

c) **IndiGau SNP Chip (Version 2)**: Featuring 788,496 SNPs, it is the world's largest cattle SNP chip, released on August 13, 2021, and represents NIAB's first publicly available product.

d) **Patent Filing**: A patent application for the high-density SNP chip was filed (Application No. 202241043917) by Sarwar Azam, Ravi Kumar Gandham, and Subeer S. Majumdar.

e) **Genotyping and Data Analysis**: Genotyping of 2,046 samples from 40 breeds was completed. Phylogenetic and genetic structures of various breeds were established, with a manuscript in preparation.

f) **Reference Genomes**: Two high-resolution genome assemblies for Sahiwal and Tharparkar were completed and are available on the NCBI portal, serving as definitive reference genomes for Indian cattle.

8. National or international collaborations associated with this technology or project? If any, please share brief details:

International Collaborations: Dr. Curt Van Tassel's Group, USDA, USA: Provided critical support in data analysis and marker identification, aiding in the development of the SNP chip.

9. What is the market potential of the technology/project in both the near term and long term?

The SNP chip has substantial near-term potential for both the scientific community and breeders. It can be utilized for Genome-Wide Association Studies (GWAS), genomic selection programs, and genotyping tasks such as identifying purebred animals, sex determination, and parentage verification. This positions the chip as a valuable tool in research and service industries. Additionally, the development of a LD chip from the HD SNP chip presents a significant opportunity. The LD chip is more affordable and feasible for large-scale genotyping, which can increase farmer accessibility for certifying animal purity and parentage. It offers a cost-effective solution for genomic selection programs in general herds, while the HD chip is suited for nucleus and well-characterized herds.

Molecular epidemiology and genomics of bovine mastitis-associated staphylococci

Name of the Institution

National Institute of Animal Biotechnology, Hyderabad
National Institute of Animal Biotechnology (NIAB), Opp. Journalist Colony, Near Gowlidoddy, Extended Q City Road, Gachibowli, Hyderabad, Telangana, India - 500 032

1. Brief Description of the Technology / Project

This was a research project where several bovine mastitis-associated pathogens were studied. As part of it, whole genome sequences of *Staphylococcus aureus* (34), *Staphylococcus chromogenes* (2), *Staphylococcus epidermidis* (4), *Staphylococcus haemolyticus* (3), *Mammaliicoccus sciuri* (1), *Staphylococcus xylosus* (2), *Staphylococcus hominis* (1), *Staphylococcus pseudointermedius* (1), *Staphylococcus gallinarum* (1), and *Mammaliicoccus lentus* (1) were submitted to GenBank.

2. Problem solved / addressed

Based on genome sequences and other data, genotype, virulence factors, and antimicrobial resistance determinants were investigated.

Whole genome sequencing of B. melitensis IND1 isolated from goat

Name of the Institution

National Institute of Animal Biotechnology, Hyderabad
National Institute of Animal Biotechnology (NIAB), Opp. Journalist Colony, Near Gowlidoddy, Extended Q City Road, Gachibowli, Hyderabad, Telangana, India - 500 032

1. Brief Description of the Technology / Project

Sequencing and annotation of genome of a B. melitensis strain (IND1) isolated from an aborted goat.

2. Problem solved / addressed

Comparative genome analysis identified 141 unique SNPs, 78 VNTRs, 51 Indels, 2 putative prophage integrations and many secreted proteins. The data may help to develop improved epidemiological typing tools and efficient preventive strategies to control brucellosis. The institute has Collaborated with Dr. Vivek Kumar Gupta (former Principal Scientist at Central Institute for Research on Goats (Indian Council of Agricultural Research, Ministry of Agriculture, Government of India), Makhdoom, P.O. Farah, Mathura, 281 122, U.P. India.

Whole genome sequencing of Leptospira isolated from cattle urine

Name of the Institution

National Institute of Animal Biotechnology, Hyderabad
National Institute of Animal Biotechnology (NIAB), Opp. Journalist Colony, Near Gowlidoddy, Extended Q City Road, Gachibowli, Hyderabad, Telangana, India - 500 032

1. Brief Description of the Technology / Project

Sequencing and annotation of genome of Leptospira isolated from cattle urine.

2. Problem solved / addressed

Comparative genome analysis of more than 300 serovars identified clade specific genes and virulence factors. Technology is used to design and test Multi-Epitope Vaccine candidate against Leptospirosis. The data will help to develop improved vaccine and diagnostics against zoonotic disease Leptospirosis.

Metagenome sequences of bovine vaginal fluid of Gir and Kankrej breed; Genotyping data of five breeds (Gir, Sahiwal, Kankrej, Tharparker, Ongole) for milk yield

Name of the Institution

National Institute of Animal Biotechnology, Hyderabad
National Institute of Animal Biotechnology (NIAB), Opp. Journalist Colony, Near Gowlidoddy, Extended Q City Road, Gachibowli, Hyderabad, Telangana, India - 500 032

1. Brief Description of the Technology / Project

To understand the microbial prospect of bovine infertility in RBS animals; to understand genetic variants association in milk yield in low and high milking yield.

2. Problem solved / addressed

The project addresses the challenge of improving milk yield in dairy animals by identifying genetic variants associated with both high and low milk production. The project is focused to identify microbial association with RBS infertility which may lead to diagnosis or treatment; identify genetic variants associated with high and low milk yield which may help to develop elite dairy animals. The collaboration is within Gujarat Biotechnology University, Gujarat (Dr. Vishal Suthar) and NDDB, Gujarat (Dr. Nilesh Nayee).

Complete genome sequence of Lumpy Skin Disease virus directly from a clinical sample

Name of the Institution

National Institute of Animal Biotechnology, Hyderabad
National Institute of Animal Biotechnology (NIAB), Opp. Journalist Colony, Near Gowlidoddy, Extended Q City Road, Gachibowli, Hyderabad, Telangana, India - 500 032

1. Brief Description of the Technology / Project

This study reports the first complete genome sequence and analysis of a pathogenic LSD virus (LSDV) from India (LSDV/208/PVNRTVU/2020) obtained by direct sequencing of a suspected clinical sample using Illumina and Nanopore sequencing technologies.

2. Problem solved / addressed

The first complete genome sequence and analysis of a pathogenic LSD virus (LSDV) from India (LSDV/208/PVNRTVU/2020) obtained by direct sequencing of a suspected clinical sample using Illumina and Nanopore sequencing technologies. The complete genome sequence of LSDV/208/PVNRTVU/2020 is 150445 bp long, codes for 156 putative genes and carries identical 2254 bp inverted terminal repeats at either ends. The unique features reported in the LSDV isolates from the recent outbreaks in Asia, namely, the insertions of 12 nucleotides in the viral G-protein coupled receptor (GPCR) and 27 nucleotides leading to duplication of 9 amino acids in the extracellular enveloped virus-specific (EEV) genes were also conserved in LSDV/208/PVNRTVU/2020. Phylogenetic analysis of the complete genome sequence of LSDV/208/PVNRTVU/2020 revealed its close relation with Kenyan strains and clustered away from vaccine strains.

Published: Putty K, Rao PL, Ganji VK, Dutta D, Mondal S, Hegde NR, Srivastava A, Subbiah M. First complete genome sequence of lumpy skin disease virus directly from a clinical sample in South India. Virus Genes. 2023 Apr;59(2):317-22. (DOI: 10.1007/s11262-023-01967-3).

Whole genome sequencing of rumen microbiome

Name of the Institution

National Institute of Animal Biotechnology, Hyderabad
National Institute of Animal Biotechnology (NIAB), Opp. Journalist Colony, Near Gowlidoddy, Extended Q City Road, Gachibowli, Hyderabad, Telangana, India - 500 032

1. Brief Description of the Technology / Project

To understand the microbiome of indigenous cattles in events of dysbiosis

2. Problem solved / addressed

Identification of key microbial communities or core microbiota is under progress. The project will broaden our knowledge about how rumen microbiota change impacts rumen functionality in terms of feed utilization and metabolic disease induction.

Sree Chitra Tirunal Institute for Medical Sciences and Technology

Name of the Institution

Medical College campus. Trivandrum 695011

The following details are of 6 projects handled in SCTIMST in paediatric neurology. The titles of all six projects are listed below:

1) Spectrum of Leukodystrophy and Genetic Leukoencephalopathy in Indian Population Diagnosed by Clinical Exome Sequencing and Clinical Utility.
2) Metabolic causes of paediatric developmental & epileptic encephalopathies (DEE)- genetic variant analysis in a south Indian cohort.
3) Clinical Utility of Proband Only Clinical Exome Sequencing in Neurodevelopmental Disorders.
4) Utility of clinical exome sequencing in progressive myoclonus epilepsy syndromes: An exploratory analysis.
5) Genotype-phenotype correlations and predictors of cognitive outcomes in Dravet syndrome & Dravet borderline phenotypes.
6) Clinical and Genetic Profile of Autism Spectrum Disorder-Epilepsy (ASD-E) Phenotype: Two Sides of the Same Coin!

1. Brief Description of the Technology / Project

For our clinical and research projects focusing on childhood-onset neurological disorders, we are utilizing Next Generation Sequencing technologies such as Clinical exome sequencing and whole exome sequencing. Additionally, we are submitting samples for chromosomal microarray, karyotyping, and Multiplex ligation probe amplification techniques. We are conducting thorough endophenotyping for most of these projects to identify genotype-phenotype correlations and the diagnostic yield of these tests. However, many cases remain undiagnosed, necessitating whole genome sequencing.

2. Problem solved / addressed

We identified the genetic causes in 61.6% of patients with genetic leukoencephalopathy, 41% with neurodevelopmental disorders, and 43.8% with metabolic causes of pediatric epilepsy.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The projects listed from 1-6 have already been published in reputed national and international journals.

4. During development and/ or implementation, have you encountered any regulatory or other challenges?

All Data were generated after the projects got IEC clearance (Institutional Ethic Committee), and samples were obtained with informed consent of parents as per IEC. IEC procedures in

SCTIMST are a well-documented and formalized protocol and regulatory challenges were not encountered.

5. Suggestions on policy / regulatory interventions for the technology being described

Treatment for certain genetic disorders such as spinal muscular atrophy and enzyme replacement therapy for Mucopolysaccharidosis are expensive, making them inaccessible to those who need them. It is important to establish mechanisms to make these treatments available to patients or to develop more affordable therapies along similar lines.

6. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

It's important to establish an accurate diagnosis, as it provides closure for the parents and prevents any further unwanted investigations. Once the diagnosis is established, we can provide a prognosis and treatment if available. This information will also help the parents make family planning decisions to prevent the birth of another offspring with a genetic disorder.

7. National or international collaborations associated with this technology or project?

Rajiv Gandhi Centre for Biotechnology (RGCB), Trivandrum was part of the project 2.

Study of Gut Microbiome in coronary artery disease

Name of the Institution

Sree Chitra Tirunal Institute for Medical Sciences and Technology Trivandrum Medical College campus. Trivandrum 695011

1. Brief Description of the Technology / Project

Cardiovascular diseases continue to pose a major public health challenge globally, with India facing a particularly high burden due to prevalent risk factors such as hypertension, diabetes, and smoking. Despite significant advancements in treatment options, the underlying mechanisms of these diseases, including heart failure, remain complex and involve multiple interacting factors, including genetic, environmental, and lifestyle elements. Growing evidence suggests that the gut microbiome plays a crucial role in sustaining overall health. The gut-heart axis (GHA), which represents the two-way communication between the gut microbiome and the heart, significantly affects cardiovascular health and the development of diseases like coronary artery disease (CAD). In this context, we propose a study aimed at thoroughly exploring the dynamics of the gut microbiome and its impact on the pathophysiology of CAD, particularly within the Indian population.

2. Problem solved / addressed

Current research largely concentrates on Western populations, highlighting a significant gap in comprehensive studies that examine the gut-heart axis (GHA) across various ethnic and geographical contexts. Previous investigations have shown that the gut microbiome of Indian individuals differs markedly from that of foreign populations, with notable variations even among different regions within India, such as North-Central and South India. Given the unique dietary, cultural, and genetic influences on gut microbiome composition, it is crucial to explore these factors, specifically within the Indian demographic, to create tailored interventions for CAD prevention and management.

This study aims to fill this important knowledge void by utilising a metagenomic approach to analyse the gut microbiome in Indian patients with CAD. Our goal is to gain insights into microbial profiles and to link microbiological and biochemical parameters with clinical indicators, thereby uncovering new information regarding the role of the GHA in CAD pathophysiology. The study will include sample collection (stool and blood) from patients and controls, including DNA isolation, biochemical analysis by mass spectrometry, metagenomic analysis by nanopore sequencing, and data analysis for clinical correlation.

Additionally, this study is vital for identifying biomarkers and paving the way for future diagnostic and therapeutic developments.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

New study - This is a preliminary study proposal that will hopefully lead to establishing new investigative modalities to detect the potential for CAD very early and encourage the adoption of preventive measures.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

This study does not directly involve any technology development. It will generate data that addresses the current knowledge gap in the study of GHA concerning CAD in an Indian context.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

Since it involves patient samples and samples from normal individuals, Institute Ethical Clearance is needed. An informed consent for taking samples is also needed.

