reduced in *Scaphiopus couchii* as a consequence of adaptation to ephemeral breeding ponds. As a result of this adaptive process, *S. couchii* now presents several features that resemble an accelerated version of *P. cultripes*: from overall morphology to fat storages to metabolic rate and endocrine regulation of development. To understand how the transcriptional regulation may have evolved between these divergent species, we have also characterized the gene regulatory network underlying developmental rate in both *P. cultripes* and *S. couchii*. We have investigated whether the same underlying transcriptional profile is conserved across species, and whether it varies between species in its environmental sensitivity. Spadefoot toads provide a good example of how canalization of ancestrally plastic traits can contribute to adaptive divergence and evolutionary novelty.

S4.P.6

First-Time Cis-Regulatory Interactions between Mammalian-Specific TFs and the Zebrafish Genome: Understanding First Time Encounters in Molecular Evolution

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Biological entities, whether proteins, blue whales, sensory organs or cis-regulatory elements are continuously interacting with other structures, establishing complex networks through which biological information is exchanged. These interaction networks are assembled and maintained during the course of evolution. But, what happens when new elements are incorporated for the first time into these systems? We have expressed highly divergent mammalian-specific homeodomain transcription factors (TFs), such as LEUTX and ARGFX, in the completely foreign chromatin environment of zebrafish embryos. We show that LEUTX mRNA injection disrupts early zebrafish development and embryos are arrested during early gastrulation. In the case of ARGFX, ChIP-seq experiments of injected zebrafish embryos show that the ectopic binding sites in zebrafish are preferentially found in chromatin regions that are open and accessible during zebrafish development, some of them are found in the zebrafish orthologues of ARGFX endogenous

target genes in mammals. Our results suggest that biological molecular structures, such as TFs, have inherent capacities to interpret and read the information contained in other biological systems, even when these systems have not co-evolved with and are foreign to these biological structures.

S4.P.7

Genome-wide studies of the dynamic of regulatory information during sea urchin development

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Animals exhibit an astonishing morphological disparity in body plans but also they share many genomic features. Indeed, comparative studies suggest that the several factors composing gene regulatory networks defining developmental tissue layers are conserved in triploblastic animals. A regulatory code of interactions between transcription factors (TFs) and cis-regulatory elements (CREs) determines whether target genes are transcribed in a strict spatial and temporal domain. Therefore, the identification of CREs is crucial to elucidating transcriptional programs across taxa and, because active CREs lay in accessible regions of the chromatin, ATAC-seq method has been exploited to systematically profile regulatory elements associated to open chromatin regions. To better understand modules of regulation during the development of deuterostomes, we generated ATAC-seq libraries of sea urchin, a distant related to vertebrates, at different developmental stages. Then, we identified several clusters of CREs based on the dynamic of the ATAC signal over time. These clusters are characterized by different enrichment in binding motifs of TFs. By combining these temporal data of regulation with the expression level of gene associated to CREs, we aim to define different temporal categories of regulation in sea urchin as a new tool to compare different organisms regardless their anatomy in order to gain insights into the role of regulatory landscape changes in the evolution of gene expression throughout animal development.