V Taller de Biología Celular y del Desarrollo

PROGRAMA & LIBRO DE RESÚMENES

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Biología Celular y del Desarrollo

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and the well-established and crucial function of the phytohormones auxins in hook development. In this work we dissect different aspects of auxin biology in HYL1 mutants (auxin sensitivity, transcriptional responses, biosynthesis and transport) and found that HYL1 is needed to establish the auxin gradient in apical hooks. Our research led us to propose that HYL1 might integrate light/dark and auxin signals to control skotomorphogenic growth in Arabidopsis.

036- ¿PUEDEN LOS MODELOS MATEMÁTICOS CONTRIBUIR A UNA MEJOR COMPRENSIÓN DE LOS PROBLEMAS BIOLÓGICOS?

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El creciente uso de modelos cuantitativos en Biología es evidente. Esto se debe en parte a las enormes innovaciones tecnológicas de los últimos tiempos que permiten el acceso a una gran cantidad y variedad de datos experimentales. Para poder abordar, sistematizar y comprender estos datos los modelos matemáticos son herramientas poderosas, que además, permiten hacer predicciones. En esta charla discutiré dos problemas de interés en Biología del Desarrollo: la señalización a través de la vía de Notch y la formación de patrones espacio-temporales. Mostraré que el análisis teórico de un modelo para inhibición lateral asociado al estudio de imágenes de microscopía confocal de células del intestino de Drosophila permite entender por qué los destinos de células madre vecinas no siempre son asimétricos. También discutiré la relevancia de la señalización a distancia a través de filopodios en la inhibición lateral, y su impacto en los patrones espacio-temporales de diferenciación celular.

037- A NEUROPEPTIDE SCREEN TO IDENTIFY MODULATORS OF BEHAVIORAL ALTERATIONS INDUCED BY CONFINEMENT

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The relevance of the word “confinement” and the negative effects it has on physical, mental, and emotional wellbeing has become particularly evident to humanity during the COVID-19 pandemic, when mandatory or fear-induced self-confinements were highly effective in reducing viral spread, but they also severely disrupted human behavior. The molecular and neural mechanisms underlying the translation of physical confinement to internal state changes and how these alter behavior are poorly understood and very difficult to study in natural settings due to an excessive number of possible confounding factors. Innate behaviors, which are complex, genetically-encoded behaviors that proceed with a predictable sequence, provide a unique window to study the effects of confinement on behavior. We used the wing expansion behavior that Drosophila juveniles perform upon eclosing from their puparium to unravel both the molecular and cellular correlates of behaviorally-relevant, confinement-induced changes in internal states. Newly emerged flies select a suitable place to perch and initiate a stereotyped behavior that leads to the expansion of the folded wings. The execution of this behavior, which is triggered by the hormone Bursicon, is strongly negatively-regulated by spatial confinement.

Placement of flies in small chambers extends the perch selection phase, but the environmental cues, neural circuits and molecular mechanism that mediate this decision remain unknown. Here, we describe our experimental setup and present the preliminary results of our pan neuronal RNAi silencing screen devised to test the requirement of neuropeptides and neurotransmitters in this behavioral choice.

038- RAPID IMMUNOPRECIPITATION MASS SPECTROMETRY TO IDENTIFY PROP1 PARTNERS THAT DIRECTS PITUITARY GLAND DEVELOPMENT

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Prop1 is the first pituitary specific transcription factor that leads gland development and lineage differentiation into the hormone-expressing cell types, but little is known about the regulation of this process. The general objective of this work was to elucidate the PROP1 protein complexes in order to understand its role during pituitary development and to evaluate them as candidate genes that can cause related disorders. We used the murine pituitary cell line GHFT-1, engineered to express biotinylated PROP1, and conducted RNA-seq and Rapid Immunoprecipitation Mass spectrometry (RIME). Differential gene expression analysis indicated that PROP1 upregulated 240 genes and downregulated 201 genes in Prop1 cell line compared to control (fold change=l1.5l). DAVID analysis showed that the most regulated GO terms were related to extracellular matrix, cell adhesion and junctions and positive regulation of proliferation and cell migration. Ontology enrichment analysis shows that PROP1 immunoprecipitated with several nuclear proteins related to transcriptional regulation and splicing and also with many non nuclear proteins related to cell adhesion and migration. These results are in agreement with previous observations from our group, where we showed that Prop1 induces the EMT-like process in the stem cell population. To further unveil PROP1 partners we used LISA which predicts transcriptional regulators using chromatin accessibility and histone mark ChIP-seq data. We used as input the genes that intersected from the PROP1-ChIP-Seq and RNA-seq experiments and obtained 536 genes. Of these genes, 37 were present in the RIME. We took advantage of scRNA-Seq data from postnatal mouse pituitaries to test their expression in Prop1 + cluster cells. We found enrichment for the Nuclear Factor I/B or NFIB. Furthermore, we observed by RNAscope a similar expression pattern of Nfib and Prop1 in e12.5 mouse embryos, consistent with the idea of being part of the same protein complex. Further experimental work is needed to validate PROP1 interaction partners. Understanding the transcriptional complex formed will shed light on the pivotal role of Prop1 in pituitary development.

039- ROL DE LAS CÉLULAS VECINAS EN EL PROCESO DE REGENERACIÓN DE NEUROMASTO EN ZEBRAFISH

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