A KJELDGAARD LECTURE

Thursday 20 April 2017 at 13:15
1534-125 Auditorium F Mathematics
Same location for the PhD session

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USA

Codon optimality is a major determinant of mRNA stability in Eukaryotes

Work in my laboratory over the last decade has help define the relationship between mRNA translation and decay. We first demonstrated that mRNA degradation occurs co-translationally - such that both the initiation of degradation and 5′-3′ exonucleolytic digestion of the mRNA occurs while the transcript is associated with translating ribosomes (Hu et al., Nature 2009; Hu et al., Nature Struct. Mol. Biol. 2010). We next implicated DHH1 as an activator of mRNA decapping and regulator of translation that acts post-initiation (Coller and Parker, Cell 2005; Sweet et al., PLoS Biol. 2012). More recently, we uncovered that the identity of codons within the protein-coding region of mRNAs is a critical determinant of mRNA stability in yeast (Presnyak et al., Cell 2015). With regards to the latter, we have shown that mRNA decay rates are dictated by the percentage of codons deemed 'optimal' (based on the abundance of their cognate tRNAs relative to demand). We hypothesize that optimal codons are decoded by ribosomes more rapidly, while non-optimal codons are read more slowly (due to limiting tRNA concentration; Richter and Coller, Cell 2015), and that these differences in the kinetics of translation elongation are communicated by DHH1 to the mRNA decapping machinery as a means to modulate mRNA levels in the cell (Radhakrishnan et al., Cell 2016).

Host: Christian K. Damgaard, Gene Expression and Gene Medicine
Department of Molecular Biology and Genetics, Aarhus University

The lecture will be followed by a chalk-board session for PhD students

The Kjeldgaard Lecture Series is organised by
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