6. Suggestions on policy / regulatory interventions for the technology being described

At the time of developing testing modalities, approvals for clinical studies in an accredited hospital will be needed.

7. Project impact/outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

The expected outcome of the proposed study is a comprehensive characterization of the gut microbiome in Indian subjects with CAD. The data generated can bring out microbial signatures with the potential for the discovery of specific biomarkers of CAD.

8. What is the market potential of the technology/project in both the near term and long term?

If risk of CAD can be detected early in life, lifestyle modification will be more easily taken up, leading to a healthy population. The testing methods developed will be extremely popular.

Real time Isothermal Nucleic acid based early diagnosis of pulmonary tuberculosis – a novel approach of developing open platform technology

Name of the Institution

Sree Chitra Tirunal Institute for Medical Sciences and Technology Trivandrum Medical College campus. Trivandrum 695011

1. Brief Description of the Technology / Project

Tuberculosis (TB) is a serious global health issue, with an estimated 10 million new cases and 1.5 million deaths each year. The World Health Organization (WHO) classifies TB as a priority infectious disease as it is so difficult to diagnose and treat. Traditional methods, such as smear microscopies, are often inconclusive because of very low sensitivity. The nucleic acid amplification test (NAAT) is a rapid TB screening test that detects TB bacteria from sputum samples in less than three hours. PCR (polymerase chain reaction)-based tests such as CBNAAT and Truenat are available to confirm positive TB cases. Though these technologies are highly accurate, they can handle only a few samples at a time and are developed as a closed system (requiring a proprietary PCR machine to run the rest).

An open platform nucleic acid amplification test, which can utilise the existing PCR testing infrastructure established during the COVID-19 pandemic, could be a game-changer in large-scale population-based screening for pulmonary TB.

2. Problem solved / addressed

The AG Chitra real-time isothermal LAMP Tuberculosis diagnostic kit has the following features:

1. It is a rapid and sensitive test that can be performed at a laboratory in less than 1 hour.
2. The test shows an accuracy of 97.71% with a sensitivity of 93.33% (95% CI 83.80-98.15) and a specificity of 98.62% (95% CI 96.51-99.62) compared to Xpert MTB/RIF. With microbial reference standard (MRS) - MGIT culture the kit showed a sensitivity of 89% (95% CI 76.9-96.45%) and a specificity of 94% (95% CI 90.77-96.44%).
3. An automated DNA isolation protocol for TB bacterium from sputum samples is also included in the technology.
4. It is cost-effective compared to that of PCR-based tests.
5. The open-platform technology for TB diagnosis will have a significant impact in early diagnosis of missing cases and achieve the TB free status by the year 2030
6. The technology has been developed indigenously and is protected by intellectual property rights.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Technology transferred to M/S Agappe Diagnostics, Kochi. CDSCO approved the kit for commercialization. ICMR validation has been initiated to bring the technology to national programme.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

Commercial implementation is ongoing.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

A faster implementation of ICMR validation would speed up the technology implementation at national level.

6. Suggestions on policy / regulatory interventions for the technology being described

A proactive technology validation at ICMR level is essential in bringing the technologies that are highly promising for early diagnosis of diseases like TB. A long winding path of regulatory approvals discourage the industry to be part of commercializing innovative technologies from academic institutions.

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

The AG Chitra RT-LAMP TB diagnostic kit is developed to achieve an affordable technology for screening a large population to “find the missing cases”. This diagnostic tool is based on the Real-Time Loop-Mediated Isothermal Amplification (RT-LAMP) protocol, which is accurate, faster, and more cost-effective. During the assay, 40 data points will be collected from each sample to detect the presence of TB bacteria accurately. This test is a nucleic acid amplification technique that is simpler than PCR. The test can be easily performed with minimal training and run on any PCR machine having fluorescence detection.

Table 1: Comparison of the accuracy of AG Chitra TB RT-LAMP kit with other WHO-approved pulmonary tuberculosis tests in adult patients.

Patient population	Xpert MTB/ RIF	Xpert Ultra	Truenat	PCR	TB-LAMP	AG Chitra RT-LAMP
Adults PTB, MRS	Se: 0.85	Se:0.90	Se: 0.73	Se: 0.93	Se: 0.80	Se: 0.89
	Sp: 0.98	Sp: 0.96	Sp: 0.98	Sp: 0.97	Sp: 0.97	Sp: 0.94
Adults PTB, SS-, MRS	Se: 0.67	Se: 0.77	Se:0.39		Se: 0.40	Se: 0.73
	Sp: 0.98	Sp: 0.96	Sp: 0.98		Sp: 0.97	Sp:0.94
Xpert MTB/ RIF					Se: 0.84	Se: 0.93
					Sp: 0.97	Sp: 0.98

PTB: pulmonary tuberculosis, Se: sensitivity, Sp: specificity, SS-: sputum smear-negative MRS: microbiological reference standard (MGIT culture); PCR: Pooled data of Abbott Realtime MTB, BD Ma MDR-TB, Hain Flurotype MTBDR and Roche Cobas MTB. Data from *WHO Consolidated Guidelines on Tuberculosis. Module 3: Diagnosis - Rapid Diagnostics for Tuberculosis Detection, 2021 Update. Geneva: World Health Organization; 2021. Licence: CC BY-NC-SA 3.0 IGO.*

The data shows that the AG Chitra RT-LAMP assay meets the accuracy of Xpert MTB/RIF and Xpert Ultra compared to the Microbiological reference standard (MGIT culture). The AG Chtira RT-LAMP kit is superior to the TB LAMP (Eikon Chemical Company, Japan) in sensitivity to the detection of pulmonary tuberculosis (see Table 1).

8. National or international collaborations associated with this technology or project? If any, please share brief details:

This technology was developed in collaboration with Kerala TB centre, Trivandrum and with RNTCP network.

9. What is the market potential of the technology/project in both the near term and long term?

Regions like India and many Southeast Asian countries bear a huge burden of tuberculosis. An affordable TB diagnostic kit has a huge market potential worth millions of dollars.

Update

CASE STUDIES FROM INDUSTRY

SPIT-SEQ Test

Name of the Industry

MedGenome Labs Limited
Electronics City Phase 1, Electronic City, Bengaluru, Karnataka 560100

1. Brief Description of the Technology / Project

SPIT-SEQ is a next generation sequencing (NGS) based, culture-free, whole genome sequencing test for tuberculosis (TB). The first-of-its-kind test is performed directly in clinical samples to identify the mutations that are associated with drug resistance – one of the most common causes of TB-linked deaths. MedGenome's SPIT-SEQ test covers all drug resistance markers, both reported and novel and gives a comprehensive report in less than two weeks. It can be performed in both pulmonary and extra-pulmonary samples. It provides drug resistance report for first and second line and newer anti TB drugs. SPIT-SEQ enables rapid and effective case management and mitigates the risk of spread of multi-drug resistance in the community.

2. Problem solved / addressed

As of March 2024, nearly 10 million people were estimated to have developed tuberculosis (TB) globally. In 2022, 1.5 million people died from it. India accounted for the highest number of TB cases in the world in 2022, representing a 27% of the global burden as per WHO. TB remains one of the most pressing public health concerns in the country. TB is curable and preventable. About 85% of people who develop TB disease can be successfully treated with a 3-6-month drug regimen. The SPIT-SEQ test leverages cutting edge innovation in genomics to give doctors the tools and insights they need to prescribe the most effective drugs quickly and accurately for specific TB patient needs, drastically reducing the time to start treatment from 6-8 weeks to just 10 days. Thus, MedGenome has developed a test that is affordable, accessible and provides faster results. Please read more at What India needs to do to eradicate TB by 2025.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Already commercialised and implemented.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

MedGenome's SPITSEQ Test is currently available in India. It is a prescription-based, proprietary test which can be availed by patients either directly through MedGenome website or diagnostic labs, on doctor's advice. It is currently available in the private sector. It can be ordered directly by individuals through the MedGenome website or through healthcare providers who partner with MedGenome. SPIT-SEQ can be offered at price as low as Rs 5000 per sample which is much lower than the cumulative cost of conventional drug susceptibility testing. In the last 12 months we have had significant increase in the number of SPIT-SEQ tests performed.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

No

6. Suggestions on policy / regulatory interventions for the technology being described

N/A

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the project?

The key impact/outcomes are outlined below:

- SPIT-SEQ is a breakthrough technology that will support efforts towards TB elimination in India as envisaged in the "Pradhan Mantri TB Mukt Bharat Abhiyan" (PMTBMBA) launched by GoI in September 2022
- The test has allowed healthcare leaders to detect novel mutations associated with DR TB, providing valuable insights that inform adjustments to drug regime or dosage to improve patient outcomes
- On World TB Day in March 2023, Dr. Sameer Lote, Director & Consultant Panacea Clinic in India recommended that SPIT-SEQ test should be regarded "gold standard" for drug resistance testing. He mentioned that it has "revolutionized" treatment for DR TB
- Rapid, reliable, and increasingly affordable WGS technologies can now guide all components of TB control: diagnosis, treatment, surveillance, and source investigation

8. National or international collaborations associated with this project?

Details of partnerships:

- MedGenome has worked closely with government agencies, non-profit organizations, and other stakeholders to develop comprehensive strategies for TB prevention, diagnosis, and treatment. The SPIT-SEQ test has received recognition from trusted experts and leaders in the healthcare industry
- MedGenome has partnered with an NGO in Mumbai to incorporate SPIT-SEQ in the diagnostic algorithm

9. What is the market potential of the project in both the near term and long term?

There is tremendous market potential for the test in both the near term and long term. India's alarming disease burden statistics makes it even more imperative to identify and diagnose TB at the right time. MedGenome's strategy has always been to adopt the needs of the market in areas where we need swift action to control the incidence of certain diseases through the diagnosis at the right time. The SPIT-SEQ test is an initiative in the same direction. Over the years we expect the WHO and Revised National Tuberculosis Control Programme (RNTCP) endorsement of NGS based drug resistance tests directly in clinical samples of TB patients. The endorsement will change the algorithm followed for diagnosis and treatment of DR TB. Please see below article for more insights Betting on hi-tech and the whole genome to beat TB

ExomeMax

Name of the Industry

MedGenome Labs Limited
Electronics City Phase 1, Electronic City, Bengaluru, Karnataka 560100

1. Brief Description of the Technology / Project

ExomeMax is a cost-effective approach for genetic testing that has the power to detect genetic variants responsible for many diseases. It is a one-stop comprehensive evaluation of different kinds of genetic variants and helps in reducing the need for multiple genetic tests and the time to reach a diagnosis. Identification of the causal variant allows clinicians to offer tailored treatment and management options to the patient. Further, it also allows clinicians to inform patients about the risk of passing the disease to future generations and to make informed reproductive decisions.

At 20x coverage ExomeMax has ~4.5% better coverage than off-the-shelf exomes, and with improved coverage of exomes, the diagnostic yield can be increased by 30%.

2. Problem solved / addressed

Inherited diseases are a major cause of childhood hospitalization, ICU admission, mortality, and healthcare costs. 7,000+ rare diseases affect 3.5-5.9% of the world's population i.e., ~300 million people worldwide. Genetic diseases have progressively been acknowledged as an important public health issue, greatly impacting the lives of people with such conditions, their families, healthcare systems and society. The cost, accuracy, and effectiveness of genetic testing along with turnaround time become critical in these cases. EXOMEMAX is a comprehensive test which was introduced in India in 2022. This customized test has been validated and standardized at par with industrial clinical standards. The test offers comprehensive evaluation of variants improving the diagnostic outcome. Reports can be made available in 10-14 days which becomes crucial to many critical cases. Further clinicians can offer tailored treatment based on the diagnosis.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Already commercialised and implemented.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

Domestic (successfully introduced at a pan-India level).

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

Regulations with respect to genetic testing in India are limited.

6. Suggestions on policy / regulatory interventions for the technology being described

N/A

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the project?

Key impact / outcomes have been outlined below:

- The test has helped doctors provide appropriate treatment to the patient. For example, ExomeMax helped a very senior doctor at the Institute of Medical Genetics and Genomics at Sir Ganga Ram Hospital, New Delhi to diagnose correctly as the high-throughput sequencing capabilities of ExomeMax pinpointed a subtle mutation nestled within a specific exome and helped the doctor with thorough investigation
- A project was specially designed with MedGenome's clinician collaborator to identify disease causal variants in paediatric epilepsy, who are resistant to anti-seizure medications. Following the ethical committee approval (n=100), clinically well characterized cases were evaluated, and disease causal variants were identified, and this enabled appropriate treatment. This is one of the first genetic studies on refractory epilepsy from India.

8. National or international collaborations associated with this project?

Our Collaborations, whether or not with respect to this project, are covered by confidentiality obligations.

9. What is the market potential of the project in both the near term and long term?

The Exome sequencing market is poised to grow from ~USD 420 million in 2022 to ~USD 1.5 billion by 2030, as per various market research reports.

