



## 10 YEARS OF ACTIVITY REPORT - 2014





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# The objectives of the PLANT GENOMIC CENTER

Agricultural research must deal with major issues on various scales, in light of the changing climatic and demographic context, where energy resources are limited. In this context of plant improvement and adaptation, genome exploration is one of the strategic approaches of choice. Indeed, for species of interest, genomics defines gene content, their organization, biological function and also their variability between different samples. These knowledge facilitate the identification of interesting plant genes, which can play a role in pathogenic resistance (viruses, bacteria, mushrooms) or in the quality process (flavor of fruits and vegetables, composition in fatty acids or vitamins, quality molds) and in agronomic performance (precocity, architecture, yield). In terms of biodiversity, which exists between all genotypes of the same species and their related wild forms, genomics helps to deepen our knowledge of the main metabolic pathways and to rationalize the selection of new varieties. To manage this challenge, genomic research can take advantage of the extraordinary growth observed since the 90s. This revolution combined with specialized biological resources is key to the successful management of genomic research projects. Genomic resources are mainly represented by libraries of large DNA inserts that are essential for the exploration of complex plant genomes, which may vary in size from a few million nucleotides to several billion.

Dedicated to plant genome research, the CNRGV holds more than 14 million unique samples including plant models (*Arabidopsis thaliana*, *Medicago truncatula*) and crop plants (wheat, maize, pea, sunflower, barley, rapeseed, radish, etc.). The CNRGV is actively involved in the plant genomic effort by producing new resources as well as developing innovative molecular tools for the international scientific community.

# Genomics to better serve agricultural practices

## A Biological Resource Center dedicated to plant genomes



Genomics has seen extraordinary growth since the 1990s and constitutes a major scientific challenge. The cloning of genomes into large insert genomic DNA libraries is an invaluable tool for the study of complex genomes such as the plant genomes. The French Ministry of Research acknowledged the strategic importance of these genomic resources. In this context, a Biological Resource Centre (BRC) dedicated to plant genome, namely the French Plant Genomic Center (CNRGV) has been created in 2004.

The CNRGV is an essential part of the infrastructure underpinning biotechnology. It's a service provider and a repository for strategic biological material.

The CNRGV plays a key role in agricultural plant science that aims to increase crop productivity and the agricultural product quality while respecting the environment. Maintaining productivity and quality under conditions of reducing inputs have to be reached. Understanding plant biology is a key to improve crop production and protection in the face of climate change which is already impacting food supply and security. All of these goals have significant economic value. In this context, the plant biotechnology sector has seen extraordinary advances but still many progresses have to be done regarding the growth of the population which results in an increase of the food's needs. Among biotechnologies in the plant field, genomics has seen significant improvement. Genomics provides essential tools to speed the work of the more traditional molecular approaches. The knowledge of plant genomes will help in understanding plant's behaviors in various conditions, including many stresses that plant will have to deal due to climate changes. It will also help in understanding the evolution

and adaptation skills of the plant. However, eukaryotic genomes are more complex than prokaryotic genomes, and among eukaryotes, plant genomes are much more complex than any other. There is no direct relationship between genome size and organism complexity, which is a paradox known in science. Plant genomes complexity is one of the reasons why genomic resources are so important for understanding plant biology. Indeed, plant genomes are complex by many aspects including, large sizes that often reach gigabases, high ploidy levels and high percentages of repetitive elements that may represent the majority of the genome size. Next-generation sequencing (NGS) technologies have revolutionized genomic research in several domains, as it offers the capacity to obtain large amount of DNA sequences in a short time. However, this approach is not sufficient to decipher the high complexity of plant genomes and so understand biological processes underlying adaptive responses of plant. The genomic libraries we provide at the CNRGV are invaluable tools for plant genome analysis. They are the unique tool to answer to various scientific questions in order to isolate gene of interest, to characterize disease locus, to make positional cloning, to study

polymorphism, genome evolution and genetic variability or to explore the biodiversity. Many consortia, in which the CNRGV is involved, have been set up in order to be able to obtain a better quality of plant genomes sequence, such as wheat, barley and sunflower. These genomic resources represent a very high value for plant genomics. The existence of a structure like the CNRGV guarantees a standardization of the qualities of storage and referencing of all the genomic resources, and the largest distribution for all the laboratories involved in plant genomics projects.

