

Centre de ressources biologiques et structure d'appui aux projets de recherche en génomique végétale

Relier les caractères d'intérêts des plantes aux gènes et à la structure des génomes

## Objectifs et missions du CNRGV

Conserver et diffuser des **banques génomiques végétales** et données associées

Développer des **outils génomiques innovants** pour l'analyse des génomes

Proposer un catalogue de services cohérents afin de **soutenir des projets scientifiques de dimension et de nature variées**

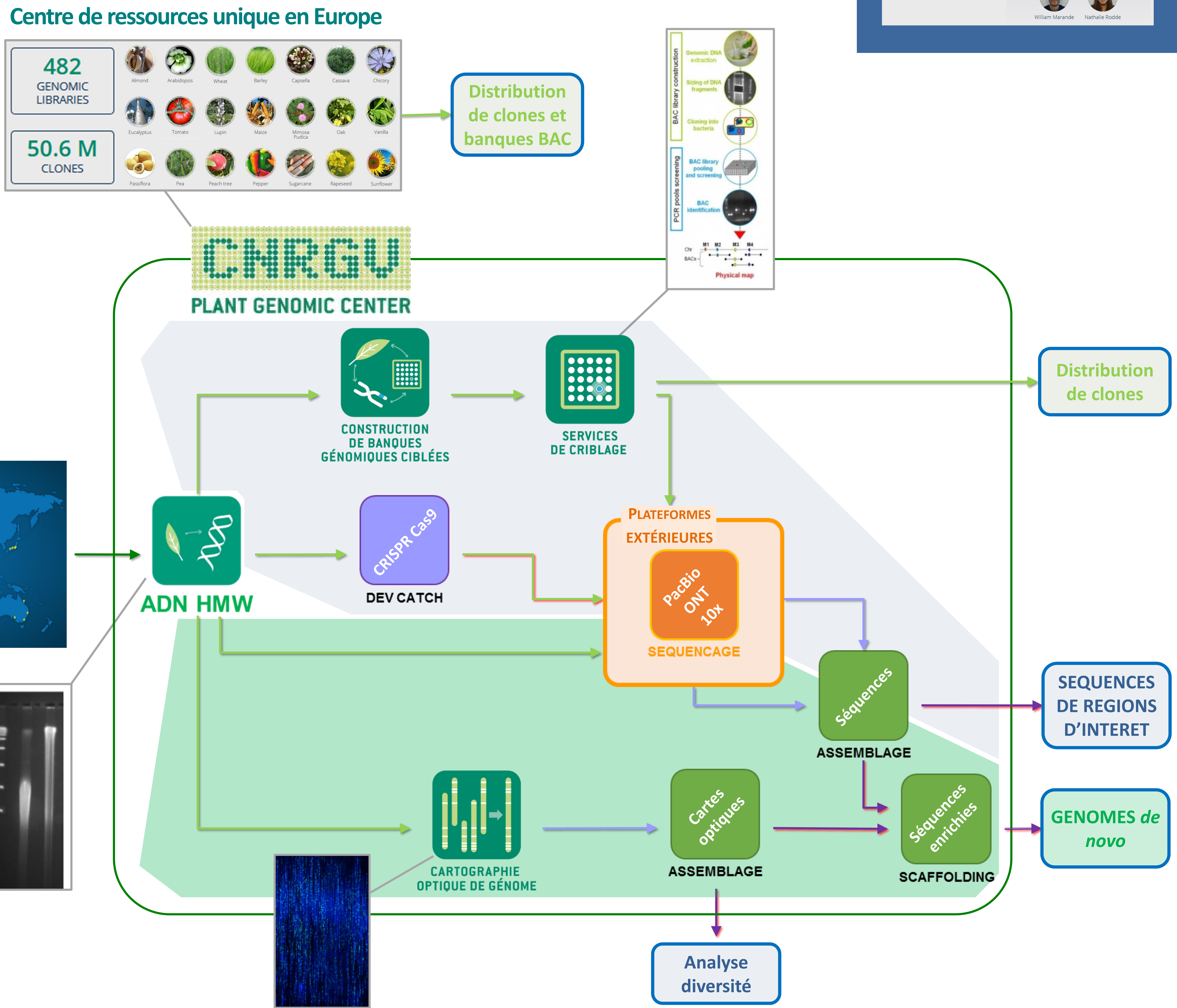
**Nouer des collaborations** et favoriser les interactions au sein de la communauté scientifique

