Expression of Interest from Industry

CSIR-IGIB is a premier scientific research institution of Council of Scientific & Industrial Research under Ministry of Science & technology, Government of India. Over the years, CSIR-IGIB through its research programs has contributed to development of health care solutions through genomics and other omics based technologies, emerging as a leader in the area of clinical genomics. The research at the institute is focused primarily in the areas of genomics, bioinformatics, biology of complex diseases, environmental biotechnology, proteomics and rare genetic diseases leading to development of various products, processes, know-how and resources useful to Pharma, Biotechnology and health care related industries.

CSIR-IGIB has transferred several of its know-how and products to the industry which include: Regen D for treating Diabetic foot Ulcers; know-how for Hyaluronic Acid useful in preparation of ingredients for Intra Ocular Lens replacement; a device for fast & accurate measurement of BOD in Industrial effluents for monitoring industrial waste disposal and pipeline for diagnosis of Mitochondrial diseases using Next generation Sequencing.

The portfolio of technologies/ know-how available for commercial use are available on the website, inviting expression of interest from industries who want to either license the technology or partner with CSIR-IGIB in co-development leading to commercialization.

Industries seeking to license any of the technologies/products/knowhow/resources listed on the website may contact Mr Pankaj Bansal, Head, Business Development on email : pbansal@igib.res.in

Industries who seek to collaborate with CSIR-IGIB on any of the research areas may contact Dr Geetha Vani Rayasam, Head, Corporate Scientific Alliance On Email : Geethavani@igib.res.in

Some of the Technologies Currently Available for Licensing are:

“Comprehensive computational pipeline for analysis and clinical interpretation of myeloid cancer panel data”

BACKGROUND

Myeloid malignancies are a clinically heterogenous group of neoplasms, which involve the haematopoietic progenitor cells, which include cells of granulocyte, monocyte, erythroid, megakaryocyte, and mast cell lineages. This haematopoietic malignancy involves the clonal proliferation of the progenitor cells resulting in malignant transformation. The disease is further classified into five types, Acute myeloid leukemia, Myelodysplastic syndromes (MDS), Myeloproliferative neoplasms (MPN), Myeloplastic/myeloproliferative neoplasms (MDS/MPN) and Myeloid neoplasms associated with eosinophilia and abnormalities of PDGFR-A or -B, or FGFR1.

The age-adjusted incidence of Acute Myeloid Leukemia is estimated to be 3.7 per 100,000 persons according to the SEER Cancer Statistics Review in the United States of America. Other Myeloid malignancies are rare in occurrence. The genetic mutations in Myeloid neoplasms have been extensively catalogued in the recent years and has significantly contributed to the understanding of the disease, pathophysiology and prognosis. Apart from the chromosomal transactions, a number of single nucleotide changes and InDels have been recently explored at much great detail. The emergence of Next generation sequencing has enabled the evaluation of a large number of genes involved and implicated in the disease, thus offering a snapshot of the mutational spectrum in the malignancy and is increasingly been used in clinical settings for classification, diagnosis, aiding treatment and prognosis.

The major limitation in the widespread utility of next-generation sequencing based gene panels in the disease has been the complexity of analysis and interpretation of Next Generation Sequencing data. In most cases, this involves in-depth analytical skills and highly trained human resource. A well-curated mutation resource with clinical implications would enable the fast and accurate clinical interpretation of the data if applied in tandem with an automated computational pipeline for data analysis and variant calling.

We have developed a comprehensive computational pipeline for analysis and clinical interpretation of Next Generation Sequencing data generated from Myeloid Cancer panels. This pipeline has application in fast diagnosis and clinical interpretation of genetic variations in Myeloid Cancers, including clinically relevant InDels associated with the disease.

ADVANTAGES

1. Easy to use web-based interface which can be used online/offline or on the cloud
2. Standard data analysis and interpretation interface with automation of all aspects from alignment, variant calling and clinical reporting (FASTQ to Report).
3. High quality data curation by expert clinicians with tagging of clinically relevant and actionable mutations and Pharmacogenetic variants.
4. Customizable database to include lab-specific /custom data of relevance.
5. Compatible with major next-generation sequencing based gene panels for Myeloid neoplasms
6. Enables identification and characterization of clinically relevant Internal Tandem Duplications (ITD)s
7. Standardized interface and reporting including option to export in standard PDF formats.

Companies with the capability to resell, host, support, maintain and commercialize may contact CSIR-IGIB.