



# PO0051 - Biodiversity Analysis in Plant Genomes : An Innovative Capture Approach to Characterize Targeted Region of Interest

## Abstract

In a context of climate change, population growth and limited energy resources, plant genomes knowledge is essential for a better understanding of mechanisms driving plant adaptation and evolution. Deciphering plant genomes is one of the strategic approaches. However, this remains challenging due to the high level of complexity of plant genomes in terms of size, polyploidy levels and repetitive elements contents.

Moreover, due to high intra-species variability, a single reference genome is not enough to understand complex biological processes, such as resistance to biotic or abiotic stresses. Understanding the link between a genomic region and a phenotype of interest requires a reliable sequence information from the specific cultivar carrying this trait of interest.

Due to the evolution of Long-Read Sequencing technology (Pacific Biosciences or Oxford Nanopore Technology) in term of chemistry and cost, genome information become more accessible. However, the cost of whole genome sequencing can remain high due to the complexity of plants, especially to study multiple genotypes at once. Focusing on a genomic region of interest is an alternative solution for diversity analysis.

Here we present an update of an innovative sequence capture approach aiming at targeting large DNA fragments in eukaryote genomes. This strategy is adapted from the CRISPR-Cap method (Cas9-Assisted Targeting of Chromosomal segments) described by Lee and al. in 2018. CNRGV adapted this protocol by using a Cas9 enzyme deprived of its endonuclease function coupled to a cluster of gRNA specific to the region of interest to be captured. We present the efficiency of this strategy to: (i) characterize complex viruses' insertions in banana genome and (ii) identify the sex locus in grapevine.

