Stochastic dynamics of a homeotic gene in the Arabidopsis flower: From models to quantitative analysis at a cellular level

Samuel Collaudin*[1,2], Aurélie Chauvet[1,2], Arezki Boudaoud[1,2], Anna Marciniak-Czochra[3], and Pradeep Das[1,2]

[1]Reproduction et développement des plantes (RDP) – CNRS : UMR5667, Institut national de la recherche agronomique (INRA) : UR0879, Université Claude Bernard - Lyon I (UCBL), École Normale Supérieure (ENS) - Lyon – bat. LR5 46 Allée d'Italie 69364 LYON CEDEX 07, France

[2]Laboratoire Joliot Curie – CNRS : USR3010, École Normale Supérieure (ENS) - Lyon – 46 Allée d'Italie 69007 Lyon, France

[3]Institute of Applied Mathematics and Interdisciplinary Center for Scientific Computing (IWR), University of Heidelberg – Im Neuenheimer Feld 294, 69120 Heidelberg, Allemagne

Résumé

The ABC model of floral organ identity determination is now a classical example of how combinatorial gene activities effect patterning during development. In the 25 years since the model was first proposed, the field has come to understand a lot about how the so-called A-, B- and C-class homeotic genes interact with each other, both genetically and molecularly, and how they in turn regulate the expression of specific target genes. However, one aspect that is still poorly understood is exactly how the ABC genes themselves become expressed in very specific spatial domains and at very specific times during flower development.

To address this question, I chose to focus on the expression dynamics of the C class gene, AGAMOUS (AG). It has been shown that AG expression first begins to appear in the centre, but not in the periphery, of 3 day-old flowers. However LEAFY and WUSCHEL, which are the main activators of AG, are present in the flower from day 1, well before the onset of AG expression. Similarly. APETALA2, which plays a key role in repressing AG expression, is also expressed at day 1. To understand how these regulators bring about the precise spatio-temporal regulation of AG, I have developed a simple dynamic model based on reaction-diffusion equations that reflected the principal known interactions of these regulators. I have also incorporated floral growth during the relevant stages in the model. A mathematical analysis of the model suggests that the auto-activation of AG coupled with the repression by APETALA2 defines a threshold in AG expression. It also suggests that AG diffusion plays an important role in its capacity to be highly expressed in the central dome just after activation.

To validate the different hypotheses output by the model, I have generated and imaged AG translational reporter lines, quantified expression at the cell level and used a statistical approach to describe AG expression in different genotypes. I observe that, contrary to the published literature, but in accordance with the predictions from the model, AG is first expressed at very low levels and in a few isolated cells, seemingly stochastically, at about

*Intervenant

day 2. Its expression then appears at slightly higher levels and in small cell clusters before expanding to occupy its known expression domain. Together, our models and observations suggest that three following features play an important role in AG regulation: (i) that AG expression appears in a stochastic manner, (ii) that AG must regulate its own expression, and (iii) that AG auto-activation must invoke a threshold. I am now in the process of testing these different features using specific molecular constructs.