REPORT

Report of the Fellow who availed Fellowship/Training under Human Resource Development for Health Research.

1	**Name and designation of Fellow**	Mitali Chatterjee, Professor
2	**Address**	Dept. of Pharmacology, Institute of PG Medical Education & Research, 244 B, Acharya JC Bose Road, Kolkata 700 020
3	**Type of Fellowship and period**	Short term HRD scheme of DHR 14th March- 15th April, 2015 (1 month)
4	**Duration of fellowship**	1 month
5	**Frontline area of research in which Training /research was carried out**	Pharmacogenomics
6	**Name & address of mentor and host institute**	Prof. Paul M Kaye, Centre for Immunology & Infection, Hull York Medical School, York YO10 5YW, UK
7	**Highlights of work conducted** **(i)Technique/expertise acquired**: ii) **Research results, including any papers, prepared/submitted for publication** (Give in about 300 words)	(i)We undertook a global transcriptomic analyses of *Leishmania* infected tissue sourced from an animal model of Leishmaniasis as also skin biopsies from patients with Post kala-azar dermal Leishmaniasis (PKDL). (ii)In India, where VL is anthroponotic, patients with PKDL are considered as the disease reservoir. Therefore the eradication of PKDL is an essential component of the VL elimination programme. Achieving this goal requires a greater understanding of the cause(s) of PKDL which is possible via a thorough understanding of the host–pathogen–vector triangle, especially a deeper understanding of the intimate interactions at the molecular level. Undoubtedly, the most rational approach would be an '-omics' approach. Accordingly, using whole-genome array technologies, we compared the gene expression profiles of liver and splenic tissues from mice infected by *L. donovani* to those of uninfected macrophages as also the impact of anti-leishmanial therapy. In parallel, dermal biopsies from patients with PKDL were similarly processed for conducting high-throughput RNA-Seq studies so as to characterize and compare the transcriptomes of skin biopsies obtained from human subjects with data from animal models of

		Leishmaniasis. Overall, the study indicated that Leishmania infection was associated with a significant upregulation of genes involved in biological pathways linked to the recruitment and activation of immune cells and to regulation of inflammatory responses. The study has provided data pivotal to better understanding the pathogenesis of PKDL. The data will provide the scientific community with a solid infrastructure for developing new diagnostics, as also develop alternative treatment strategies that could assist current programs aimed at breaking the transmission cycle of leishmaniases.
	iii) **Proposed utilization of the experience in the Parent Institute. (Please specify the project developed whether originally proposed/ new project):**	A publication is being prepared. (iii)A global transcriptomic analysis of dermal lesions in patients with Indian Leishmaniasis (both visceral and Post Kala-azar Dermal Leishmaniasis) will be undertaken. In collaboration with National Institute of Biomedical Genomics, Kalyani, a collaborative project proposal will be submitted shortly.

Signature of Fellow