

REPORT

Report on participation of the ICMR International Fellow (ICMR-IF) in Training/Research abroad.

1. Name and designation of ICMR- IF : Dr. Amitabha Bhattacharjee
2. Address : Department of Microbiology, Assam University, Silchar-788011, Assam
3. Frontline area of research in which training/research was carried out : NGS pipeline for analysis of antimicrobial resistance genes and fitness genes in bacteria.
4. Name & address of Professor and host institute : Dr. Mark Holmes
Department of Veterinary Medicine
University of Cambridge
Madingley Road, Cambridge, CB3 0ES
United Kingdom
5. Duration of fellowship : Three months
6. Highlights of work conducted : Enclosed as Annexure I
 - i) Technique/expertise acquired : NGS pipeline using software like bmap, FLASH, SPAdes, QUAST, and gene annotation by Prokka for genomic analysis of pathogens and AMR genes
 - ii) Research results, including any papers, prepared/submitted for publication : In preparation
 - iii) Proposed utilization of the experience in India : The parent institute has a DBT sponsored Bioinformatics centre. The training obtained by the fellow will help to establish the expertise the in the centre so that future research work will be initiated on combining in vitro and insilico analysis of resistome in pathogens to identify pathogen based biomarkers for their detection and newer drug targets. A joint grant proposal is already initiated which will be submitted within one month.


Signature of ICMR-IF

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Annexure I

During the fellowship tenure I have learnt the Next Generation Sequencing Pipeline for analysis of genome of pathogenic bacteria. It includes BBmap software package which is used to de duplicate the reads. Next to it FLASH software was used for merging the overlapping reads. Next de novo assembly was done by SPAdes. Next QUAST software was used for quality assessment of the scaffold. Finally gene annotation was done by Prokka software. In the study I sequenced antibiotic resistant *E. coli* isolates with and without acquired resistance mechanisms to analyse fitness genes which also takes part in resistance. I was able to identify the fitness genes *MdtO*, *MdtN*, *SugE*, *MdtK*, *MdtH*, *MdtF*, *MdtE* and stress resistance gene *BhsA*. Additionally fosfomycin and Polymixin B resistance determinants *fsr* and *arnA* respectively were also identified. Sequence of all the strains showed presence of these fitness genes signifies the potential role of them in antibiotic resistance.

Dantase
R. S. Sathyan