**Etre à l'écoute des chercheurs** pour proposer des solutions adaptées à leurs problématiques spécifiques

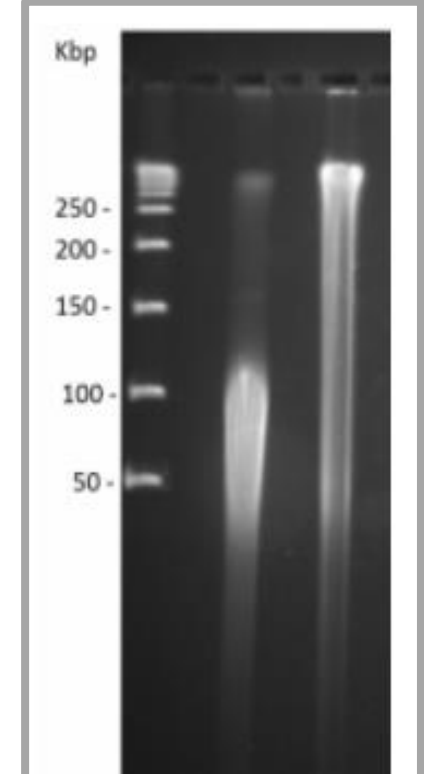


Différentes approches génomiques existent pour décrire la structure des génomes de plantes, de façon globale, ou à l'échelle de locus d'intérêt.

Nous adaptons les stratégies proposées à nos collaborateurs en fonction de la taille et complexité des espèces et régions génomiques étudiées.



— Matériel végétal  
— ADN  
— Données brutes  
— Données assemblées



Demandes de service, d'information et proposition de collaboration via le site internet du CNRGV :

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

- GENOMIC SAMPLES DISTRIBUTION
- GENOMIC LIBRARY CONSTRUCTION
- TARGETED GENOMIC LIBRARY CONSTRUCTION
- SCREENING SERVICES
- HMW DNA EXTRACTION
- GENOME OPTICAL MAPPING
- BAC CLONE CHARACTERIZATION
- ROBOTIC SERVICES

## Exemples de collaborations en cours

### Analyse des génomes

- Identifying sequences associated with virus tolerance in cassava**  
Gemini viruses represent an important threat to crop production and food security as they are the causal agents of viral diseases.
- ERC LUPIN ROOTS : Unravelling cluster root development in white lupin**  
Plants exhibit a high level of developmental plasticity that is controlled by a complex combination of perception, integration and response. In opposition to animals, where developmental patterns are highly conserved, plant organs are produced as a response to environment.
- Pyramiding strategy for durable resistance to root-knot nematodes in Prunus Rootstocks**  
Root-knot nematodes (RKN) (*Meloidogyne* spp.) are extremely polyphagous pests with a high economic impact at the global scale.
- Phylogenetic inferences in Passiflora based on the analysis of chloroplast genomes**  
Using chloroplast genome sequences (cpDNA), our research group has carried out phylogenetic analyses that resulted in strongly supported trees, providing a better understanding of the evolutionary relationships in the Malpighiales and the Fabids' clade.

### Séquençage de génomes

- CONSORTIUM for the sequencing of Vanilla planifolia - « VANISEQ » project**  
This consortium aims at providing genomic resources and data in order to better understand the genetic of *Vanilla planifolia*.
- International Consortium on Sunflower Genomics - ICSG**  
The domesticated sunflower, *Helianthus annuus L.* is a global oil crop that has promise for climate change adaptation, because it can maintain stable yields across a wide variety of environmental conditions.
- gEXTRACT**  
A gold-standard *M. pudica* genome assembly is required, but multiple protocols tested for DNA extraction finally resulted in short fragment only suitable for illumina-based sequencing. Failing to extract HMW gDNA for long-read sequencing is not specific to *M. pudica*, so the main goal of the gEXTRACT project will be to leverage the expertise of our three labs (CNRGV, LIPM, LRSV) to develop a universal protocol for plant HMW gDNA extraction.

### Développement méthodologique

- CATCH My Interest : capture of large genomic regions of interest**  
The CATCHMI project aims at developing a new approach to capture specific genomic regions of interest.