Finally, all the societal challenges request an improvement in the managing of plant, in terms of productivity, quality of the production, environment respect, or a greater use of biomass. Simultaneously, the revolution in sequencing technologies offers an exciting new perspective to answers these questions. The advances in technologies at the genomic level will help in better understanding the relationships between plant and the environment, and the CNRGV is willing to contribute by providing the tools to achieve these goals by taking advantage of conserved resources but also by helping scientist to work together.

The objectives of the CNRGV are both to produce, store, and manage genomic collections and to provide high throughput and innova-

tive molecular tools to the international community. The genomic collections are mostly represented by large inserts genomic DNA libraries. Currently, the CNRGV has a unique collection, represented by more than 14 million samples coming from genomic resources of model and crop plants (wheat, sunflower, maize, barley, rapeseed, tomato, etc...). From the very beginning, this structure was anticipated as largely opened to the European plant academic community and to industry with a rapid development toward the international community. Indeed, service platform dealing with plant species of economic interest are unique in France and very rare worldwide. The existence of this unique center in France and in Europe, guarantees a standardization of the qualities of storage and referencing, and the largest distribution for laboratories involved in plant genomics projects. The CNRGV already supplies laboratories throughout the world with genomic resources and innovative services. The CNRGV is a reliable provider and has yet interacted with more than 300 laboratories located in 32 countries around the world. We noticed a significant increase of the interactions since the beginning, which shows the increasing interest of laboratories for the services provided by the CNRGV, demonstrating that it's a recognized and essential structure

to assist plant genomics projects. The CNRGV is now appreciated by the scientific community for two main aspects, the fact that it is a public structure and the professionalism with which the CNRGV achieves its missions. Research institutes and breeding companies put their trust in INRA because of the long-term strength of its system and the efficiency and innovative services that it provides.

We provide our customers with innovative and efficient genomic tools to answer a large diversity of questions, from the fundamental knowledge of biological processes in plant to the characterization of genes involved in specific traits of agronomical interest. Among various tools we have developed a strategy aiming at focusing directly on a genomic region of interest in specific genotypes and rapidly isolate clones spanning a genomic region. This strategy combined with NGS technology, has proven to be an efficient way to directly target genomic region of interest and explore the variability among specific genotypes. Numerous projects using this strategy are in progress in the laboratory. Developing such innovative strategies based on genomic resources is our ongoing goal in order to support future research.