HRDTrack

Name of the Industry

MedGenome Labs Limited
Electronics City Phase 1, Electronic City, Bengaluru, Karnataka 560100

1. Brief Description of the Technology / Project

Homologous Recombination Repair (HRR) is one of the key mechanisms which cells harbour in repairing double strand breaks. As can be noted in different solid cancers, alterations in key regulators of HRR pathway mainly BRCA1/2 can lead to deficiency in HRR pathway (HRD) causing genome instability. Clinical findings from ovarian cancer patients with HRD show sensitivity towards PARP inhibitors (PARPi). HRD status is used as a biomarker for targeted therapy. Many commercial assays are currently available for predicting HRD status but a cost effective solution with in-depth insights is still a challenge.

2. Problem solved / addressed

To make the HRD solution more accessible with deeper insights MedGenome has developed efficient and cost-effective end-to-end DNA-based solution HRDTrack. It evaluates HRD status based on quantitative genome aberration score a measure of genomic changes from high quality SNP markers representative of multiple ethnicities and variants from BRCA1/2 genes. Assay has been validated on a large number of clinical samples (N=170) with an accuracy of 97.05%. Overall, the assay provided one of the best performance metrics in the industry with minimal assay failure rate on clinical samples.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Already commercialized and implemented

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

Global availability

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

No

6. Suggestions on policy / regulatory interventions for the technology being described

N/A

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the project?

The key impact/outcomes are detailed below:

- Cost effective solution for ovarian cancer patients
- 50% of High-Grade Ovarian Cancer (HGOC) patients are HRD positive but BRCA negative, such patients can be checked for HRD status through this test and they can get benefit from PARP inhibitors - This test can be easily accessible. It is efficient and adequately validated to give accurate results (with >97% sensitivity)

8. National or international collaborations associated with this project?

Our Collaborations, whether or not with respect to this project, are covered by confidentiality obligations.

9. What is the market potential of the project in both the near term and long term?

Quite high potential for further market penetration. The current global market size for HRD testing is around USD 1.2 billion (as per various sources as well as

MedGenome estimates) MedGenome website: https://diagnostics.medgenome.com/

Liquid Biopsy: Promising Diagnostic Tool in Clinical Oncology

Name of the Industry

MedGenome Labs Limited
Electronics City Phase 1, Electronic City, Bengaluru, Karnataka 560100

1. Brief Description of the Technology / Project

A liquid biopsy is used to detect genomic biomarkers in circulating tumour DNA (ctDNA) which is shed into the bloodstream from dying tumour cells. It is a beneficial alternative in the absence of tumour biopsy, can be used as complementary to tumour biopsy to understand complete mutation profile of the disease or reflex to tumour biopsy to monitor the disease after treatment and determine acquired resistance in specific clinical situations and offer significant benefits. Liquid Biopsy based mutation profiling proves to be a powerful tool to monitor the treatment response, predict relapse and identify acquired resistance mechanisms. In EGFR mutated non-small cell lung cancer patients, tyrosine kinase inhibitors are used for targeted treatment but after a certain period of time, the disease becomes unresponsive to these drugs and relapse occurs. Liquid Biopsy test helps to identify the specific changes (mutations) that may have led to the resistance to therapy and further guides in changing the treatment.

2. Problem solved / addressed

Liquid biopsy is a breakthrough that will change the face of cancer treatment in India. In India, the number of cancer cases reported annually is set to rise from 14.6 lakh in 2022 to 17.3 lakh in 2025. Unfortunately, a whopping 75-80% of those diagnosed are estimated to have advanced stage tumours, making treatment challenging and the outcomes less favourable. With cancer, timing is everything. Detecting cancer at Stage 1, translates to an 85% chance of a cure while with Stage 3 cancer, that drops to about 30%. The rising incidence of cancer has made preventive diagnostics and accurate screening for cancer the need of the hour. Availability of cost-effective liquid biopsy tests would be a game changer under these conditions.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Already commercialised and implemented.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

Domestic (available in India). The liquid biopsy test was first launched by MedGenome in 2018 and has already yielded tremendous results. The laboratory-developed liquid biopsy test offered by the company meets global standards (CAP-accredited and well-validated) while being developed for the Indian market. The test is offered in India at a much lower price when compared to similar tests in the US and EU to ensure affordability for a wider population base.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

No

6. Suggestions on policy / regulatory interventions for the technology being described

N/A

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the project?

The key impact/outcomes are detailed below:

- Liquid biopsy test is a non-invasive technique
- Liquid biopsy offers a valuable alternative to invasive tissue biopsy testing (which can be inadequate, expensive, less accessible, and difficult to repeat for disease surveillance)
- Liquid biopsy-based mutation profiling proves to be a powerful tool to monitor the treatment response, predict relapse and identify acquired resistance mechanisms
- Physicians can significantly improve treatment outcomes for patients with lung cancer using liquid biopsy, which will open the door to more effective and precise oncology procedures. Lung cancer is on the rise in India (5.9% of all cancer cases are lung cancer, making it the country's fourth most common kind)
- MedGenome offers the test in India at a much lower price than in the US to make it more affordable

Please also refer below articles:

Lung Cancer Management: Why You Need to Know About Liquid Biopsy?

Know The Role Of Liquid Biopsy In Precision Medicine In Lung Cancer

8. National or international collaborations associated with this project?

MedGenome has collaborated with the Tata Memorial Hospital (a premium Oncology hospital in India) for liquid biopsy testing in lung cancer cases. MedGenome has also collaborated with AstraZeneca on homologous recombination repair (HRR) testing

9. What is the market potential of the project in both the near term and long term?

Liquid biopsy is emerging as the best alternative or complementary option to molecular testing using tissue biopsies. Hence, it is expected to witness substantial growth in India both in the near term and long term.

MedGenome's Research Paper on Liquid Biopsy:
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5757203/

Please also refer below article:
Is Liquid Biopsy the future "Gold Standard" for cancer detection?

Predictive Health and Precision Medicine for Indian Population using Imputation aware, population specific high throughput Microarray genotyping

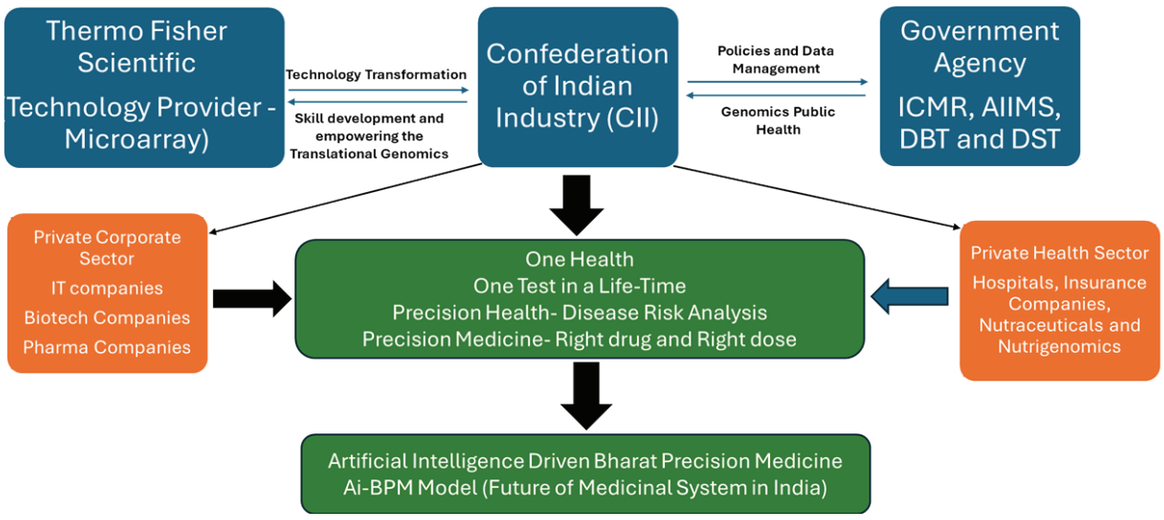
Name of the Industry

Thermo Fisher Scientific India Pvt Ltd.
Thermo Fisher Scientific India Pvt Ltd., 403-404, Delphi B Wing, Hiranandani Business Park, Powai, Mumbai 400076.

Objectives:

1. To develop predictive disease risk analysis by screening 1Lakh the Indians distributed across different geographical regions using Microarray Technology
2. Corroborate the India specific Pharmacogenomic variations and develop precision medicine model to provide right drug at right dose for the precision medicine.
3. To develop large India population GWAS data for the future Surveillance Studies
4. To develop Artificial Intelligence based Precision medicine to serve the "One Health" in the public health stream.

Figure 1: Ai-BPM model- Future of medicinal system in India



1. Brief Description of the Technology / Project

Predictive Genomics is a powerful capability to help predict disease risk and understand drug response to improve health outcomes and manage costs. The predictive health approach demands a high throughput, reliable, consistent genotyping technology at an affordable price for Indian population. Axiom Microarray is the well-established method for direct genotyping

of 1,000s to 100,000s of variants per sample at highly scalable cost and throughput. Millions of genotypes can be imputed from genome-wide array data "imputation-aware population specific" Axiom microarrays are designed for optimal genome coverage and imputation accuracy. The Applied Biosystems Axiom PangenomiX Array is a human genotyping research array designed for whole-genome imputation with diverse and global population coverage. It is a valuable research tool for human genomics, including applications such as genome-wide association studies (GWAS), population health initiatives, polygenic risk score research and development, and clinical research for trials in drug discovery. The Axiom PangenomiX Array can scan the whole genome from as little as 100 ng genomic DNA. It can enable target single nucleotide polymorphism (SNP) identification, copy number variant analysis, human leukocyte antigen (HLA) typing and more in a single, cost-effective assay with ready-to-use data analysis.

2. Problem solved / addressed

Predictive Genomics is a powerful capability to help predict disease risk and understand drug response in order to improve health outcomes and manage costs. The Microarray Genomic data enable researchers to improve health outcomes and manage costs in the following ways:

1. Stratify population to high-risk individuals and
2. Tailor prescription drugs based on person's biology.

Thermo Fisher has the capabilities, skills, experience, and vision to achieve these goals and to work closely with all other essential partners to ensure the overall success of the program. We also have the broad network of KOLs, thought leaders, all of which strengthen the efficiency, flexibility, know-how, and capability to enable the India to establish a successful program to manage NCDs. Thermo Fisher has been at the forefront of multiple programs involving screening for disease risk, pharmacogenomics deployment and diagnostic applications. Learnings from example highlighted below can help build a health platform that can be deployed at-scale. The technology has been deployed in several large-scale precision medicine initiatives with the goal of identifying risk factors for common diseases and preventative medicine.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Axiom Microarray is the most widely used technology for the GWAS analysis and stablish the polygenic risk score for the diseases that are prevalent in given a region. Many cohort studies on Indian population are evident to delineate the population diversity, key associated markers for the various diseases like diabetes, coronary heart disease etc. However, a massive population screening in different metro and tier 1 or 2 cities is required for understanding the population heterogeneity and identify the highly associated markers for the various disease. To implement such programs, there is a need of joint efforts of National Government agencies and private sector organizations especially pharma sector.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

Microarray has been commercialized for the past few years and has been used in India as well as Globally by multiple Reference Labs, Cancer Hospitals, Regional Cancer Centres, Research institutes etc. for various applications.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

Predictive Genomics is a powerful capability to help predict disease risk and understand drug response to improve health outcomes and manage costs. Predictive Genomics requires a holistic ecosystem approach for success.

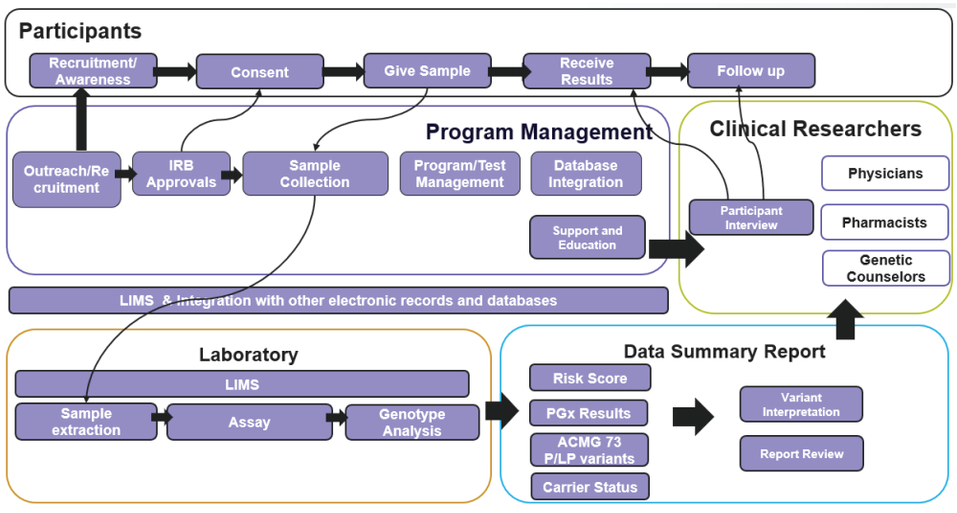
In brief, we propose a multi-pronged approach in our vision:

1. Sample recruitment and Electronic Health Record (EHR) integration strategy – The first step involves implementing sample recruitment strategies and EHR strategies. National screening programs require deploying educational material and appropriate training for physicians, nurses and participants in participating in health screening. Educational material needs to be deployed at each of the sites where participants in a national screening program can sign up. Electronic health integration of clinical records needs deployment strategies to integrate upstream clinical and downstream recommendations with participant records through systems such as Cerner or Epic systems.
2. A national program should involve a first step that includes deploying a Multiple-Disease Risk Screening Assay (MDSA) using cost-effective microarrays to help identify at risk individuals for inherited disease and inappropriate polypharmacy. The goal of this step is to screen for risk across multiple disease areas.
3. Return of screening results to participants with an appropriate genomic consultation (could be optional).
4. Implementation of Data management and machine learning for the future precision medicinal application demand Genomics and Bioinformatics Skill and Talent development.
5. Creating Awareness Programmes in the Hospitals and Pharma sector for the precision medicine and avoid adverse drug reactions.

