NANYANG TECHNOLOGICAL UNIVERSITY

School of Biological Sciences

Seminar Announcement

Translational Control Mechanisms Governed by tRNA Modifications in the *Plasmodium falciparum* Intra-erythrocytic Developmental Cycle

Date: 16 Sep 2016 Friday

Time: 4pm

Venue: Classroom 1, SBS

Speaker: Prof. Peter Preiser
School of Biological Sciences, NTU

Abstract

Poor correlation of mRNA and protein levels suggests a role for translational control of gene expression during the Plasmodium intra-erythrocytic life cycle. Among the components of translational machinery, the dozens of ribonucleoside modifications on transfer RNAs (tRNA) are emerging as critical regulators of cell physiology and stress response. However, little is known about malaria tRNA modifications and their roles in gene expression, making it an unexplored area of Plasmodium translational biology. We have now characterized the repertoire of tRNA modifications of *P. falciparum* and identified critical functions in tRNA maturation and stage-specific translation. *Plasmodium falciparum* has a standard set of eukaryotic tRNA modifications that resembles the model organism *Saccharomyces cerevisiae*. We show that these modifications are tightly regulated in two ways throughout the intra-erythrocytic developmental cycle (IDC) of the parasite. First, we observed a synchronized increase in most of the modifications from ring to trophozoite stage, suggesting tRNA maturation to meet stage-dependent translational needs of the parasite. To better understand the relevance of these changes in modifications, we use proteomics to quantify the abundance of >1000 proteins across the IDC. Strikingly, the most abundantly expressed proteins in the late stage of the IDC, but not early stages, have a marked codon bias that can be directly correlated with the corresponding increase in tRNA modifications. Based on these results, we propose a model for how tRNA modifications govern the late-stage of the malaria IDC by controlling the abundance of stage-specific proteins through facilitating selective translation of codon-biased transcripts. These findings together provide new insights into the translational control mechanisms in the development and pathogenesis of Plasmodium parasites.