CRBM external seminar
BIOLuM
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Linking the bursting dynamics of transcription with the rapid onset of precision in the Bicoid system

Nathalie DOSTATNI

Institut Curie, Paris, France

Nathalie Dostatni obtained her PhD in 1991 under the supervision of M. Yaniv at the Pasteur Institute and was recruited as a CR2 at INSERM in 1989. After a five-year post-doc with Claude Desplan at the Rockefeller University, she started her team at the IBDM in Marseille with ATIPE funding. In 2001, she was appointed DR2 at INSERM and moved her team to the Institut Curie. Interested in combining research with teaching, she was recruited in 2001 as a professor in charge of teaching in Biology at Ecole Polytechnique, and became in 2012, Professor of Epigenetics at Sorbonne University. All along her carrier, her research focuses on the process of gene expression in eukaryotic cells using different models at the interface between the mechanistic aspects of transcription and chromatin dynamics, patterning and maintenance of cell identity during development, quantitative imaging, and mathematical modeling.

Abstract

Drosophila embryogenesis is characterized by rapid transitions in gene activity, whereby crudely distributed gradients of regulatory proteins give way to precise ON/OFF pattern of gene expression. To understand the underlying mechanism and explore the dynamics of gene expression in a quantitative manner, Nathalie Dostatni and her team have recently adapted to living embryos the MS2-MCP system, which allows the fluorescent tagging of RNA and the detection of ongoing transcription across development. This novel approach showed that a precise transcriptional response downstream of the Bicoid morphogen gradient is established in a very short time (3 minutes). The reconstruction of this regulation with synthetic reporters and modeling indicated that its spatial feature and temporal dynamics are compatible with an equilibrium model with a short decay length Bicoid activity gradient as a sole source of positional information. Meanwhile, Bicoid's partners sped-up the process either by lowering the Bicoid concentration threshold required for transcriptional activation or by reducing burstiness through increasing the length of transcription bursts.

Selected publications

Fernandes G, Tran H, Andrieu M, Diaw Y, Perez Romero C, Fradin C, Coppey M, Walczak AM, Dostatni N. Synthetic reconstruction of the *hunchback* promoter specifies the role of Bicoid, Zelda and Hunchback in the dynamics of its transcription. *Elife*. 2022. 11:e74509. doi: 10.7554/eLife.74509.

Zhang L, Perez Romero CA, Dostatni N and C Fradin. Using FCS to accurately measure protein concentration in the presence of noise and photobleaching. *Biophys J*. 2021. 120 : 4230-4241.

Tran H, Walczak A. M. and Dostatni N. Constraints and limitations on the transcriptional response downstream of the Bicoid morphogen gradient. Academic Press, *edited* by *Stephen Small and James Briscoe, Current Topics in Developmental Biology*. 2020.137, 119-142

Lucas T, Tran H, Perez Romero CA, Guillou A, Fradin C, Coppey M, Walczak AM and Dostatni N. 3 minutes to precisely measure morphogen concentration. *PLoS Genetics.* 2018. 14, e1007676.