# PLANT GENOMIC CENTER Team



Hélène Bergès  
*Director*



Laetitia Hoarau  
*Administrative  
Quality Manager*



Stéphane Cauet  
*Informatic Manager*



Arnaud Bellec  
*Technical Manager*

## Informatic staff



David Pujol



Nicolas Théron

## Technical staff



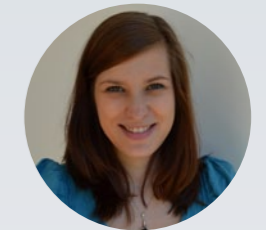
Sonia Vautrin



William Marande



Audrey Courtial



Nathalie Rodde



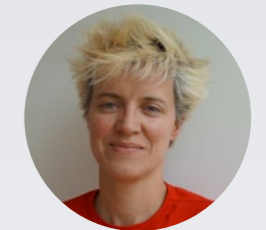
Genséric Beydon



Elisa Prat



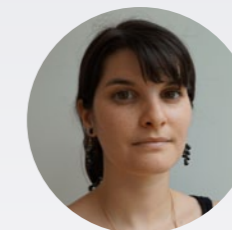
Joelle Fourment



Nadège Arnal

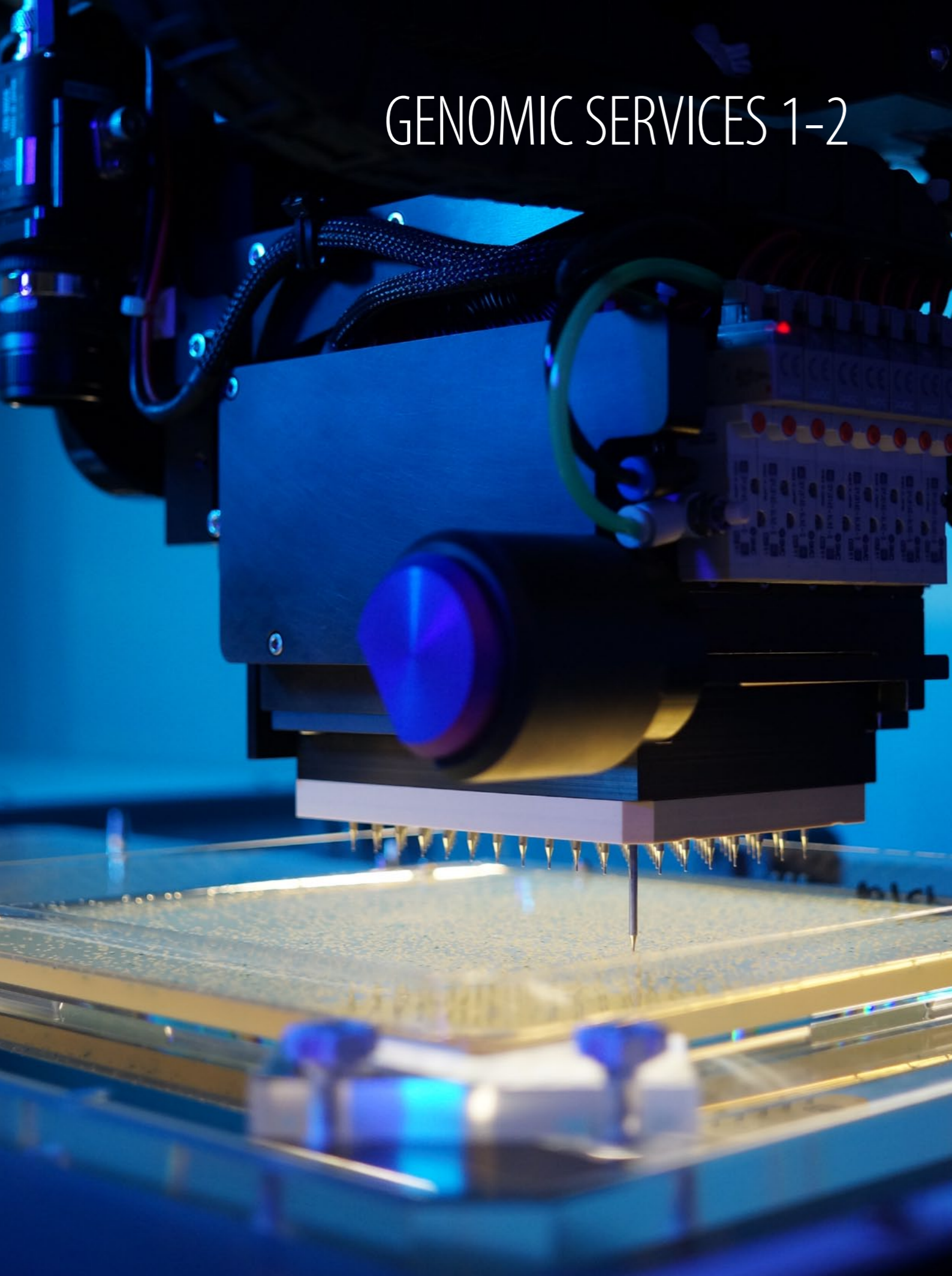


Nadine Gautier



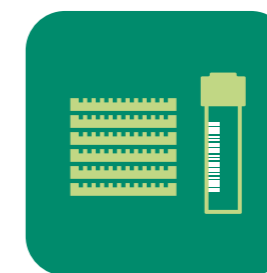
Justine Mas

# GENOMIC SERVICES 1-2



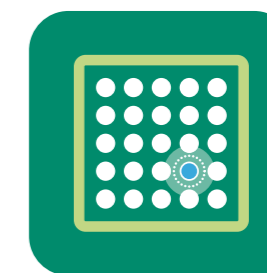
## Construction of BAC (bacterial artificial chromosome) libraries of large genomic DNA inserts