6. Suggestions on policy / regulatory interventions for the technology being described

The major elements of a typical Predictive Genomics program implementation in screening involves the multiple sub-components that are shown in the illustration below figure 2.

Figure 2: Genomic Program Implementation Schematics



The program includes:

1. An entity responsible for the program management is at the centre of overseeing the program, participant recruitment and sample collection.
2. Integration with existing databases or electronic records may be a requirement.
3. The laboratory generates genotyping data and processes samples at different government designated or CII governed centralized genomics facility.
4. The data summary report provides the findings in a form appropriate for clinical researchers. In case the results are provided to the participants, follow up or a participant interview is included.

The implementation of such a screening program involves complete genomic ecosystem including

1. Sample collection strategy
2. sample extraction and storage
3. Laboratory workflows and infrastructure
4. Whole-genome content on arrays
5. Reporting
6. Integration with EHR

The Figure1 on Ai-BPM model- Future of medicinal system in India also highlight the need of collaborative efforts of National Government Funding Agencies like ICMR, AIIMS, DBT and DST to fund massively and support data generation.

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

Business Impact: Economic evaluation has demonstrated that screening using Polygenic Risk Scores (PRS) is a dominant option compared to usual screening methods, for identifying individuals that are at a higher risk from a variety of NCDs including cardiovascular disease1, breast-cancer2, diabetic nephropathy3 etc. For example, coupling polygenic risk scores (PRS) with traditional risk factors is a promising, cost-effective method for targeted statin treatment in the prevention of coronary heart disease. For coronary artery disease, compared with the use of traditional risk factors only, the optimal use of polygenic risk score data in a population of 100,000 would decrease the total costs of a preventative intervention program by approximately $300,000 in a 10-year follow-up period, while increasing health outcomes by 1.7 quality-adjusted life-years (QALYs)1.

National Impact: This massive microarray GWAS screening data will help in stratifying the high-risk disease associated population in the early stages of an individual's life or even before the rise of clinical symptoms. Thus, with this technology one could make paradigm shift of current sick care treatment to preventive care treatment. In the future it is an essential factor to implement an AI based tools and solutions of the precision health and provide healthy life using genomics data generated by microarray. The implementation of this technology will help in1. Understand genetic disease risk for common diseases and adverse drug effects in Indian

population. 2. Make individual health care system with personalized health care plans and create EHR for all. 3. Improve health outcomes and reallocate health care spend.

Commercial Impact: Microarray remains the best-established technology of choice for the genome-wide imputation plus direct genotyping to be scaled from small to very large cohorts with well-established and low complexity assays and data analysis at an affordable price. A single microarray test with multiple application performed once in a life span of an individual can help to manage the healthy status and to have precise tailored medications in the future, thereby reduce the overall burden on the health expenses.

8. National or international collaborations associated with this technology or project?

1. **Taiwan Precision Medicine Initiative (TPMI)**[4,5,6]: TPMI is a partnership between Academia Sinica and 12+ medical centers to bring genetic information generated on Axiom Genotyping Solution into clinical practice. The platform deployed at 5 hospitals and genotyping center in Taiwan have genotyped 300,000+ of 1 million participants. TPMI aims to optimize patient care by preventing drug side-effects, early cancer screening for those at high risk, and encouraging life-style changes for those at risk for other serious diseases.

2. **India Genome Project (IGP)**[7]: IGP is a national genome project funded by the Department of Biotechnology, which aim to delineate the India population diversity and identify the polygenic research score for high prevalent non-communicable diseases like neuromuscular disease, diabetes, hypertension, cardiac disease etc. The Central for Brain Research, Indian Institute of Science (CBR) is one of the premier nodal site for massive genotyping and cataloguing south Indian population using our Axiom Microarray. The CBR scientists have accomplished more than 15000 south Indian samples genotyping and focusing to establish polygenic risk score for the neuromuscular diseases like Alzheimer's disease, Schizophrenia, Perkinoson's disease and stroke etc. The aim is to early prediction of these neuromuscular disease in an healthy individual and optimize the health care by implementing good life-style practice and food.

3. **Million Veteran Project (MVP), USA**[8,9]: MVP is a national program funded by the U.S. Department of Veterans Affairs Office of Research & Development. The goal of MVP is to partner with Veterans receiving their care in the VA Healthcare System to study how genes affect health. MVP is now piloting return of results to participants through their clinical program called Million Veteran Program – Return of Actionable Results (MVP-ROAR) Study . MVP-ROAR is a randomized controlled trial of immediate vs. delayed (after 6 months) return of medically actionable, clinically confirmed genetic testing results. Participants that have been identified at risk of developing a condition requiring intervention go through follow-up process that involves confirmation with a separate technology. Disclosure of clinically confirmed medically actionable genetic testing results and post-test genetic counselling session.

4. **UK Biobank Cohort**[10]: UK Biobank is one of the largest GWAS based Biobank studies in the world. This study genotyped over 450,000 European ancestry participants using Axiom arrays and Affymetrix BiLEVE Array. More than 100s of research studies are published using the Axiom UK Biobank datasets. Axiom microarrays are used to estimate p.C282Y associations with brain MRI features plus incident dementia diagnoses during follow-up in a large community cohort. Male p.C282Y homozygotes had more brain iron deposition, smaller specific gray matter volumes, and increased incidence of dementia compared to

those without HFE mutations. Overall, these results suggest that p.C282Y homozygosity is a significant risk factor for dementia in men with European ancestries.

5. **FinnGen Project's role in epilepsy, drug adherence studies**[11]: The FinnGen study brings together 500,000 samples from the Finnish nationwide network of biobanks that was built with our solution. The study is sparking new national achievements in biomedicine.

8. What is the market potential of the technology/project in both the near term and long term?

Non-communicable diseases (NCDs) such as diabetes and hypertension have become the leading cause of death and suffering, contributing to 65 per cent of deaths in India over the past three decades12. Post covid the number has gone up significantly. The projected cancer burden in India for 2021 was 26.7 million and expected to increase to 29.8 million in 2025. The highest burden was in the north (2408 per 100,000) and northeastern (2177 per 100,000) regions of the country and higher among males. More than 40% of the total cancer burden was contributed by the seven leading cancer sites — lung (10.6%), breast (10.5%), oesophagus (5.8%), mouth (5.7%), stomach (5.2%), liver (4.6%), and cervix uteri (4.3%). India has additional burden of genetic diseases in some populations due to consanguinity, An estimated 495,000 infants with congenital malformations, 390,000 with G6PD deficiency, 21,400 with Down syndrome, 9,000 with beta-thalassaemia, 5,200 with sickle cell disease, and 9,760 with amino acid disorders are born each year. The prevalence of late-onset multi-factorial disorders (including coronary artery disease, hypertension and psychiatric disorders) is also large 13. Due to inadequate diagnostic, management and rehabilitation facilities, the burden of these disorders is greater than in Western countries. India needs strong cost-effective solution to identify/screen its population to understand disease burden to improve healthcare of its people.

India can capitalize on a unique and historical convergence of need, knowledge, technology, and support to improve the health and wellness of its' people. We propose herein a Microarray Predictive Genomics solution focused on genomics tests that have clinical utility, for the population level screening and establish the precision medicine. Furthermore, the proposed plan will engage all stakeholders, industrial and academic partners, clinicians, and patients, and will also improve future participatory and preventive medicine through the active involvement of patients and individuals at large.

NGS (Next Generation Sequencing) systems

Name of the Industry

Thermo Fisher Scientific India Pvt Ltd.
Thermo Fisher Scientific India Pvt Ltd., 403-404, Delphi B Wing, Hiranandani Business Park, Powai, Mumbai 400076.

1. Brief Description of the Technology / Project

Next-generation sequencing (NGS) utilizes massively parallel sequencing to generate thousands of megabases of sequence information per day, opening doors to new research studies that were once difficult to accomplish in a practical manner. Powered by semiconductor chips, Ion Torrent next-generation sequencing technology helps to implement a fast and simple workflow that scales to your clinical research needs across multiple applications including inherited diseases, oncology, infectious diseases, reproductive genomics, human identification, agrigenomics and more.

2. Problem solved / addressed

Ion Torrent NGS enables analysis and discovery of multi-biomarker types (fusions, insertion/deletions (indels), single nucleotide variants, and copy number variations) using scalable sequencing with optimized bioinformatics and reporting solutions designed for clinical research in oncology.

Our complete NGS solutions are uniquely suited to understand how the combination of genetics and environment influences development of complex diseases such as autoimmune disorders, neurodegenerative diseases, and many others. Ion Torrent NGS solutions can also be used for Expanded carrier screening and preimplantation genetic testing for positive impact on families around the world.

Ion Torrent NGS solutions can help uncover microbial diversity, study pathogen outbreaks and identify mutations that may be associated with antibiotic resistance.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Since last 7 to 8 years, Ion Torrent NGS systems are being used worldwide for various applications in the field of Oncology, Reproductive Health, Infectious diseases and Inherited disorders.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

NGS has been commercialized for the past few years and has been used in India as well as Globally by multiple Reference Labs, Cancer Hospitals, Regional Cancer Centres, Research institutes etc. for various applications.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

Cost: Biggest challenge of adopting or implementing NGS in India is the cost involved in performing an NGS test. Due to lack of insurance coverage and expensive out of pocket expenditures the NGS test adoption is limited to only a small percent of eligible patients.

Lack of trained manpower: NGS implementation across labs requires trained resources who can help bring this technology to Tier 2/Tier 3 cities.

Data privacy: NGS generates massive amounts of data and results that vary in terms of known clinical relevance. It is important to determine appropriate processes for protecting, managing and communicating the data.

6. Suggestions on policy / regulatory interventions for the technology being described.

India holds a huge potential to be one of the biggest genomics markets based on NGS technology due to its rich genetic diversity. Healthcare diagnostics is currently the focus of various industry players. Promoting public-private partnerships, regulated by policies, human resources with the right skill set and training can push India to the front on the global stage.

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

Societal: Sequencing of the SARS-CoV-2 using NGS has helped to develop vaccines in record time, track the emergence of viral variants and invest in timely strategic plans to control the spread.

National: Having Indian population specific genomics data will ease the process of developing companion diagnostics and personalised medicine.

Commercial: NGS can help in early cancer detection, interrogate multiple biomarkers simultaneously to provide personalized treatment, screen populations for inherited disorders, check spread of pandemics by tracking emergence of known and novel variants. The above utilities can help in reducing overall healthcare expenditures significantly.

8. National or international collaborations associated with this technology or project? If any, please share brief details:

Oncomine Assay on Ion Torrent NGS systems are used globally by large oncology clinical trials such as NCI-MATCH, LC-SCRUM and Myelo-MATCH. More details on below links.

https://ascopubs.org/doi/10.1200/JCO.2023.41.16_suppl.3047,

https://www.oncomine.com/assays

https://cancerletter.com/in-brief/20201002_5l/

Thermo Fisher Scientific has partnered with multiple Pharma companies globally for developing Oncomine based NGS Companion Diagnostics (CDx) solutions which are approved by US-FDA. More details on link - https://www.oncomine.com/ngs-for-pharma

In 2023 Thermo Fisher Scientific Inc. and Pfizer entered into a collaboration agreement to help increase local access to next-generation sequencing (NGS)-based testing for lung and breast cancer patients in more than 30 countries across Latin America, Africa, the Middle East and Asia where advanced genomic testing has previously been limited or unavailable. Access to local NGS testing can help to provide faster analysis of genes associated, empowering healthcare providers to select the right therapy for that individual patient.

https://hcn.health/hcn-trends-story/thermo-fisher-scientific-pfizer-partner-to-expand-localized-access-to-next-generation-sequencing-based-testing-for-cancer-patients-in-international-markets/

9. What is the market potential of the technology/project in both the near term and long term?

Every year 1.4 million new cancer cases are detected in India. Currently only 8 to 10% of these cases can afford an NGS test for molecular profiling. Wide scale adoption of NGS through reduced cost per test, trained manpower and increased awareness on clinical utility of these tests can help improve accessibility of NGS for larger populations.

NGS can also play an important role in predicting risk probability for inherited cancers which constitute 10% of the total cancer cases identified each year.

In India an estimated 495,000 infants with congenital malformations, 390,000 with G6PD deficiency, 21,400 with Down syndrome, 9,000 with β-thalassaemia, 5,200 with sickle cell disease, and 9,760 with amino acid disorders are born each year. NGS can play an important role in reducing the burden of genetic disorders in India.

https://karger.com/cmg/article-abstract/5/3/192/67699/The-Burden-of-Genetic-Disorders-in-India-and-a?redirectedFrom=fulltext

Digital PCR system

Name of the Industry

Thermo Fisher Scientific India Pvt Ltd.
Thermo Fisher Scientific India Pvt Ltd., 403-404, Delphi B Wing, Hiranandani Business Park, Powai, Mumbai 400076.

