

Cyclin G deregulation, a tool to decipher gene network(s) controlling developmental stability

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Cyclin G deregulation, a tool to decipher gene network(s) controlling developmental stability





A central challenge in developmental and evolutionary biology is to understand **developmental stability**, the process that buffers developmental noise. In bilaterians, developmental stability is estimated by Fluctuating Asymmetry (FA), the random deviation from perfect symmetry within an isogenic population bred in a standardized environment.

Overexpression of Cyclin G (CycG), encoding a cyclin involved in the regulation of transcription and in the cell cycle, induces an unprecedented increase in wing FA. This phenotype is associated with loss of correlation between total cell number and mean cell size in adult wings. Moreover, it is linked to the role of Cyclin G in transcriptional regulation. CycG deregulation is used as a tool to identify gene networks underlying developmental stability.

- Developmental stability and Fluctuating Asymmetry

V - The effect of Cyclin G on developmental noise is related to its role in transcription

Developmental robustness Canalization Environmental Genetic variations variations **Developmental stability** — Developmental noise

Developmental noise is assessed by Fluctuating Asymmetry (FA) in isogenic lines raised in a standardized environment



II - CycG misregulation increases developmental noise





VI - Several Polycomb-group (PcG) or Trithorax-group (trxG) gene mutants modify CycG-induced developmental stability





VII - Identification of Cyclin G transcriptional targets

RNA-seq of wing imaginal discs overexpressing *CycG* reveals a sub-network of 189 deregulated genes potentially involved in developmental stability

Network of 189 co-deregulated genes



Ontology of co-deregulated genes: (mRNA splicing, translation, EGFR and insulin signaling, glucose metabolism)



IV - Cyclin G is a trancriptional regulator

Cyclin G interacts with two chromatin regulators of the Enhancers of Trithorax and Polycomb family (Corto, ASX)



Cyclin G binds polytene chromosomes where it extensively co-localizes with ASX



(C. Dupont in preparation)

Ongoing projects and Future investigations

- ✓ Determine genome-wide binding sites of Cyclin G (Chip-Seq), to identify direct transcriptional targets by correlation with RNA-seq
- Continue the candidate gene approach to find modifiers of CycG-induced FA (gene) encoding direct interactors, genes involved in epigenetic memory, in growth pathways)
- \checkmark Build gene network(s) that control developmental stability based on modifiers of CycGinduced FA

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