

Challenging the validity of the stoichiogenomic theory

The emerging field of 'stoichiogenomics' (Elser et al. 2011) aims at understanding the influence of nutrient limitations on the elemental composition of the genome, transcriptome, and proteome. The 20 amino acids, as well as the 4 nucleotides, differ in the number of nutrients they contain (e.g., carbon, nitrogen, oxygen, or sulfur). Thus, changes in the elemental composition of DNA, RNAs, or proteins may to some extent decrease nutrient requirements and increase the fitness of an organism facing environmental limitations. This hypothesis conceptually applies to any element, but it proved particularly relevant on nitrogen (N), as this nutrient is frequently limiting in natural ecosystems while making up a large proportion of the biological macromolecules (proteins & nucleic acids). Thus, N limitation could theoretically select for changes in the composition of proteins or RNAs through the preferential use of N-poor amino acids or nucleotides.

Such N-saving mechanisms have been reliably evidenced in marine microorganisms (Luo et al. 2015; Lv et al. 2008; Grzymski and Dussaq 2012), but they remain controversial in multicellular eukaryotes. Recent studies on metazoans or plants supposed to face N-limitation have described stoichiogenomic-like patterns, which were interpreted as evidence for N-saving adaptive mechanisms. However, most of these studies lacked a robust phylogenetic framework and/or were based on inaccurate comparisons of elemental composition between sequence bulks (and not between orthologous sequences). Moreover, non-adaptive processes such as changes of mutational pattern or variation of the strength of GC-Biased Gene Conversion, which may both create stoichiogenomic-like patterns, were not considered. The few studies accounting for these pitfalls (Günther et al. 2013; Francois et al. 2016) did not validate any of the stoichiogenomic assumptions in multicellular organisms, even when considering strongly N-depleted environments such as groundwater. The absence of stoichiogenomic mechanisms may be explained by the small effective population size of multicellular eukaryotes, natural selection being not efficient enough to retain weakly beneficial N-saving point mutations. Alternatively, other N-saving mechanisms might have been selected faster at higher organization levels, relaxing the selective pressure on nutrient requirements (e.g. through a decrease in metabolic rate).

These methodological issues call for a comprehensive revision of all stoichiogenomic evidence published so far. This internship project will assess the reliability of the stoichiogenomic theory across the tree of life, by applying to all stoichiogenomic-relevant datasets (plants, microorganisms, metazoa) a common robust procedure to detect any signature of N-saving mechanisms in N-limited environments. Phylogenetic structure of the datasets will be accounted for when comparing the elemental composition of orthologous sequences (proteins & nucleic acids). When possible, expression levels will also be considered. At a finer scale, the 'strand-asymmetry' test developed in Francois et al. (2016), which allows to discriminate between adaptive and non-adaptive mechanisms, will be used to detect the strand-asymmetric signature that stoichiogenomic selection should leave in the substitution pattern. This project will require good bioinformatic skills to retrieve, process and analyze genomic datasets.

References:

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Supervision and application:

The student will be supervised by Clémentine Francois, Tristan Lefébure and Laurent Duret. The intern will be hosted at the research team LEHNA (Laboratoire d'Ecologie des Hydrosystèmes Naturels et Anthropisés, UMR-CNRS 5023), and collaborate with the LBBE (Laboratoire de Biométrie et Biologie Evolutive, UMR-CNRS 5558), in Lyon.

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