



Seminar/Talk

Evolution of transcriptional and post-transcriptional regulation: insights from a sea anemone

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How complex animal body plans could arise in evolution is one of the fundamental questions in biology. We address this question by investigating the underlying genomic, molecular and developmental processes that led to the diversification of animal body plans. We use cnidarians (jellyfish, corals and anemones) as model organisms to understand the evolution of key bilaterian features: bilaterality, central nervous systems and three germ layers. Our approaches to these questions are comparative and functional genomics in combination with developmental biology: The sequenced genome of the sea anemone *Nematostella vectensis* revealed many genes usually associated with the formation of the two body axes, the three germ layers and the nervous system in Bilateria and we are now studying their function by means of overexpression, morpholino-mediated knockdown, CRISPR/Cas9 knockouts and transgenics. Since the presence of these genes does not necessarily enforce the formation of the structure they are responsible for in bilaterians, the difference between cnidarians and bilaterians is likely in the gene regulatory network, both on the transcriptional level as well as on the post-transcriptional level. In order to address the question how gene regulatory networks could evolve, we established a number of molecular tools and genomic resources for *Nematostella vectensis*.

Wednesday, September 27, 2017 12:30pm - 01:30pm

I22 Lakeside View (I22.01)



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