Libraries of large genomic DNA inserts are essential to genomics research. The cloning of large genomic DNA inserts into BAC vectors facilitates handling and multiplication as well as long-term conservation. BAC libraries help to identify and isolate genes of interest but also to carry out the physical mapping and sequencing of plant genomes. We manage all the stages of BAC library construction, from the extraction of genomic DNA from plant tissue to the cloning and rearraying in microplates.



## Genomic sample distribution

The CNRGV distributes biological samples from more than 200 different genomic libraries, both nationally and internationally, representing the biodiversity of model and crop plants. In terms of distribution, we can distribute single clones, whole genomic libraries or subset libraries. Sample preparation is carried out by dedicated robots, which ensures traceability and quality of distributed samples. Each process is tracked by our data management system.



## Screening services

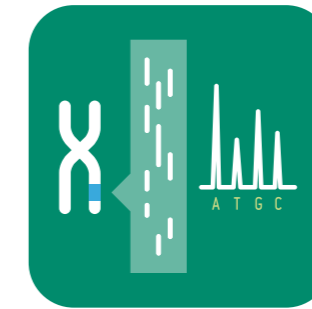
The CNRGV provides screening services for BAC libraries to successfully identify and isolate genes or genomic regions of interest. Starting from a BAC library we establish the genomic tools required for your research needs. Genomic tools consist of high-density filters or DNA pools. Both approaches allow the effective identification of BAC clones carrying a marker of interest. Screening is performed either by hybridization of high-density filters or by Real-Time PCR on DNA pools. The use of these genomic tools combined with high throughput equipment ensures rapid access to BAC clones of interest, with an accurate traceability of BAC clones.

# GENOMIC SERVICES 2-2



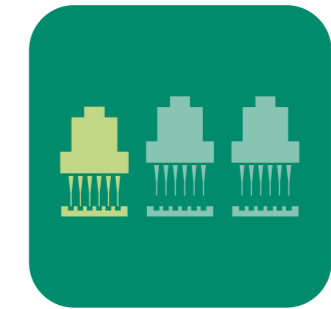
## Targeted genomic library construction

A BAC library provides an efficient tool for map-based cloning, physical mapping or sequencing, facilitating multi-faceted projects. However, the construction of a BAC library is too great an undertaking if it only aims to answer one or even a few scientific questions. In order to reduce consuming steps of the BAC library construction and improve access to genomic regions of interest, the CNRGV has developed a targeted genomic library strategy. BAC clones of targeted genomic libraries are screened immediately after their transformation, which allows the isolation of clones of interest, whilst avoiding the expensive and time-consuming steps of BAC clones organization in microplates. Targeted genomic libraries have proven their efficiency and are notably useful in investigating the diversity of specific regions among various plant cultivars.



## BAC clone characterization

The CNRGV aims to offer a comprehensive service from plant DNA extraction to the characterization of genetic information underpinning a trait of interest. To meet this goal the CNRGV currently utilizes Next Generation Sequencing (NGS) technologies to effectively analyze BAC clones of interest. We consider that a comprehensive and reliable view of a DNA sequence is extremely helpful in investigating biological mechanisms. To reach this end we focus in particular on the quality of the assembly and on finding various solutions that enable us to achieve this.



