To dissect the role of ISWI-mediated chromatin remodeler in controlling stem cell self-renewal, I developed a strategy to purify a large numbers of pure GSCs from the Drosophila ovary. Using this approach I generated a genome-wide transcriptome and chromatin-binding profile of ISWI on GSCs chromatin. To identify the potential regions of the genome that are bound by ISWI in GSCs, I conducted a ChIP-Seq analysis and found nearly 7000 ISWI bound coding genes. Moreover, RNA-Seq experiments conducted in ISWI mutant GSCs revealed ISWI as major regulator of about 70 % of its target genes in GSCs. Furthermore, by gene ontology analysis I identified specific gene networks under the control of ISWI. Particularly, I found that the ISWI regualtes genes playing an essential role in the maintenance of GSCs.

Our data suggest that the ATP-dependent chromatin remodeler ISWI works as a master regulator of GSCs self-renewal in the Drosophila ovary.

Reevaluating the function of a transcription factor: MBF-1 as a sea urchin chromatin organizer ?

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The Zinc-finger MBF-1 factor is involved in the expression of the early histone genes during development of the sea urchin embryo (1, 2). In spite of being a transcription activator, the DNA-binding domain of MBF-1 shares high sequence similarity with that of the chromatin organizer CTCF of vertebrates and drosophila (3). On the other hand, extensive *in silico* analysis failed to identify the sea urchin CTCF ortholog (4). This led us to speculate that MBF-1 somehow could have co-opted the function of CTCF during evolution of the echinoderms. Since in vertebrates CTCF binds *Hox* chromatin, to support our hypothesis, we first identified high-score putative binding sequences for CTCF/MBF-1 within the single sea urchin *Hox* gene cluster. Moreover, we observed the full evolutionary conservation of these binding sites in *S. purpuratus* and *P. lividus* species. Worth of mention, by chromatin immunoprecipitation (ChIP) assay, we detected the occupancy of MBF-1 on *hox11/13-a*, *-b*, and *-c* regulatory sequences at distinct stages of development. As expected from the binding of an activator, we found that the association of MBF-1 to the *cis*-regulatory sequences of both *hox11/13-a* and *-b* genes relates to the transcriptional status of these genes. Strikingly, we also mapped the physical binding of MBF-1 to *hox11/13-c*, which is instead not expressed during embryogenesis. Altogether, these observations indeed suggest the possibility that MBF-1, besides being a transcription activator, could also function as a general chromatin organizer. To further support this hypothesis, we are planning ChIP-seq experiments to identify the association of MBF-1 to the sea urchin chromatin at a genome-wide level.

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