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Translation research in malaria: Molecular aspects of complicated human malaria

Ashis Kumar Das
Birla Institute of Technology and Science, India

Malaria is caused by protozoan parasites belonging to the genus Plasmodium. The four most prevalent of the human malaria parasites are *P. falciparum*, *P. vivax, P. malariae* and *P. ovale*. These infect humans in tropical and subtropical regions of the world and are thought to cause upwards of 2 million deaths annually. Malaria remains a very important vector borne disease in India, which is estimated as possessing the most disease burden amongst all the countries in the S.E Asia region. It has been projected that, outside Africa, half of the global population at risk from malaria resides in India. Plasmodium falciparum has long been known to cause complicated malaria including cerebral malaria. It is only recently that *P. vivax* has also been accepted as causing the same. We along with our collaborators published in 2005 an article in Emerging Infectious Diseases on complicated *P. vivax* malaria from India which was one of the first to attract the attention of scientists and public health professionals to this phenomenon. The talk will be in 3 parts. Initially, the significance of Natural Antisense Transcripts (NATs) in patient isolates of *P. falciparum* and *P. vivax* will be presented along with the probable significance of changes in sense/antisense ratios in complicated disease and some insights into the mechanism and significance of generation of NATs from microarray experimentation. This part will be based on our publications in both the parasite species and first reports in their own right. The second part of the presentation will provide highlights of certain aspects of the *P. falciparum* transcriptome based on our analysis of microarray data of non-cerebral complicated malaria. This analysis suggests the up-regulation of predominantly Var B and C of the members of the multigene family long thought to be implicated in complications from *P. falciparum* infections along with limited up-regulation of Var A. The expression of these families will be correlated with the exportome of the parasite. The WGCNA (Whole Genome Co-expression Network Analysis) leading to the identification of disease specific modules and hub genes in complicated *P. falciparum* malaria will be shown along with possible implications of the same.

Biography

Ashis Kumar Das joined BITS, Pilani, as an Assistant Professor in the year 1998 and is currently a Professor in the Department of Biological Sciences, BITS, Pilani, Pilani. He enjoys teaching, research and administration. He was formerly the Dean, Research and Counseling Division and Group Leader, Biological Sciences Group (now Department). He completed his Masters from Ballygunj Science College, Kolkata, and obtained his PhD from National Institute of Immunology, New Delhi, India.

adas@pilani.bits-pilani.ac.in

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