## Robotic services

The CNRGV has set up a complete robotic range dedicated to genomic resources handling and treatment. This leading-edge equipment allows the CNRGV to support most genomic projects that require reliable and high-throughput treatment of large numbers of samples. Robots are most frequently used in bacterial colony organization, bacterial clone rearranging and DNA extraction. However we will consider the needs of any project and will always do our very best to meet your project needs.

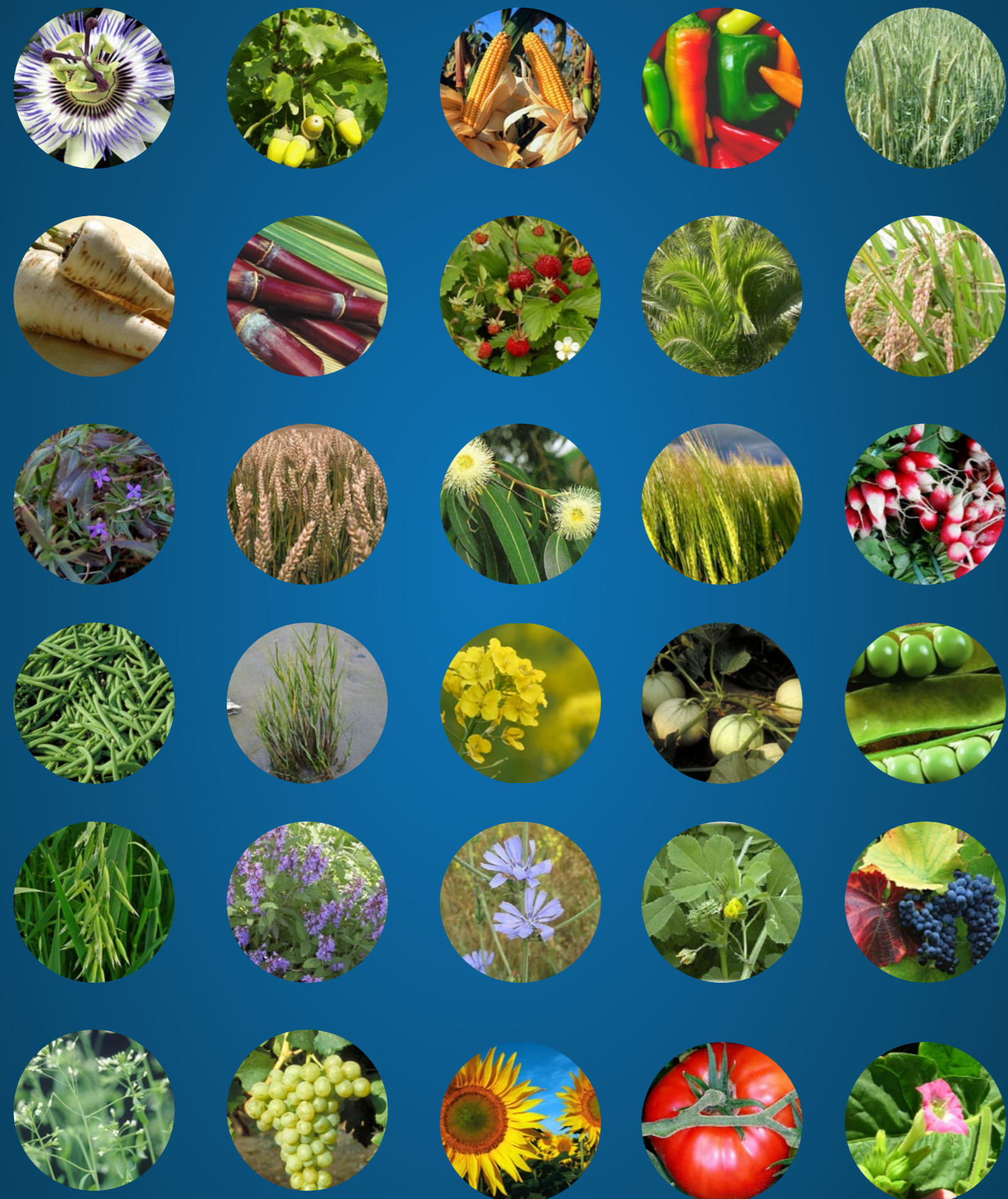


Interactions with  
laboratories around  
the world



# Plant genome sequencing

Collaborating to uncover the mystery surrounding plant-life



The evolution of the plant kingdom has shaped the extraordinary complexity of plant genomes. Plants have evolved over 250 million years, adapting to all biotopes through a multitude of forms, like the simple but informative form of the thale-cress for example, which was the first sequenced plant genome at the beginning of the year 2000, or the spectacular millenary redwoods, or the nourishing cereals whose cultivation has allowed for the development of human civilization.

The diversity of plants is notably explained by their capacity to support the comprehensive duplication of their genomes or polyploidy. The presence of two copies per gene in the newly polyploid plant genome, allows for a new mutated function of one of the copies in the progeny. Whilst polyploidy is a major asset in plant evolution, it poses a great challenge in terms of plant genome sequencing. The different sequencing strategies are based on the same principle of splitting the genomes into small molecules ranging from few dozens to some thousands of nucleotides, depending on the technology used, then sequencing these small fragments and finally assembling the sequences obtained based on their similarities, in order to provide a step by step reconstruction of the pseudo-molecule sequence. The ultimate aim of sequencing therefore consists in reducing the number of pseudo-molecules to the number of chromosomes of the plant. With regards to polyploidy, as well as high levels of repeated sequences, another characteristic of plant genomes, the assembly process is complicated by the ambiguities. These specificities result in generally more complexity in plant sequencing, compared to the sequencing of microorganisms and animals, which have not experienced recent developments of polyploidization and show weaker levels of repeated elements.

