July 16-21, 2017 at UC San Diego, CA, USA

Molecular innovation in ciliates with complex genome rearrangements

R. Neme[1*] and L. F. Landweber[1,2],
[1]Columbia University, Department of Biochemistry and Molecular Biophysics, [2] Columbia University, Department of Biological Sciences
* rn2419@cumc.columbia.edu

Molecular innovation, as the process that produces new functions in an organism, provides a window of opportunity to understand the transitions from non-genic, non-functional material into new genes, functions and structures.

Ciliates, unicellular eukaryotes with two types of nuclei, possess the remarkable ability to rearrange their genomes in processes that involve the selective deletion, ligation and reorganization of genetic information from a sexual genome into a somatic genome. These arrangements can be simple or complex, depending on whether fragments of DNA are joined in the same order in the final product, or whether the rearrangements require translocation or inversion. This type of genomic architecture provides abundant plasticity and increased potential for innovation relative to other eukaryotic lineages.

Molecular innovation profits from the organization of biological information. Most organisms obtain novelty from mechanisms such gene duplication, gene fusions, alternative splicing, or de novo. In ciliates, it can be assumed that all such mechanisms are generally active. Furthermore, it has been shown that alternative DNA processing is able to produce new genes [1], and as such constitutes a ciliate-specific innovation that produces further innovation. This is likely to have contributed greatly to the molecular and functional diversification on stichotrich lineages. We are interested in the evolutionary steps leading to this type of genomic architecture, and the influence it has had on evolutionary innovation.

We undertake phylogenomic analyses of various ciliate species, and explore how the rate of acquisition of new protein-coding genes has accelerated in lineages of ciliates with complex genome rearrangements. Further, we assess genome-wide error rates of the rearrangement process in the model species *Oxytricha trifallax*, aiming to understand how the cellular machinery deals with errors, and how much of those errors could contribute to the conversion of non-coding elements in the genome into new genes.

[1] Chen X et al. 2016. *Genome Biology and Evolution* 7: 2859-2870