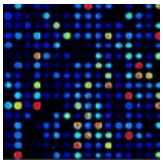
Séminaire – Math For Genomics

Séance du mercredi 17 juin 2020. 11h.
Evry. IBGBI. LaMME.

Co-adaptation in plant genomes



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GENOPOLE

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Detecting the effects of co-adaptation in plant genomes

Mitochondria and chloroplasts play crucial roles in energy metabolism and environment sensing and response. Although these roles heavily rely on nuclear genes, both organelles contain a tiny proportion of the genes necessary for their respective functions in energy metabolism, respiration and photosynthesis. Coadaptation between organellar genomes and the nuclear genome at the specific level has been observed for many years, in many eukaryotic lineages. More often it is revealed by deleterious phenotypes appearing in individuals associating the organelle genome(s) from one species with the nuclear genome from another species. This coadaptation is considered to result from responses, throughout evolution, to variation in either genetic compartment by compensating variation in the other.

At the within species level, interest for intraspecific variation in organellar genomes has arisen as evidence accumulate for its potential adaptive role. However, because the functions ensured by organellar gene products rely on their interactions with nuclear-encoded factors, the cytonuclear interactions need to be taken into account while exploring the phenotypic effects of cytoplasmic variation. We used dedicated genetic resources to address this question in the model plant Arabidopsis thaliana: cytolines designate genotypes associating the nuclear genome of one natural variant (accession) with the organellar genomes of another.

We will present various experiments, from molecular phenotyping to global phenotyping in the field, performed on cytolines and their parental accessions, and the analyses developed to detect the phenotypic effects of cytoplasmic variation and of the disruption of cytonuclear coadaptation at the within species level.