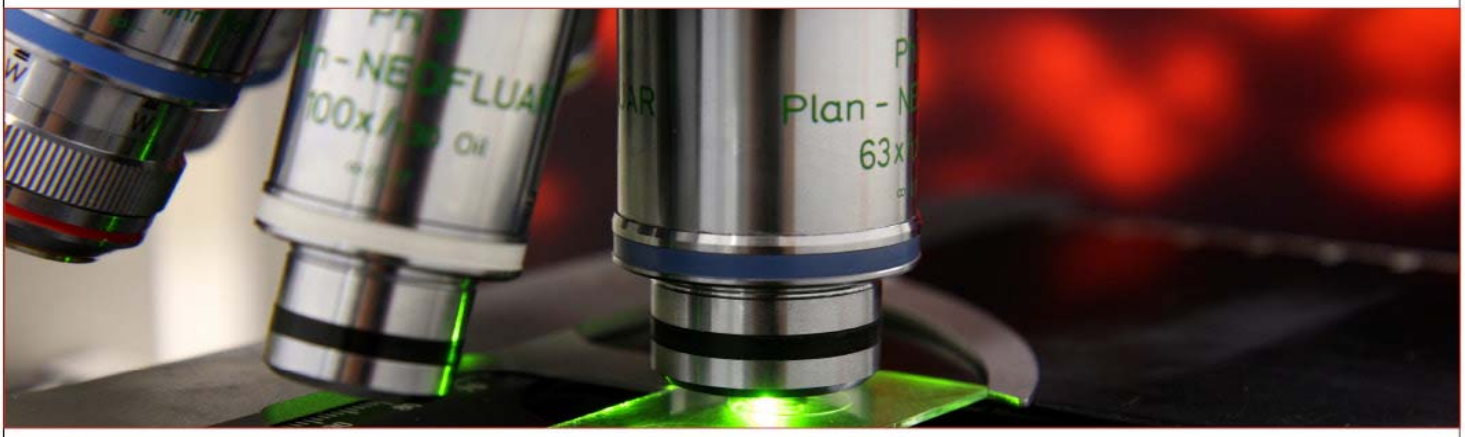
SÉMINAIRES ET CONFÉRENCES



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« Programmed translational bypassing in mitochondria: mechanism, mobility and origin »

A dramatic type of non-canonical translation called 'programmed translational bypassing' allows ribosomes to 'ignore' (jump across) a defined mRNA interval of several dozen nucleotides. Well-characterized bypassed sequences include the hop and byp elements, which are present in bacteriophage T4, and yeast (*Magnusiomyces capitatus*) mitochondria, respectively. Bypassing in T4 was shown to proceed by ribosome stalling at a stop codon, formation of a hairpin in mRNA, dissociation of peptidyl-tRNA and its reassociation at a matching site downstream. Further, hop is a mobile genetic element. The stunning number of byps (81) in mtDNA of *M. capitatus* further suggests that these elements are mobile, testifying to a recent burst of proliferation. Yet, the mobility of byps relies on fundamentally different mechanisms. Byps are more likely to spread like miniature DNA transposable elements known as GC clusters that are present in mtDNAs across hemiascomycetes.

Our findings evoke a host of questions. Which are the constituents of the *M. capitatus* translation machinery that accommodate translational bypassing - ribosomal proteins, ribosomal RNAs, elongation factors, tRNAs, and/or newly evolved components? Are extant byps still mobile, or a dead end of mobile element propagation? Further, how did hop and byps emerge in the course of evolution? Are byps related to mobile GC clusters that propagate like DNA transposons and that are common in fungal mtDNAs?

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Le lundi 23 janvier 2017, 12h00

Pavillon Roger-Gaudry
Salle : D-225

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