Genome Biology Talk

Human Malaria: drug resistance, genetic structure, evolution and complexity of infections

Speaker:
Dr. Surendra Kumar Prajapati
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Time and location:
September 24 (Wednesday) 10:00-11:00am, Room 4B104

Abstract:
Malaria is an ancient infectious disease caused by five species of *Plasmodia* in the human. *Plasmodium falciparum* and *P. vivax* are major human malaria parasites, known for causing mortality and morbidity to their vertebrate host, respectively. The disease still remains one of the major threats for public health, mainly due to emergence of virulence strains and spread of drug resistance against various chemical based interventions. The molecular age, population structure, and genetic heterogeneity of parasite play significant role in the manifestation of clinical pathology, disease transmission and success of malarial control program. We have identified and mapped mutations conferring resistance to Sulfadoxine-Pyrimethamine, Chloroquine and Artemisinin based combination therapy (ACT), which reveals signature of resistance against these drugs. Parasite genetic structure and evolutionary history were inferred by using a panel of novel molecular markers that was designed from *P. vivax* genome, uncovered an ancient existence of this parasite in the Indian subcontinent. Further, we have identified genetic polymorphism from major vaccine candidate genes and evaluated their impact on the efficacy of inhibitory antibodies. In addition, we have identified distinct genetic repertoire of *var/stevor* gene families that was associated with clinical complications. To further extend our knowledge on the level of parasite genetic structure within a host, we are identifying extent of heterogeneity of parasite in the patients. In conclusion, our data suggest a highly complex parasite genetic structure in the Indian geographical regions, higher level of genetic heterogeneity 'within host' and signature of drug resistance against various anti-malarials. These outcomes would be highly relevant in further designing of an effective control measures against malaria disease.

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