1. Brief Description of the Technology / Project

The Applied Biosystems QuantStudio Absolute Q Digital PCR System is a plate-based digital PCR (dPCR) platform powered by proprietary microfluidic array plate (MAP) technology that enables all the necessary steps for dPCR —compartmentalizing, thermal cycling, and data acquisition—to be conducted on a single instrument. The dPCR workflow is identical to the qPCR workflow to improve ease of use, minimize hands on steps, and maximize consistency across multiple applications in oncology, reproductive health, inherited disease, infectious disease, wastewater monitoring & cell & gene therapy workflow.

2. Problem solved / addressed

QuantStudio Absolute Q Digital PCR System addresses the challenges of multi instrument workflow by providing Single fully automated instrument workflow thus helps reduce errors and manual input steps. System also minimizes wasted sample volume and provides industry leading consistency.

Digital PCR enables quantitative detection of rare sequences in Cancer and Disease research. System provides flexible as well as cost effective solution in liquid biopsy especially for disease and therapy monitoring. It also addresses the need of Environmental surveillance and wastewater-based epidemiology used to monitor public health threats by testing for specific environmental DNA (eDNA) and RNA (eRNA) which are found in low copies.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Since last 3 years, Quantstudio Absolute Q systems are being used worldwide for various applications in the field of Oncology, Reproductive Health, Infectious diseases, Inherited disorders & Cell & Gene Therapy.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

Quantstudio Absoloute Q digital PCR system has been commercialized for the past few years and has been used in India as well as Globally by multiple Reference Labs, Cancer Hospitals, Diagnostics chains & Research institutes etc. for various applications.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

Awareness: One of the challenges of adopting or implementing Digital PCR in India especially in Oncology is the awareness of the technology among clinicians.

Kits: Implementation of Digital PCR across labs requires various validated kits in oncology which can help bring this technology to Tier 2/Tier 3 cities especially in Oncology.

6. Suggestions on policy / regulatory interventions for the technology being described.

India holds a huge potential to be one of the biggest genomics markets based on its rich genetic diversity. Healthcare diagnostics is currently the focus of various industry players. Promoting public-private partnerships, regulated by policies, human resources with the right skill set and training as well as can push India to the front on the global stage.

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

Societal: Environmental surveillance and wastewater-based epidemiology are used to monitor public health threats by testing for specific environmental DNA (eDNA) and RNA especially for SARS CoV2 to track the emergence of viral variants and invest in timely strategic plans to control the spread.

National: By utilizing digital PCR system for disease monitoring using liquid biopsy based solutions in Oncology, a cost effective solution in disease monitoring, will improve the process of personalised medicine and patient management.

Commercial: Digital PCR can help in early cancer detection as well as disease monitoring by using different assays in Oncology, check spread of pandemics by tracking emergence of known and novel variants through waste water monitoring as well as clinical surveillance. The above utilities can help in reducing overall healthcare expenditures significantly.

8. National or international collaborations associated with this technology or project? If any, please share brief details:

Multiple 3rd party kit manufacturers/developers are utilizing Quantstudio Absolute Q digital PCR system to develop and launch new tests in Oncology, Reproductive Health as well as other applications.

9. What is the market potential of the technology/project in both the near term and long term?

Every year 1.4 million new cancer cases are detected in India. 8 – 9% of these cases are from Lung Cancers & Breast Cancers. Wide scale adoption of Digital PCR in therapy monitoring through liquid biopsy solutions across different kinds of cancers can help improve accessibility of the technology for larger populations in Tier2/3 cities.

Digital PCR can also play an important role in clinical surveillance or wastewater surveillance for early detection of outbreaks thus assisting public health departments in well planned strategy deployment.

DNA Capillary Electrophoresis (CE)/Genetic Analyser

Name of the Industry

Thermo Fisher Scientific India Pvt Ltd.
Thermo Fisher Scientific India Pvt Ltd., 403-404, Delphi B Wing, Hiranandani Business Park, Powai, Mumbai 400076.

1. Brief Description of the Technology / Project

Applied Biosystems genetic analysers are a trusted standard for Sanger sequencing and fragment analysis by capillary electrophoresis (CE). This simple and most time efficient technology uses fluorescently labelled oligonucleotide primers to seek out specific DNA regions to conduct targeted sequencing of various genes for many different usage-Clinical, Research, diagnostics, manufacturing, Forensics. The technology adds simplicity, scalability, speed and most importantly flexibility to genomics workflow, enabling user to analyse most difficult samples with complete confidence, whether you are running a few samples or need larger scale options. Analysis of nucleic acids using capillary electrophoresis (CE) is performed via two methods: Sanger sequencing and fragment analysis. Both provide simple, sample-to-answer workflows for highly accurate sequence interrogation and fast turnaround time. Sanger Sequencing: Gold-standard technology for accurate sequence determination with single-base resolution. Ideal for targeted sequencing and confirmation analysis. Fragment Analysis: Simple, most time efficient 4-step method for multiplexed detection of pathogens, variants, SNPs or size analysis.

CE technology helps to implement a fast and simple workflow that scales to your clinical research needs across multiple applications including inherited diseases, oncology, infectious diseases, reproductive genomics, human identification, Agrigenomics, Gene editing, Vaccine QC and more.

Applied Biosystems Genetic Analysis Systems | Thermo Fisher Scientific - IN

2. Problem solved / addressed

This technology has multiple uses supporting multiple sectors enabling analysis for multi-biomarker types (fusions, insertion/deletions (indels), single nucleotide variants, and copy number variations):

1. **Infectious Disease**: Microbial Identification, Virus and Bacteria Strain identification, Drug resistance
2. **Inherited diseases**: Detecting genetic variations in inheritable diseases with high incidence and disease burden (eg. Haemoglobinopathies, Muscular dystrophies), Rare and undiagnosed genetic disorders (RUGD).
3. **Oncology**: Single gene or small panel testing for various different types of cancer, methylation analysis
4. **Human Forensics**: Solving crime through DNA, Establishing databases for offenders/ Convicts, Missing persons.

5. **Clinical Research**: Vaccine manufacturing & QC; plasmid sequencing, supporting gene editing technologies for different clinical research projects and rare inherited disease studies like Duchenne muscular dystrophy and MECP2 duplication syndrome, cell line authentication, quality control of stored human tissues and fluids,and assessment of the nature of known mixtures.

6. **Agrigenomics**: Marker Identification and screening for crops, animals with better characteristics like climate resistance, insect resistance, high yields.

Sanger Sequencing and Fragment Analysis by CE | Thermo Fisher Scientific - IN Human Identification | Thermo Fisher Scientific - IN

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Since last 3 decades, Sanger sequencing and Fragment Analysis using CE technology is being used worldwide for various applications in the field of Clinical Research, Inherited Disorders, Oncology, Reproductive Health, Infectious diseases, and Academic Institutes, Agri & Animal Research, Human Forensics.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

CE has been commercialized for the past many years and has been used in India as well as Globally by multiple Reference Labs, Academic Institutes, Cancer Hospitals, Regional Cancer Centres, Research institutes, Forensic Science Laboratories etc. for various applications.

5. During development and / or implementation, have you encountered any regulatory or other challenges?

Policies: Due to lack of insurance coverage and expensive out of pocket expenditures the gene testing is limited to only a small percent of eligible patients. There are very few centres like AIIMS which have the expertise and the know how to provide clinically relevant answers.

Our country has been discussing about developing a database of convicts for managing crimes. Although there's an increased interest and discussions however clear directions are required on implementation.

Lack of trained manpower: For mass adoption and screening, the technology requires basic understanding of molecular biology and medical genetics. The technology awareness and implementation across labs requires trained resources who can help bring and implement the usage of this technology to Tier 2/Tier 3 cities.

6. Suggestions on policy / regulatory interventions for the technology being described

India holds a huge potential to be one of the biggest genomics markets based on its rich genetic diversity. Healthcare diagnostics is currently the focus of various industry players. Involving some key disorders/diseases under Insurance will help in better uptake of these cutting-edge technologies.

Solving crime through DNA & DNA Databases has a huge potential and is already being adopted in many countries. Current structure of Central and state Forensic Science Laboratories does not have universal processes, have back logs which is slowing down the process of Justice.

Promoting public-private partnerships, regulated by policies, human resources with the right skill set, training and most important quality solutions can push India to the front on the global stage.

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

Societal: Sequencing of Inherited disorders, microbes routinely like HIV, Measles, Rubella using CE has helped provide timely treatment, manage drug resistance and develop vaccines in record time, track the emergence of viral variants and invest in timely strategic plans to control the spread. Technology has been routinely used to solve crime through DNA which directly impacts social burden.

National: Having the technology available in Tier 2 & 3 cities and at affordable prices will help manage many disorders like thalassemia, sickle cell anaemia, Fragile X, DMD, SMN, Down's syndrome which have a lifelong disability effect.

Providing timely DNA evidence in criminal cases and having a relevant DNA database will help solve crimes faster today and prevent victims tomorrow.

Commercial: CE technology can help in screening microbial infections, carrier screening, check spread of pandemics by tracking emergence of known and novel variants. early cancer detection, provide valuable investigative leads, DNA evidence for solving crime, The above utilities can help in reducing overall healthcare expenditures significantly and improving Law and order situation in the country.

8. National or international collaborations associated with this technology or project? If any, please share brief details:

CE Technology has been an integral part of genomics solutions all over the world for better management of Cancers, Genetic Diseases, Microbial Infections & drug resistance.

Many countries around the world have National Criminal databases, Missing person databases where CE technology is being used routinely.

9. What is the market potential of the technology/project in both the near term and long term?

With a very large population and high birth rate, and consanguineous marriage favoured in many communities, there is a high prevalence of genetic disorders in India. Hemoglobinopathies including sickle cell anemia, thalassemia, muscular dystrophies pose a significant burden in India. Down syndrome is another genetic disorder, which is the major cause of mental retardation, with a frequency of approximately 1 in 1000 births The prevalence of rare genetic diseases in India is a significant public health concern. Estimates suggest that over eight crore individuals in India suffer from rare diseases, which encompass a spectrum of over 5000 conditions, typically of genetic origin. The reported prevalence of birth defects in India is 64.4 per 1000 live births, highlighting the country's high genetic burden.

Approximately, 40% of the rare diseases can be attributed to genetic factors. The Foundation for Research on Rare Diseases and Disorders has estimated that about 70 million people are affected by rare diseases. Microbial infections and related drug resistance is increasing every day. Every year 1.4 million new cancer cases are detected in India. These diseases together contribute to a significant number of individuals and the disease burden in a populous country such as India. Genomics-based solutions can enable accelerated diagnosis and management of genetic disorders, rare diseases, early detection and management of cancer, drug resistance.

DNA databases have an undisputed capability to enable solve crimes faster, can support missing person identification. Currently there's a population of approximately 2.5milion individuals where if database is created it will immensely support the cause.

Wide scale adoption of CE technology, trained manpower and increased awareness on clinical utility of these tests, public private partnerships can help improve accessibility and optimal use of these technologies for larger populations.

Genomics of rare genetic diseases—experiences from India | Human Genomics | Full Text (biomedcentral.com)

NCRB's Crime in India 2022 Report (drishtiias.com)

State of Prisons in India (drishtiias.com)

The Criminal Procedure (Identification) Bill, 2022 (prsindia.org)

pib.gov.in/PressReleaseIframePage.aspx?PRID=2007872

Genome Surveillance of SARS-Cov2 using Next Generation Sequencing led by INSACOG (The Indian SARS-CoV-2 Genomics Consortium).

Name of the Industry

Illumina/Premas Life Sciences
Level 7, Embassy One Pinnacle Tower, 8, Bellary Rd, Dena Bank Colony, Ganganagar, Bengaluru, Karnataka 560032

The Indian SARS-CoV-2 Genomics Consortium (INSACOG) is a network of laboratories in India established in December 2020 to monitor the genomic variations of the SARS-CoV-2 virus. The consortium was formed in response to the COVID-19 pandemic to track the emergence of new variants and to understand the transmission dynamics of the virus in India. INSACOG's efforts have been crucial in identifying variants of concern (VOCs) and variants of interest (VOIs) through large-scale genomic sequencing.

Next-Generation Sequencing (NGS) Efforts by INSACOG

INSACOG employed Illumina Next-Generation Sequencing (NGS) technologies to sequence the genomes of SARS-CoV-2 samples collected from across the country. The consortium's network includes multiple regional sequencing laboratories, which are tasked with collecting samples, sequencing the viral RNA, and analyzing the data to track mutations and the spread of different variants. The data generated is then shared with the global scientific community to aid in global efforts to combat the pandemic.

Support by Illumina and Premas Life Sciences

The entire project used Illumina's Next Generation Sequencing as the core technology to sequence the various samples. Illumina's core sequencing technology and the Covid-Seq assay, along with the analysis pipelines were key to interrogating the various virus strains. Premas Life Sciences has played a supportive role in INSACOG's genomic sequencing efforts. The company has provided crucial technical expertise, and hands on trainings to support this high-throughput sequencing project in India.

