



DynaGeV

Dynamique des Génomes Végétaux

Workshop on Plant Genome Dynamics and Evolution

CIRAD Campus de LAVALETTE - MONTPELLIER

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Evaluation of methodologies for the characterization of plant mosaic genomes

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Hybridization events between species and subspecies are considered as major evolutionary steps, possibly contributing to the advent of new phenotypes. These events are widespread in several crop species and are expected to produce genomes with a mosaic structure of sequence blocks from different ancestry. Characterizing the inter(sub)specific mosaic structure of crop plant genomes that result from recent hybridization events can help understanding how they were formed, their domestication history, and possibly the ancestral origin of phenotypic traits.

With the development of NGS genotyping technologies, several population genomics approaches have been proposed to infer the ancestry of genome segments, by comparing polymorphism patterns across individuals along chromosomes. However, these Local Ancestry Inference (LAI) methods have mainly been developed for applications in animal models, and human most particularly. They are based on assumptions which do not always fit plant models due to more complex genome structures (e.g. different ploidy levels, variable heterozygosity levels within species) or different reproductive systems (e.g., vegetative propagation, selfing). In this context, there is a need to evaluate available methods on plant models.

To that end, we developed a small and flexible R program to simulate data under a wide variety of scenarios representative of plant model characteristics. We use this tool to evaluate two main types of LAI methods: exploratory approaches (based on multivariate analysis) and full probabilistic approaches (based on Hidden Markov Model). First results will be presented and discussed.