COEVOL COÉVOLUTION MULTI-ECHELLES

EQUIPE GÉNOMIQUE EVOLUTIVE ET FONCTIONNELLE

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A primary goal in biology is to construct a functional map of the genome, linking each DNA sequence to its molecular roles and to the cellular and organismal processes in which it takes part. Thanks to the development of molecular technologies, which provide genome-wide maps of transcription, protein and RNA binding, chromatin state and topology, etc., we are now considerably closer to this goal. However, uncovering the biochemical activity associated with each DNA sequence is not sufficient to prove its functionality, as numerous active genomic elements may be redundant or altogether dispensable, resulting from inherent noise in cellular processes. Evolutionary genomics approaches can help bridge the gap between biochemical activity and biological functionality, by identifying genomic elements that are subject to purifying natural selection to maintain their functional properties or to positive selection following the acquisition of new functions. With this motivation, I am interested in the evolution of long non-coding RNAs, a class of transcripts that are pervasive in mammalian genomes and whose functionality is still largely debated (Necsulea et al., 2014; Darbellay & Necsulea, 2020). I have addressed this question through comparative transcriptomics analyses across multiple species, tissues and developmental stages.

Another facet of my research focuses on the evolution of gene expression regulatory mechanisms. I am particularly interested in the organization of mammalian cis-regulatory landscapes, in particular in the long-range interactions between gene promoters and distant regulatory elements. Data on long-range contacts between promoters and regulatory elements is rapidly accumulating. However, it remains unclear how these regulatory relationships evolve and how they contribute to the establishment of robust gene expression profiles. Alexandre Laverré, currently a PhD student jointly supervised with Eric Tannier, addresses this question by exploiting high-throughput chromatin conformation capture data for human and mouse (Laverré, Tannier & Necsulea, in revision).