



## **ABSTRACT**

### **“Unraveling the organization and evolution of biological regulatory systems in eukaryotes”**

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The diversity and complexity of multicellular eukaryotes is caused by the underlying molecular interactions driving development, growth and adaptations to various environmental conditions. Based on the assumption that the diversity in protein functions is responsible for this variation, many studies have focused on the evolution of these protein-encoding regions. Nevertheless, given the limited amount of species-specific genes in contrast to the large amount of homologous genes in the genomes of many species, it is obvious that additional mechanisms like variation in gene expression and post-transcriptional/translation modifications, together with different types of functional elements, also contribute to phenotypic diversity. Although the availability of whole genome sequences, accelerated by recent technological innovations, offer a detailed view on the raw DNA of an increasing number of model species, our understanding of the different types of information encoded within the genetic material remains limited. Consequently, expanding our knowledge about the regulatory mechanisms embedded in the genomic DNA of uni- and multicellular plants remains a highly relevant and topical research objective. Whereas the identification of functional elements in an organism's genome (using comparative genomics) provides a draft map of all potential molecular interactions, the integration of various experimental data sources such as gene expression profiling and transcription factor protein-DNA interactions will undoubtedly reveal new insights about the components and regulatory mechanisms controlling biological processes. Complementary, establishing the evolutionary constraints on biological system architectures and identifying the molecular mechanisms that generate organismal robustness and diversity are major challenges for understanding growth, development and potential adaptation to new environments.

(iii) New molecular tools to study diatoms have been developed in then recent years including genome sequencing and transformation techniques.