

## Universités de Paris, Master BMC

## Master 1 : Biomolécules et Cellules / Biologie Cellulaire Fiche de Projet de Stage, Année 2019-2020

Unité INSERM ou CNRS ou Université :

**UM7592** 

Institut Jacques MONOD

Intitulé Equipe:

Team Development, Signaling and trafficking

Responsable de l'Equipe : Pr. A. Plessis

Responsable du Stage : Dr. M. Sanial

**Contacts** 

Adresse: IJM 15 rue Hélène Brion

Email: matthieu.sanial@ijm.fr

Tel: 01 57 27 80 16

Titre du projet: Post-translational regulation of the RNA Binding Protein Smaug in Drosophila

Résumé du Projet de Stage (en 300 mots maximum, mots clés en gras)

A challenge in cell and developmental biology is to understand how inter- and intracellular signaling systems control gene expression. While post-transcriptional regulation of cytoplasmic transcripts is known to modulate their stability, localization and/or translation, knowledge of how these processes are regulated by cell signaling remains rudimentary. Cytoplasmic mRNA regulation is mediated by RNA-binding proteins (RBPs) and non-coding RNAs which co-recruit specific sets of mRNAs and protein factors that regulate the mRNA fate. Notably, these RBPs and their bound mRNAs often form dynamic membrane-less ribonucleoprotein (RNP) granules with liquid droplet-like behaviour whose assembly can be dynamically regulated in response to external and internal factors.

We are asking these questions in the context of Smaug, a conserved RNA-binding proteins which destabilizes and represses the translation of numerous target mRNAs from fly to mammals. Despite Smaug's central roles in Drosophila early embryonic development and the large number of transcripts regulated by Smaug, the regulation of its activity remains understood. We have recently obtained evidence that Smaug's protein levels, mRNA repressive activity—assessed thanks to a novel assay- and ability to form cytoplasmic bodies are all downregulated by its phosphorylation in response to the activation of a major morphogen and oncogenic pathway; the Hedgehog pathway. These data constitute the first evidence for a post-translational regulation of Smaug and suggest that the fate of one or several mRNAs bound to Smaug might be regulated by Hedgehog signaling.

The specific aims of this project are to

- (i) Assess the effect of their phosphorylation on the ability of Smaug to binds its target mRNA
- (ii) Analyze the impact of their mutation on Smaug function in vivo



## Universités de Paris, Master BMC

## Master 1 : Biomolécules et Cellules / Biologie Cellulaire Fiche de Projet de Stage, Année 2019-2020

Publications de l'équipe, relatives au stage proposé

1 page maximum SVP!