1. Problem solved / addressed

The NGS efforts by INSACOG have been instrumental in:

- Identifying and tracking the spread of various SARS-CoV-2 variants, including the Delta and Omicron variants.
- Informing public health responses and vaccine strategies.
- Providing insights into the efficacy of vaccines against emerging variants.
- Contributing to global databases like GISAID (Global Initiative on Sharing All Influenza Data).

2. Stage of the Technology / Project (Development stage / already commercialized and implemented):

Already implemented, however modifications can be made in the technology to tailor it to any pathogen of interest or even human genetic diseases.

3. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

The modified method, where the primer sequence is changed to interrogate another pathogen of interest/human genes can be used both domestically or globally.

4. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

INSACOG's COVID-19 sequencing efforts have led to several key outcomes that have significantly impacted India's public health response during the pandemic. Here are the primary outcomes:

a) Detection and Monitoring of Variants

- **Identification of Key Variants**: INSACOG played a crucial role in identifying and monitoring variants of concern (VOCs) and variants of interest (VOIs) in India. For example, the Delta variant (B.1.617.2), which was first detected in India, was quickly identified and tracked by INSACOG. This variant became the dominant strain globally and was associated with the second wave of COVID-19 in India.
- **Omicron and Its Sub-lineages**: INSACOG also tracked the emergence and spread of the Omicron variant and its sub-lineages, providing data on how these variants affected transmissibility, vaccine efficacy, and public health measures.

b) Informed Public Health Responses:

- **Policy and Response Shaping**: The data generated by INSACOG informed government policies, including lockdown decisions, travel restrictions, and quarantine measures. This data was also crucial in deciding which regions required more stringent public health interventions based on variant prevalence.
- **Vaccination Strategy**: Insights from genomic data helped shape India's vaccination strategy, particularly in understanding how variants might impact vaccine effectiveness. This informed booster dose rollouts and the development of variant-specific vaccines.

c) Contribution to Global Databases and Research

- **Data Sharing**: INSACOG contributed large amounts of sequencing data to global databases like GISAID, aiding international efforts to track the virus's evolution and spread. This data sharing was essential for global surveillance and the development of vaccines and therapeutics.
- **Scientific Research**: The consortium's findings have been published in numerous scientific journals, contributing to the global understanding of SARS-CoV-2, its mutations, and the implications for public health.

d) Capacity Building in Genomic Surveillance

- **Infrastructure Development**: INSACOG's efforts led to significant advancements in India's genomic sequencing infrastructure. Laboratories across the country were equipped and trained to perform high-throughput sequencing, which will be beneficial for future pandemics or public health emergencies.
- **Enhanced Surveillance Capability**: The establishment of INSACOG created a robust surveillance network that continues to monitor not only COVID-19 but also other pathogens, strengthening India's overall public health infrastructure.

e) Public Awareness and Communication

- **Public Communication**: INSACOG's work also contributed to public communication efforts, providing accurate information about the virus's behavior and the importance of vaccination. This helped to combat misinformation and build public trust in health measures.

Overall, INSACOG's COVID-19 sequencing efforts have been pivotal in managing the pandemic in India, enabling the country to respond more effectively to the challenges posed by the evolving virus.

5. National or international collaborations associated with this technology or project?

Technology Partners: Illumina and Premas Life Sciences Pvt Ltd.

National Collaborations: INSACOG group of institutions: National Institute of Virology (NIV), Institute of Genomics and Integrative Genomics (IGIB), Centre for Cellular and Molecular Biology (CCMB), National Centre for Disease Control (NCDC), Institute of Lifesciences (ILS) etc

Subsequent to the initiation by INSACOG, organizations like UNICEF and WHO funded infrastructure creation for pathogen surveillance in India across different states to develop regional capacity.

6. What is the market potential of the technology/project in both the near term and long term?

As mentioned before, the CovidSeq test, from Illumina, first developed for SARS-CoV2 sequencing can be modified to interrogate different viral pathogens causing human or animal diseases. This test has been subsequently called the Illumina Microbial amplicon Prep (IMAP). In the context of One Health, it is increasingly becoming important to create viral surveillance tools across species as zoonotic transmission of many pathogens has been convincingly established. These need to be cost effective and should have an easy workflow to implement. The CovidSeq/Illumina Microbial Amplicon Prep test is cost effective, easy to execute and scalable to accommodate higher sample loads. Research scientists have also demonstrated the use of the test in various human genetic diseases, and hence it can be successfully used to address this segment too.

The global infectious diseases market is around $20 Bn + with a CAGR of 5.5% and the global sequencing market is $30 bn + with a CAGR of 12%. This market can be tapped into with cost effective, scalable solutions like the CovidSeq test or its modified assay (Illumina Microbial Amplicon Prep).

PURedit™ CAS9: Development of the best-in-class CAS9 protein for RNP genome editing

Name of the Industry

Merck KGaA Darmstadt Germany

1. Brief Description of the Technology / Project

Though Streptococcus pyogenes CRISPR Cas9 (SpCAS9) is widely used as a gene editing tool, it has several properties that are sub-optimal for efficient and safe gene editing. To alleviate issues with off-target effects and mismatch tolerance, while maintaining high editing efficiency, we undertook a protein engineering effort to create a CAS9 protein for RNP applications. Balancing high specificity and high activity, we screened critical protein residues to create an optimized variant designed to work with synthetic single guide RNA (sygRNA™) formats. Additionally, we screened for enhancement of CAS9 RNP editing efficiency at challenging genomic sites. We developed a complete workflow system to create RNP complexes with our optimized CAS9, enhancer solution, and buffers in our PURedit™Cas9 protein kit.

2. Problem solved / addressed

Off-target activity by wild-type SpCas9 is a major concern in genome editing as it can lead to erroneous conclusions in biological research and cause adverse side effects in therapeutics. Previous efforts to improve SpCas9 specificity have drawbacks including high levels of residual off-target effects and editing efficiency constraints. We engineered a new CAS9 variant with well-balanced specificity and efficiency and paired it with an enhancer to provide a workflow solution that allows researchers to edit difficult genomic sites.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Commercialized and implemented

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

This product is fully implemented by our organization and available globally.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

The team tackled complicated purification parameters and documentation needs to provide a high-quality product.

6. Suggestions on policy / regulatory interventions for the technology being described

Streamline and standardize documentation policies.

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

As gene editing technology moves forward into clinical applications, improved CAS9 editors like PURedit™ Cas9 protein offer safer options. The increased efficiency of PURedit™ Cas9 makes it a good candidate for sensitive applications that cannot tolerate off-target effects. Additionally, the increased efficiency of PURedit™ Cas9 will save researchers significant time and money by reducing repeated work and screening needs.

8. What is the market potential of the technology/project in both the near term and long term?

We believe this product has the potential to improve gene editing workflows by improving screening applications, and facilitating successful gene-editing for a wide-range of systems and researcher needs.

PURedit® Cas9 Protein from Streptococcus pyogenes, recombinant, expressed in E. coli, 3X NLS | Sigma-Aldrich (sigmaaldrich.com)

W O 2021/183771 AI: High fidelity SpCas9 nucleases for genome modification

Genomics Assisted Breeding

Name of the Industry

Mahyco Private Limited
19 Rajmahal, 84 Veer Nariman Road, Mumbai 400020

1. Brief Description of the Technology / Project

The technology involves the prediction of likely phenotype of the lines or hybrids using ML and AI approaches. Here the lines are characterized, where both whole genome genotype data and the phenotype data such as morphology, yield, disease resistance, line performance, hybrid performance, General combining ability and Specific combining ability are estimated. Once the data is generated prediction models using AI/ML, are applied and performance of the new lines/hybrids is predicted based on the historical data of the lines and hybrids. In addition to this, genetic relationships between the germplasm lines are estimated to enable breeders to make decisions on the crosses to be made. Further by developing markers for traits of interest (through GWAS or QTL analysis), indirect selection for the trait can be made with minimum phenotyping or no phenotyping. It is also possible to accelerate the breeding programs through rapid background selection. Additionally, estimation of genetic purity of the lines and hybrids can also be done through this process.

2. Problem solved / addressed

Using this technology, it is possible to scale up the development for better products, in a precise, sustainable, faster manner. While developing new lines/hybrids, it is not possible to test and evaluate all the lines and hybrid combinations in the field. By using Genomics and AI/ML approaches to identify lines/hybrids with higher potential, we can reduce the amount of field testing and attempt new and possible better combinations that breeders would not have otherwise known. Hence this technology helps in utilizing a larger portion of germplasm to develop better products and reduce the level of field testing.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Developmental stage

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

Several applications of genomics assisted breeding have been implemented commercial development of lines and hybrids in Rice, Wheat, Cotton and Chilli and plans are in place for expanding this effort to other crop breeding programs. For Genomics assisted predictive breeding, testing has been done at the domestic level. Commercialization is yet to be achieved.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

The project has the potential to be game changer in product development and is likely to have a positive impact on business by reducing testing costs and time as well as on the environment as it would reduce the land and water use.

6. Suggestions on policy / regulatory interventions for the technology being described

Yes, as there is global interest in this technology, a number of academic and commercial providers offer services in this area allowing scope for collaborations.

7. What is the - market potential of the technology/project in both the near term and long term?

The potential is there for this technology to be applicable to any minor or major crop. And it is possible for smaller companies without a high capex investment to potentially apply this technology to product development. This technology has the potential to make a breeders decision making process more data driven and accurate.

Development of insect resistant vegetable – Brinjal for South Asia region

Name of the Industry

Sathguru Management Consultants P.Ltd
54 Sagar Society Road No 2 Banjara Hills Hyderabad 500034

1. Brief Description of the Technology / Project

The project has adopted transgene infused in the genomics of Brinjal to develop and deliver insect resistant Brinjal in South Asian region.

2. Problem solved / addressed

Fruit and shoot borer infestation in Brinjal is devastating for the crop. Farmers spray pesticide over 50 times in a crop cycle of 90 to 120 days harming the grower health and environment. There are no solutions in chemical crop protection currently beyond the application of toxic chemicals.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Commercialised in Bangladesh, while the introduction of the crop is stalled in India.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

The technology is well applied in Bangladesh with over 75,000 farmers successfully producing Brinjal without application of toxic pesticides. The technology has enhanced Brinjal productivity per acre by 40%.

In India, the product was approved but withheld for release by the Ministry of Environment.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

Introduction of transgenic crop in India is long hampered (since 2009) due to rigid unscientific policy of withholding transgenic crops. Hence the efforts were suspended for introduction in India where 12 public varieties of Brinjal were developed by public institutions funded by us. The private hybrids developed were also suspended due to policy rigidity.

However, we have successfully applied the Indian technology for Bangladesh and Philippines. In both the countries the product is approved.

6. Suggestions on policy / regulatory interventions for the technology being described

Application of genomic tools beyond molecular breeding in India is restricted today due to policy limitations. Though gene editing is now encouraged, most gene edited products would require transgenic technologies to transfer traits to wider crop segments. At this time, we are also hampered by the pending decision of Supreme Court in permitting biotechnology derived crops to be introduced. India has lagged behind neighbouring countries in introduction of biotechnology derived crops.

In agriculture genomics, we need to pursue policy reversal to permit any public institution or private enterprise to engage in biotechnology derived crop improvement.

7. What is the - market potential of the technology/project in both the near term and long term?

In Bangladesh 70,000 farmers derive more than $ 1000 per acre as incremental income with reduction of over $ 100 million pesticide application so far. The health benefits of farmers are enormous due to non-application of toxic pesticides.

In Philippines, the crop is just introduced, and we do perceive benefits similar to Bangladesh too.

8. National or international collaborations associated with this technology or project? If any, please share brief details:

The project involved collaboration of India, Bangladesh and Philippines. The product was entirely developed in India, but well commercialised in Bangladesh and now in Philippines.

9. What is the market potential of the technology/project in both the near term and long term?

In India, if introduced, it can benefit half a million acre of crop grown commercially. It can save application of toxic pesticide worth $ 50 Million annually.

Retrospective Analysis of Pharmacogenomics Data from Array-Based Genotyping in Indian Cohort

Name of the Industry

Indus Health Plus Pvt Ltd.
Indus House, Pride Port, Model Colony, Pune - 411 016, Maharashtra, India

1. Brief Description of the Technology / Project

This project involves the retrospective analysis of array-based genotyping data from over 8000 clients at Indus Health Plus, using the Illumina GSA v3 platform. Our aim was to explore the pharmacogenomics landscape of the Indian cohort, which includes clients from various regions of India. The study focused on 20 pharmacogenes that play a crucial role in the metabolism of drugs across 18 medical specialties, such as cardiology and psychiatry. We included only drug-gene associations with a high level of scientific evidence, i.e., PharmGKB LoE 1A/1B. We utilized an in-house developed bioinformatics pipeline to process and analyse the genotyping data.

