Report of the Host Institute

1. Name of the Professor: Dr Sandeep Dave

2. Name and Address of the Host Institute: Duke Institute for Genome Sciences & Policy, Duke University,2177C CIEMAS ,101 Science Drive ,Durham, NC 27708

3. Duration of Fellowship: Three months (from Feb 1st to April 30th)

4. Brief Highlights of the achievements:

   Dr. Parihar worked hard to learn a number of different methods. These include the application of microarrays for measuring gene expression and cytogenetic abnormalities. He also learned the application of next generation sequencing for the identification of genetic mutations in cancers.

5. Your Assessment of the ICMR International Fellow

   Dr. Parihar is an exceptionally bright and committed individual who applied himself fully to learning cutting-edge molecular techniques. He has learned the basics of high throughput methods including microarrays and next generation sequencing and is well-poised to apply these methods and lead collaborative projects.

6. Any Other Comments

   Signature

Sandeep Dave, MD, MS

Name Designation and Host Institute address
Associate Professor
Duke Institute for Genome Sciences and Policy
Duke Cancer Institute
Duke University, 2177C CIEMAS
101 Science Drive, Durham, NC 27708
Duke University
Durham, NC 27708

Report

Report on participation of the ICMR international fellow (ICMR-IF) in Training Research abroad

1. Name and designation of the ICMR-IF: Dr Mayur Parihar, Consultant Cytogenetics and Lab Hematology

2. Address: Cytogenetics Laboratory, North Lab,Tata Medical Center, 14 Major Arterial Road (EW),New Town, Rajarhat, Kolkata -700156

3. Frontline area of research in which training /research was carried out: Microarray, array CGH and Next generation sequencing in B cell leukemias and lymphomas.

4. Name and address of Professor and host institute : Dr Sandeep Dave, Duke Institute for Genome Sciences & Policy, Duke University,2177C CIEMAS ,101 Science Drive ,Durham, NC 27708

5. Duration of fellowship : Three Months (February 1, 2013 to April 30, 2013)

6. Highlights of the work conducted:

   i) Technique /expertise acquired:
   During my tenure here I was trained in using the Array CGH and microarray technology to better understand their role of in diagnosis of B cell leukemias and lymphomas. The training included

   - Understanding the use of micro arrays in different experimental settings and standardizing the running of a microarray facility.
   - Running SNP arrays on the Affymetrix platform.
   - Running Affymetrix gene expression microarrays.
   - Data interpretation of microarrays.
   - Understanding of Next generation Sequencing

- Concepts of targeted Next generation sequencing
- Preparation of libraries for Next gen Sequencing
- Capturing of Exomes for Exome sequencing
- Concepts of CHIP sequencing
- Concepts of RNA sequencing
- RNA and DNA extraction from FFPE
- Trisol RNA and DNA and extraction
- Running a next generation sequencing machine (Illumina) platform

ii) Research results, including any papers, prepared/submitted for publication

Started work on a project involving the exome sequencing of hepatosplenic lymphomas. It is a project in work and shall continue in collaboration with the Dr Sandeep Dave's Lab.

iii) Proposed Utilization of the experience in India

My experience here at Dr Dave's Laboratory at Duke will aid in setting up the microarray and sequencing facility at Tata Medical center and Tata Translational Research center. The understanding of use of arrays and next gene sequencing will be used for various different studies in Tata Medical center and the Tata Translational Research Center.

The proposed studies are listed below

- SNP arrays in Mydelodysplastic synromes in an already IRB approved study involving the microenvironment and correlation with the karyotyping and array findings "Polycomb Repressive Complex and Rho GTPasee in Myelodysplastic stem cell, Microenvironment"
- Sequencing or microarrays on patients with acute lymphoblastic leukemia, with normal karyotypes to identify genetic abnormalities beyond the resolution of conventional cytogenetics and FISH.
- Sequencing or microarray analysis of hyperdiploid acute lymphoblastic leukemia to look for further sub classification and risk stratification.
- Sequencing and comparison of genetic findings in minimal residual positive (MRD) positive ALL samples and MRD negative ALL samples and look for a definitive predictive marker for MRD positivity at the end of induction
- Targeted Sequencing using customized baits in ALL to look form mutations in Ikaros, PDGF,CREBBP,PAX5, JAK1/2,CRLF2,ERG,RAS genes and correlate with their cytogenetic findings and MRD status.
- Exome Sequencing of the iamp 21 ALL samples and define the genetic landscape.
- Proposal to genetically define the squamous carcinoma of tongue in young women with no risk factors in collaboration with Dr Sandeep Dave's Lab
- The array and technology and the next generation sequencing will be also useful in studying other solid tumors in different studies.