NUS National University of Singapore | Department of Biological Sciences
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VIRTUAL BIOLOGY COLLOQUIUM

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Hosted by A/P Cynthia He

Spatiotemporal differences in codon recognition—due to changes in tRNA modifications—drive translational regulation during brown adipogenesis

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~1,500 protein components are needed to make a mitochondrion, but only 13 of these are encoded within the mitochondrial genome. We set out to understand the coordination mechanisms, in terms of translation regulation, that take place when massive mitochondria biogenesis is needed.

To this end, we used ribosome profiling and RNA-Seq, coupled with cellular fractionation, to measure RNA and translation levels in different cellular compartments during brown fat differentiation. Our sequencing data indicate that upon differentiation induction, increased translation capacity can be detected in the vicinity of mitochondria. Intriguingly, mRNAs enriched around the mitochondria tend to be more translationally upregulated, early on in differentiation, if they contain more G- and C- ending codons. This phenomenon is not seen in the rest of the cytoplasm until late differentiation. Such a shift in codon recognition implies that tRNAs around mitochondria might be differentially modified compared to those in the rest of the cytoplasm. Mass spectrometry analysis of tRNA modifications corroborates these findings.

This phenomenon could be linked to the production of reactive oxygen species (ROS) when mitochondria biogenesis is triggered upon differentiation. Changes in ROS levels are likely to alter the activity of tRNA modification enzymes and lead to codon recognition differences. These observations have implications in other disease contexts in which mitochondria biogenesis plays an integral role.

About the Speaker

Huili Guo graduated from the University of Cambridge in 2005 with a B.A. degree in Natural Sciences. In 2011, she received the Ph.D. degree in Biology from the Massachusetts Institute of Technology. She performed her thesis research in the laboratory of Prof. David Bartel at the Whitehead Institute for Biomedical Research, where she used ribosome profiling and RNA-Seq to study the molecular consequences of microRNA-mediated repression in mammalian systems. Huili is a recipient of National Science Scholarships from the Agency for Science, Technology and Research (A*STAR) in 2002 (BS) and 2006 (PhD). She is currently an Independent Fellow at the Institute of Molecular and Cell Biology in Singapore. She is also an Adjunct Assistant Professor at the Department of Biological Sciences at the National University of Singapore. Huili is a recipient of the L'Oréal Singapore For Women In Science National Fellowship (2014) and the President's Young Scientist Award (2016).

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