



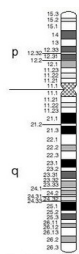
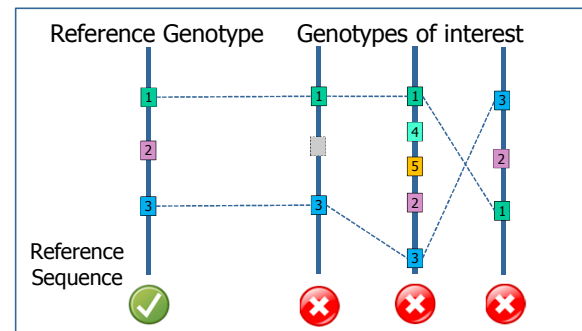
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- The **CNRGV** (French Plant Genomic Resources Center) aims to support plant genomics research as service provider or in the framework of collaborative projects
- Its mission: **link traits of interest to the genomic regions** underlying them to better understand genetic factors governing plant evolution and adaptation

❖ Plant genomes display a high complexity (large size, polyploidy, repetitive elements)

- ❖ The scientific question must define the relevant strategy to decipher this complexity
- ? Exhaustive information on whole genome vs reliable information of the region of interest
- ? Interest to characterize the genomic diversity within or between species

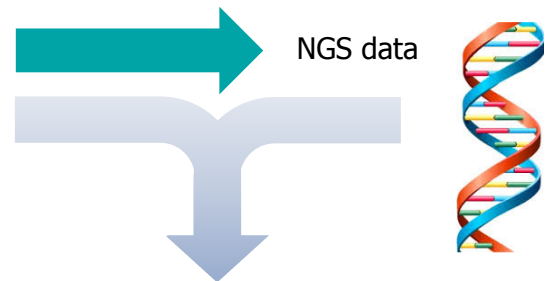
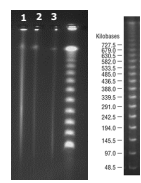
✓ The CNRGV proposes **combined strategies to deliver high quality data** on genomic regions of interest while making allowance for the scientific question and the dimension of the project



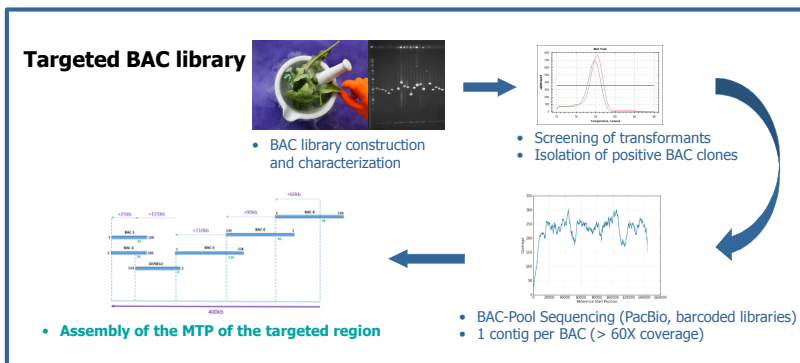
Genetic & sequence data

## High Molecular Weight DNA extraction

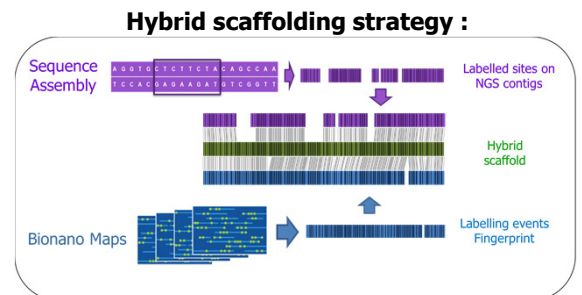
Pulse field gel electrophoresis of sunflower high molecular weight DNA  
Starting material : 2g of frozen leaves  
Dilution 1 (1), 1/3 (2) and 1/6 (3)



## Deciphering plant genome complexity to target the genomic region of interest



## Optical Map production using the Saphyr system from Bionano Genomics



### 1 - Whole genome assembly

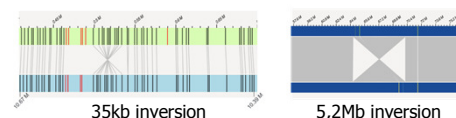
Case study of the sunflower XRQ genome

	Statistic	Original BNG	Original sequence	Sequence used in hybrid scaffold	Hybrid scaffold	Hybrid A + leftover unscattered sequence
DLE-1	Number of maps	69	11676	8738	25	5317
	N50 (Mb)	175.21	0.52	0.46	176.33	175.95
	Total length (Mb)	3057.67	2926.51	2792.45 (95.42%)	3000.44	3134.36

2359 cuts were made on 1167 sequences during chimera detection. Cuts can be due to chimera or allelic difference.

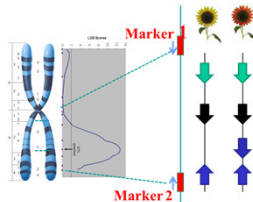
### 2 - Structural variations detection

Example of structural variation between cultivars



## CRISPR-CATCH targeting strategy

We adapted a sequence capture approach to plant genomes, called CATCH (Cas9-Assisted Targeting of Chromosomal segments, Jiang et al., 2015).



Two guide RNA-guided are used to capture genomic regions up to 700 kb. Targeted genomic region is sequenced using long read sequencing technologies.

This method allows to compare the diversity of a locus of interest with between several.

**More information:**  
**PE0088** Development of a CRISPR/Cas9 Large DNA Fragment Targeting Technique for Plant Genomes

Service requests, information and proposal for collaboration:

<https://cnrqv.toulouse.inra.fr/Services/>