2. Problem solved / addressed

The project addresses the significant gap in pharmacogenomic data for the Indian population, which has been underrepresented in global genomic studies. By understanding the genetic variations that affect drug metabolism in this cohort, we aim to enhance personalized medicine approaches, improve drug efficacy, and reduce adverse drug reactions (ADRs). This research helps tailor drug prescriptions to the genetic profiles of individuals, leading to better health outcomes and more efficient healthcare delivery.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

Already commercialized and implemented.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

The pharmacogenomics test developed through this project has been commercialized and is offered in both B2C and B2B models. Nationally, it is available to individual clients and healthcare providers, enhancing personalized medicine services. Internationally, we have extended our reach to global clients, offering our pharmacogenomics test to healthcare institutions and organizations seeking to incorporate personalized treatment plans based on genetic insights.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

Our challenge was the lack of a clear regulatory framework around pharmacogenomics testing offered directly to consumers, which would be instrumental in standardizing the testing and

reporting guidelines across labs and companies for the Indian population. Our challenge was also to identify if the test qualifies as healthcare services under GST.

6. Suggestions on policy / regulatory interventions for the technology being described

To facilitate the development and implementation of genomics technologies, clear and comprehensive regulatory frameworks should be established. Policies should focus on data privacy, security, and ethical use of genetic information. It is essential to create guidelines for informed consent that are understandable to participants. Ensuring compliance with local and international regulations, such as AMP guidelines to include minimum alleles to be tested in specific genes to be included in the panel and the relevant Indian Council of Medical Research (ICMR) guideline will be helpful. Additionally, promoting public awareness and education about the benefits and risks of genetic testing can help mitigate concerns. Collaboration between regulatory bodies, healthcare providers, and researchers is crucial for creating a supportive environment for genomic innovations.

- **Testing Guidelines**: ICMR or equivalent bodies coming up with relevant guidelines/best practices for predictive genetics and pharmacogenetic testing will enhance uptake and confidence among clinicians and the healthcare community
- **Implementation Framework**: An implementation framework for FDA-recommended Pharmacogenetic or genetic testing relevant to drugs would ensure proper management and mandatory testing before prescribing drugs with actionable PGx.
- **Awareness Drives**: Conduct awareness drives across the healthcare ecosystem to educate about the benefits of pharmacogenomic testing for our population. This will help in better update of these test which can benefit masses.
- **Lab Developed Test Guidelines**: Guidelines/Best practices for lab-developed tests will ensure standardization and reliability.
- **Pharma Collaboration**: Collaboration with pharmaceutical companies or bodies. FDA recommendations and PGx-related guidelines can contribute to drug development, leading to better drug outcomes.
- **Third-party Payer Awareness**: Raise awareness among third-party payers like insurance companies and corporates to facilitate the better implementation of genetic tests.
- **Documenting ADRs**: Properly document ADRs across the country, like Pharmacovigilance Programme of India (PvPI), to create a comprehensive database for studying ADR causes in our population. PGx testing in this case will increase the knowledge base.
- **Inclusion in standard treatment protocols**: PGx testing to be included in standard SOPs for important specialties like cardiology and psychiatry, where ADRs and therapeutic failures are well-studied and often due to interindividual pharmacogenetic variation.
- **Taxation**: All kind of Genetics tests to be included in exemption provided to healthcare services under GST Act.

7. Project Impact / Outcomes

This project has generated population-specific data that can help develop small panel assays tailored to the key genetic variants more prevalent in the Indian population. These panels will be cost-effective for mass screening at a population level. The data can also inform national policies on which genes to test on priority, based on mutation prevalence and the drugs impacted. This approach can help prevent ADRs by identifying high-risk individuals and tailoring their treatments, leading to improved health outcomes and reduced healthcare costs. Business-wise, it positions Indus Health Plus as a leader in personalized medicine in India, enhancing its service offerings. Nationally, it contributes to the growing body of pharmacogenomic data specific to the Indian population, aiding in more precise healthcare. Societally, it can lead to improved health outcomes through personalized treatment plans, reducing ADRs and increasing drug efficacy. Commercially, it opens up new markets for genetic testing and personalized healthcare services.

8. National or international collaborations associated with this technology or project? If any, please share brief details:

We are actively pursuing partnerships with national and international pharmacogenomics consortia to compare findings and enhance the global understanding of pharmacogenomics across diverse populations. Additionally, we are exploring potential collaborations with hospital partners in India and worldwide to integrate individual pharmacogenetic testing results into their Hospital Management Information Systems (HMIS) or Laboratory Information Management Systems (LIMS). This integration aims to prevent ADRs and move away from the traditional hit-and-trial approach in prescribing medications. By developing systems with LIMS integration and leveraging technological innovations, we aim to streamline the management and utilization of pharmacogenetic data. These efforts will reduce hospitalization costs, alleviate the socioeconomic burden on healthcare systems, and improve patient outcomes through pre-emptive pharmacogenetic testing data. As an industry leader in scientific innovation, we are committed to standardizing methodologies and sharing best practices, thereby making significant contributions to the broader scientific community.

9. What is the market potential of the technology/project in both the near term and long term?

In the near term, the market potential lies in personalized healthcare services and genetic testing within India, addressing the immediate need for tailored medical treatments. As awareness and acceptance of pharmacogenomics grow, the demand for such services is expected to grow multifolds. In the long term, we can aim for every Indians pre-emptive PGx report being available in ABDM - ABHA (or PGx passport being implemented by some developed countries). Technology can also expand globally, particularly in regions with similarly underrepresented genetic profiles.

By incorporating ICMR's views on best practices, implementing FDA-recommendations in PGx framework development, conducting awareness drives among healthcare providers, developing lab-developed test guidelines/best practices, collaborating with pharma companies, raising awareness among third-party payers, documenting ADRs, and focusing on critical specialties like cardiology and psychiatry where there is higher actionability, the potential of this project can be maximized.

Genomic Insights into the Mechanism of Action of Ayurvedic Drugs

Name of the Industry

M/s Sitaram Research Foundation
(A Public Charitable Trust, Registration No: 247/2010), III/475 A, Gandhinagar Road, Nedupuzha. P.O, Thrissur - 680 007

1. Brief Description of the Technology / Project

The project explores how traditional Ayurvedic medicines work at a molecular and genetic level. By using advanced genomic and bioinformatics techniques, the project seeks to identify the genetic and biochemical pathways influenced by Ayurvedic compounds.

- **Identification and Analysis of Active Compounds**: Isolating active ingredients from Ayurvedic formulations and studying their structures.
- **Genomic and Transcriptomic Profiling**: Examining how these compounds affect gene expression and cellular pathways in human cells or model organisms.
- **Mechanistic Studies**: Investigating the biochemical and cellular mechanisms influenced by these drugs, potentially linking traditional knowledge with modern biomedical science.
- **Comparative Analysis**: Comparing the action of Ayurvedic drugs with conventional pharmaceuticals to highlight unique and shared pathways.
- **Potential Therapeutic Applications**: Identifying possible new therapeutic uses for these drugs based on their genomic impacts.

The ultimate goal is to bridge traditional Ayurvedic medicine with modern genomics, providing a scientific basis for their efficacy and guiding the development of new treatments.

2. Problem solved / addressed

The project aims to bridge the gap between traditional Ayurvedic medicine and modern genomics.

- **Mechanistic Understanding**: It provides a scientific basis for how Ayurvedic drugs exert their therapeutic effects, which can validate and explain the efficacy observed in traditional practices.
- **Personalized Medicine**: Genomic insights can help in developing personalized treatment plans based on an individual's genetic makeup, enhancing the effectiveness and safety of Ayurvedic treatments.
- **Drug Discovery and Development**: Understanding the genomic impact of Ayurvedic drugs can lead to the discovery of new therapeutic targets and the development of novel drugs based on traditional formulations.

- **Safety and Efficacy**: The project can help in identifying any potential side effects or adverse reactions associated with Ayurvedic drugs, ensuring safer use.
- **Regulatory Approval**: Scientific validation through genomic studies can help in gaining regulatory approval for Ayurvedic drugs in various regions, expanding their use globally.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The current stage is in development/initial stage. We have planned the project as mentioned below:

YEAR 1

1. Project Planning and Design

a) **Objective Setting**: Define the main goals and hypotheses of the research.

b) **Literature Review**: Comprehensive review of existing research on Ayurvedic drugs and their genomic impacts.

c) **Methodology Development**: Design the experimental and computational methods to be used, including the selection of genomic techniques (e.g., sequencing, bioinformatics tools).

2. Sample Collection and Preparation

a) **Sample Selection**: Determine which Ayurvedic drugs and biological samples (e.g., human tissues, cell lines) will be studied.

b) **Ethical Approvals**: Obtain necessary ethical approvals for the study, especially if human subjects are involved.

c) **Sample Collection**: Collect and prepare biological samples for genomic analysis.

3. Data Generation

a) **Experimental Execution**: Conduct experiments to generate genomic data, which could include DNA/RNA sequencing, gene expression profiling, etc.

b) **Quality Control**: Ensure data quality through various checks and pre-processing steps.

YEAR 2

1. Data Analysis

a) **Bioinformatics Analysis**: Analyze the genomic data using bioinformatics tools to identify gene expression patterns, mutations, and other relevant genomic features.

b) **Integration with Ayurvedic Principles**: Correlate genomic data with Ayurvedic drug properties and mechanisms of action.

2. Validation and Verification

a) **Experimental Validation**: Validate key findings through additional experiments, such as functional assays or in vivo studies.

b) **Reproducibility**: Ensure findings are reproducible by independent verification.

YEAR 3

1. **Interpretation and Integration**

   a) **Biological Interpretation**: Interpret the genomic data in the context of Ayurvedic drug action mechanisms.

   b) **Integration with Existing Knowledge**: Integrate findings with existing scientific and Ayurvedic knowledge to build a coherent understanding.

2. **Dissemination**

   a) **Publication**: Write and publish research findings in scientific journals.

   b) **Conferences and Presentations**: Present findings at conferences and seminars.

3. **Application and Further Research**

   a) **Practical Applications**: Explore the practical applications of the research in medicine, drug development, and personalized medicine.

   b) **Future Research**: Identify new research questions and directions based on the findings.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

If commercialized, the project could significantly impact both domestic and global markets. Domestically, it would leverage India's vast traditional medicine knowledge, integrating it with modern genomic research to enhance credibility and efficacy. This could lead to wider acceptance and use within India, promoting Ayurveda as a scientifically validated alternative or complementary medicine. On a global scale, the project could attract international attention from researchers, healthcare providers, and pharmaceutical companies interested in alternative medicine. This could foster global collaborations, lead to the development of new therapeutics, and expand market reach. Overall, commercialization would bridge traditional and modern medicine, potentially transforming healthcare practices worldwide.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

Since the project is in the initial stages, we have not encountered any regulatory challenges. But there might be skepticism from the regulatory authorities regarding the validity of Ayurvedic medicine and its integration with modern genomics.

6. Suggestions on policy / regulatory interventions for the technology being described

- Establish standardized protocols for genomic research on Ayurvedic formulations to ensure consistency and reproducibility.
- Implement stringent guidelines for clinical trials to assess the efficacy and safety of these drugs using genomic data.

- Promote collaboration between traditional Ayurvedic practitioners and modern scientists to integrate traditional knowledge with contemporary genomic techniques.
- Ensure ethical guidelines are followed, particularly concerning consent and data privacy.
- Encourage regulatory bodies to create a framework for the certification and approval of Ayurvedic drugs based on genomic evidence, facilitating their integration into mainstream healthcare while ensuring patient safety and drug efficacy.

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

The project aims to bridge traditional medicine with modern science, enhancing both fields. For businesses, it opens avenues for the development of novel therapeutics, potentially leading to new markets and revenue streams. Nationally, it strengthens the healthcare system by integrating Ayurvedic practices with genomic science, offering cost-effective and personalized treatment options. Societally, the project promotes a deeper understanding and acceptance of Ayurveda, fostering cultural heritage and holistic health approaches. Commercially, it can lead to patented discoveries and collaborations between pharmaceutical companies and traditional medicine practitioners, driving innovation and economic growth.

8. National or international collaborations associated with this technology or project? If any, please share brief details:

The project involves notable national and international collaborations. Domestically, we would like to engage with premier Indian institutions such as the Centre for Scientific and Industrial Research (CCRAS), National Institute of Plant Genome Research (NIPGR), National Institute of Biomedical Genomics (NIBMG), Indian Institute of Science (IISc), the Council of Scientific and Industrial Research (CSIR), and the All-India Institute of Medical Sciences (AIIMS). These institutions contribute through extensive genomic research, traditional medicine expertise, and clinical studies. Internationally, the project partners Genomics and Data Analytics Core in National University of Singapore. These collaborations enhance the project through advanced genomic technologies, cross-disciplinary insights, and broader research perspectives, aiming to validate and elucidate the scientific basis of Ayurvedic medicine.

9. What is the market potential of the technology/project in both the near term and long term?

In the near term, it can attract investment from Ayurveda pharmaceutical companies, nutraceutical and biotech firms interested in integrating traditional medicine with modern genomics, potentially leading to novel therapeutic products. It can also capture a share of the growing global market for personalized medicine, estimated to reach $3.18 trillion by 2025. In the long term, the project could revolutionize the healthcare industry by providing scientifically validated Ayurvedic treatments, enhancing credibility, and expanding market reach. This integration could lead to new drug discoveries and more effective treatment protocols, benefiting global health and wellness markets.

