

Joint Colloquium
Ecological Colloquium
Cologne Evolution Colloquium

Wednesday, Oct. 11th at 4:00 pm, Ecological Colloquium, Biocenter Hörsaal.

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Evolutionary forces affecting base composition in coding sequences of plant genomes

Base composition is highly variable among and within plant genomes, ranging from GC-poor and homogeneous species to GC-rich and highly heterogeneous ones. Consequently, synonymous codon usage is biased in most species, even when base composition is relatively homogeneous. The extent and causes of these variations are still under debate, with three main forces being possibly involved: mutational bias, selection and the recombination-associated process GC-biased gene conversion (gBGC). I will first present a global description of genic GC-content in more than 200 species across the flowering plant phylogeny. We found continuous variations in nucleotide landscapes from GC-poor and homogeneous genomes to GC-rich and highly heterogeneous ones (especially in Monocots), with GC-richness associated with sharp 5'–3' decreasing GC content gradient along genes. Reconstruction of the ancestral GC-content distribution showed that GC-richness and heterogeneity were ancestral to most Monocot genomes and have been eroded in some lineages since. Then I will present a set of methods we developed to jointly estimate the intensity of selection, gBGC and mutation bias and an application example to a population genomic dataset of 11 angiosperm species, including both Monocot and Eudicot species. We found that base composition is far from mutation-drift equilibrium in most genomes and that gBGC is a widespread and stronger process than selection. In the most GC-rich Monocots, gBGC was also found to be stronger in 5' than in 3' regions, in agreement with the observed 5'–3' GC gradient. Combining these results, I will discuss a model we proposed to explain patterns of GC content variation at the gene and genome scale in plant species: we proposed that GC content patterns could be mainly determined by the interactions between gene structure, recombination patterns, and gBGC.

Host: Juliette de Meaux