Evaluating the Influence of Ayurveda Daily Routines "Din Acharya" on Epigenetic Changes and Health

Name of the Industry

M/s Sitaram Research Foundation
(A Public Charitable Trust, Registration No: 247/2010), III/475 A, Gandhinagar Road, Nedupuzha. P.O, Thrissur - 680 007

1. Brief Description of the Technology / Project

The project, "Evaluating the Influence of Ayurveda Daily Routines 'Dinacharya' on Epigenetic Changes and Health Outcomes," aims to investigate the impact of traditional Ayurvedic daily practices on genetic and health parameters. The focus is on understanding how specific routines—such as diet, exercise, and mindfulness—affect epigenetic mechanisms, which in turn influence gene expression and health outcomes. By implementing a standardized Dinacharya routine for a diverse group of 100 participants over 6 to 12 months, the project seeks to identify beneficial epigenetic modifications and correlate these changes with improvements in health metrics such as BMI, blood pressure, and mental well-being. Advanced techniques like DNA methylation analysis and histone modification profiling will be used to uncover the molecular basis of these health benefits, providing a scientific foundation for integrating Ayurvedic practices into modern healthcare.

2. Problem solved / addressed

The project addresses the gap in understanding how traditional Ayurvedic daily routines, or "Dinacharya" can influence epigenetic changes and subsequently improve health outcomes. Despite Ayurveda's long-standing emphasis on lifestyle practices for maintaining health, there is limited scientific evidence on their molecular impact. This project aims to bridge this gap by systematically investigating the epigenetic modifications induced by these routines. It addresses problems such as the lack of personalized health interventions and the need for integrative approaches that combine traditional knowledge with modern scientific insights. By demonstrating the potential of Dinacharya to induce beneficial genetic changes, the project could lead to innovative, evidence-based lifestyle recommendations that enhance overall well-being and prevent diseases, thus contributing to more holistic and personalized healthcare solutions.

3. Stage of the Technology / Project (Development stage / already commercialized and implemented)

The project is currently in the development stage. It involves detailed planning, standardization of the Ayurvedic daily routines (Dinacharya), and recruitment of participants. The implementation phase includes a 6 to 12-month intervention period during which participants will follow personalized Dinacharya schedules. Data collection will be conducted at multiple points to analyze the epigenetic changes and health outcomes. This will be followed by comprehensive data analysis, reporting, and dissemination of findings through scientific journals and conferences. The project also includes plans for future research and potential

long-term follow-up studies to assess the durability of the observed benefits. As it is still in the research phase, commercial implementation has not yet been realized.

4. If commercialized, please brief about the scale of its implementation, and whether it is at a domestic or global level?

If commercialized, the project could have a significant impact both domestically and globally, particularly in the context of modern health applications and chronic disease management. Domestically, the project could be integrated into healthcare systems, wellness centres, and digital health platforms to provide personalized AyurvedicDinacharya routines aimed at managing chronic conditions such as diabetes, hypertension, and mental health disorders. Globally, the scientific validation of these Ayurvedic practices would attract international interest, especially in regions with a growing focus on integrative and holistic health practices. The commercialization strategy could include developing mobile apps and online platforms offering personalized health plans, collaborating with global health and wellness brands, and running educational campaigns to inform the public and healthcare professionals about the benefits of Dinacharya. By demonstrating the efficacy of these routines in managing modern health issues through epigenetic changes, the project has the potential to transform health and wellness practices on a global scale, making ancient wisdom accessible and relevant in the fight against chronic diseases.

5. During development and/ or implementation, have you encountered any regulatory or other challenges?

As the project is currently in the development stage, several regulatory and logistical challenges have been encountered. Regulatory challenges primarily involve ensuring compliance with local and international health regulations for conducting clinical studies. This includes obtaining necessary approvals from health authorities, adhering to ethical guidelines, and ensuring the safety and efficacy of Ayurvedic practices.

Additionally, there are challenges related to the standardization and validation of Ayurvedic routines, which can vary widely. Ensuring consistent implementation of Dinacharya practices across diverse participant groups requires meticulous planning and strict adherence to protocols.

Another significant challenge is integrating traditional Ayurvedic practices with modern scientific research methods. Bridging the gap between traditional knowledge and contemporary scientific standards necessitates multidisciplinary collaboration and innovative approaches.

Logistical challenges include recruiting and retaining participants for long-term studies, managing large volumes of biological data for epigenetic analysis, and securing adequate funding to support comprehensive research efforts.

Addressing these challenges involves close collaboration with regulatory bodies, engaging both Ayurvedic practitioners and modern scientists, and designing rigorous study protocols to validate the health benefits of AyurvedicDinacharya.

6. Suggestions on policy / regulatory interventions for the technology being described

To support the development and implementation of AyurvedicDinacharya interventions with a focus on genomics, several policies and regulatory interventions are recommended. Firstly,

establishing a dedicated regulatory framework for integrative genomics research that includes traditional systems like Ayurveda can streamline the approval process for studies involving epigenetic changes. This framework should ensure safety, efficacy, and standardized protocols for combining traditional practices with genomic research.

Secondly, fostering collaboration between genomic researchers and Ayurvedic practitioners can enhance the credibility and integration of Ayurvedic interventions in genomics. Government grants and incentives for interdisciplinary research can support these collaborative efforts.

Thirdly, implementing specialized training programs for regulatory bodies on genomics and traditional health practices can ensure informed decision-making and better evaluation of such interventions.

Lastly, creating public awareness campaigns about the scientific validation of Ayurvedic practices through genomics can encourage wider acceptance and adherence, promoting preventive healthcare. These interventions can bridge the gap between traditional wisdom and modern science, enhancing health outcomes through personalized genomic approaches.

7. Project impact / outcomes (business/ national/ societal/ commercial aspects) of the technology / project?

The AyurvedicDinacharya and genomics project promises significant impact across multiple domains. From a business perspective, it can lead to the development of personalized health plans, new wellness products, and services tailored to individual genetic profiles, opening new revenue streams and market opportunities.

Nationally, the project supports the integration of traditional medicine with modern science, enhancing healthcare delivery and potentially reducing the burden of chronic diseases through preventive measures. This aligns with health policies promoting integrative and personalized medicine.

Societally, the project promotes a holistic approach to health, combining lifestyle practices with scientific validation. This can lead to improved public health outcomes, greater awareness of preventive health measures, and increased acceptance of traditional practices.

Commercially, successful validation and implementation can position the project as a pioneer in the growing field of genomic-based personalized health, attracting global interest and investment, and driving innovation in the wellness and healthcare industries.

8. National or international collaborations associated with this technology or project? If any, please share brief details:

The Ayurvedic Dinacharya and genomics project involves several key national and international collaborations. Nationally, partnerships with leading Ayurvedic institutions and universities in India are crucial for standardizing the Dinacharya routines and ensuring the integration of traditional knowledge. Collaborations with genomic research centers and biotechnology firms within India will facilitate advanced epigenetic analysis and validation.

Internationally, the project aims to collaborate with renowned research institutions and universities specializing in genomics and integrative medicine. These collaborations will provide access to cutting-edge genomic technologies and global expertise, enhancing the project's scientific rigor and credibility. Additionally, partnerships with global wellness and healthcare

organizations can help in the dissemination and commercialization of the findings, ensuring a broader impact.

These collaborations will not only enhance the quality and scope of the research but also foster cross-cultural exchange of knowledge, ultimately contributing to the global recognition and acceptance of Ayurvedic practices in modern healthcare.

9. What is the market potential of the technology/project in both the near term and long term?

In the near term, the AyurvedicDinacharya and genomics project has significant market potential in the wellness and preventive healthcare sectors. The growing interest in personalized health solutions and integrative medicine can drive demand for customized Dinacharya routines based on individual genetic profiles. Wellness centers, digital health platforms, and healthcare providers can integrate these personalized plans, creating new revenue streams and enhancing customer engagement.

In the long term, the project's market potential expands significantly as scientific validation and global awareness increase. It can revolutionize the approach to preventive healthcare by offering scientifically backed, personalized lifestyle interventions. This could attract investments from global healthcare and wellness industries, leading to the development of new products and services. Additionally, the integration of traditional practices with genomic insights can position the project at the forefront of the emerging field of personalized medicine, tapping into a multi-billion-dollar market focused on enhancing health outcomes through tailored interventions.

> Illumina has undeniably ushered in the genome era, to unlock the power of the genome and to improve human health for all and is driven by a commitment to life-changing discoveries and better health, fueled by a passion for continual innovation and deep collaboration. India is on its way to becoming the world's third largest economy by 2030 and it continues to confront public health issues such as tuberculosis, HIV/AIDS, malaria, and other infectious diseases. It is estimated that up to 96 million people in India have a rare disease, and one in nine people in India are likely to develop cancer in their lifetime. NIPT's integration into prenatal care in India is a significant step forward, providing expectant parents with crucial genetic information about their baby, which can lead to better management and early intervention when necessary. This aligns perfectly with the broader goals of the genomics drive. Expanding access to genomics in India will help unlock opportunities for advancing healthcare and combating the effects of climate change.
>
> **Mukesh Kumar Jaiswal,** Manager, Field Applications Service and Support Department, Illumina

> I firmly believe that genomics has revolutionized the global healthcare landscape from disease diagnosis to accelerated drug discovery. In the past decade, science and technology led innovations have driven our mission to make advanced genomic solutions accessible and affordable across emerging markets. Tests like Exome Max, Spit Seq, HRD Track, and Liquid Biopsy, among others, are designed to equip clinicians with the tools they need for timely intervention ensuring better patient outcomes. I extend my congratulations to CII for making this compendium available to the public. With so many exciting innovations taking place in the healthcare space, I am truly excited to be part of this transformative revolution.
>
> **Dr VL Ramprasad**, CEO (India), MedGenome Labs Limited, India

Supported by

ThermoFisher SCIENTIFIC

illumina®

MEDGENOME®

The Road Ahead

The CII Compendium of Cutting-Edge Genomic Technologies highlights the transformative potential of genomics across healthcare, agriculture, biodiversity, and industry. These case studies reflect India's growing capability to harness advanced genomic technologies to address unique challenges, enabling both innovation and socio-economic development.

From pioneering work in personalized medicine to revolutionizing agricultural practices with genome editing, the compendium underscores the significance of strategic investments in genomic research and innovation. It also showcases how genomics is improving health outcomes and fostering economic growth through cross-sector collaborations and partnerships.

A common theme throughout the compendium is the convergence of technology, policy, and education. These elements have been pivotal in scaling genomic solutions and ensuring equitable access. The efforts detailed here also emphasize the need for continued investment in research infrastructure, skill development, and ethical frameworks to maximize the benefits of genomics while addressing societal concerns.

Looking ahead, India is well-positioned to lead the global genomic revolution, leveraging its rich biodiversity, robust talent pool, and innovative spirit. By fostering collaboration between academia, industry, and government, India can create scalable solutions that not only benefit its population but also contribute to global advancements in genomics. This compendium is a testament to the transformative power of genomics and serves as a call to action for continued exploration and application of this critical field.

For any further details on the subject,
please feel free to contact:

Priyanka Thakur (priyanka.thakur@cii.in)
Namita Bahl (namita.bahl@cii.in)

Confederation of Indian Industry

The Confederation of Indian Industry (CII) works to create and sustain an environment conducive to the development of India, partnering Industry, Government and civil society, through advisory and consultative processes.

CII is a non-government, not-for-profit, industry-led and industry-managed organization, with around 9,000 members from the private as well as public sectors, including SMEs and MNCs, and an indirect membership of over 365,000 enterprises from 294 national and regional sectoral industry bodies.

For more than 125 years, CII has been engaged in shaping India's development journey and works proactively on transforming Indian Industry's engagement in national development. CII charts change by working closely with Government on policy issues, interfacing with thought leaders, and enhancing efficiency, competitiveness, and business opportunities for industry through a range of specialized services and strategic global linkages. It also provides a platform for consensus-building and networking on key issues.

Through its dedicated Centres of Excellence and Industry competitiveness initiatives, promotion of innovation and technology adoption, and partnerships for sustainability, CII plays a transformative part in shaping the future of the nation. Extending its agenda beyond business, CII assists industry to identify and execute corporate citizenship programmes across diverse domains including affirmative action, livelihoods, diversity management, skill development, empowerment of women, and sustainable development, to name a few.

For 2024-25, CII has identified "Globally Competitive India: Partnerships for Sustainable and Inclusive Growth" as its Theme, prioritizing 5 key pillars. During the year, it would align its initiatives and activities to facilitate strategic actions for driving India's global competitiveness and growth through a robust and resilient Indian industry.

With 70 offices, including 12 Centres of Excellence, in India, and 8 overseas offices in Australia, Egypt, Germany, Indonesia, Singapore, UAE, UK, and USA, as well as institutional partnerships with about 300 counterpart organizations in almost 100 countries, CII serves as a reference point for Indian industry and the international business community.

Confederation of Indian Industry
The Mantosh Sondhi Centre
23, Institutional Area, Lodi Road, New Delhi – 110 003 (India)
T: 91 11 45771000

E: info@cii.in • W: www.cii.in

Follow us on

cii.in/facebook | cii.in/twitter | cii.in/linkedin | cii.in/youtube

Reach us via CII Membership Helpline Number: 1800-103-1244