Plant genomes' intrinsic complexity calls for the combination of specific resources and original strategies to carry out sequencing. In light of this, the libraries of large DNA inserts (BAC) kept in the CNRGV are an extremely useful resource. The average 120 kb insert size corresponds to a

DNA molecule size that is easy to assemble from the data produced by the sequencing and at the same time useful in pseudo-molecule reconstruction. Furthermore, to simplify the assembly process it is extremely valuable to have a physical map of a genome by ordering of the BAC clones from the specific enzymatic restriction profiles of every DNA insert. Physical genome mapping can be used to select which inserts to sequence and reduce assembly complexity by only identifying similarities that exist between contiguous insert sequences.

Plant sequencing requires quality genome resources and varied competences in order to manage and diffuse resources, define physical maps, carry out sequencing and undertake bio-informatic analysis. To put such synergies in place and meet the existing significant costs of such projects, laboratories form international consortia. Thus, today the CNRGV is a recognized partner of numerous international sequencing projects. In particular, it has played a key role in wheat sequencing projects IWGSC\* (International Wheat Genome Sequencing Consortium) and barley sequencing projects IBSC\*\* (International Barley Sequencing Consortium). It is also a partner in the sugarcane sequencing project SUGESI (Sugarcane Genome Sequencing Initiative). Within these projects, the CNRGV regroups, organizes and distributes BAC libraries to different international partners. The CNRGV also participated in the now published work of tomato genome sequencing (International Tomato Genome Sequencing Project\*\*\*) and *Medicago truncatula*. Recognized for its ability to manage genome resources, the CNRGV has also shown its expertise in producing BAC libraries. Testament to this is the use of CNRGV resources in Sunflower sequencing (Genomics of Sunflowers\*\*\*\*) a tripartite project involving France, Canada and the USA.

Such international collaboration in plant genome sequencing will bear fruit in the form of future scientific discoveries and improvements in plants. Acquiring this knowledge is fundamentally necessary when faced with the challenge of sustainably feeding 9 billion people in 2050.

IWGSC\* - International Wheat Genome Sequencing Consortium - funding by all the countries involved in the project - coordinated by six co-chairs R. Appels (Australia), J. Dvorak (USA), C. Feuillet (France), B. Gill (USA), B. Keller (Switzerland), Y. Ogihara (Japan) and K. Eversole (USA).

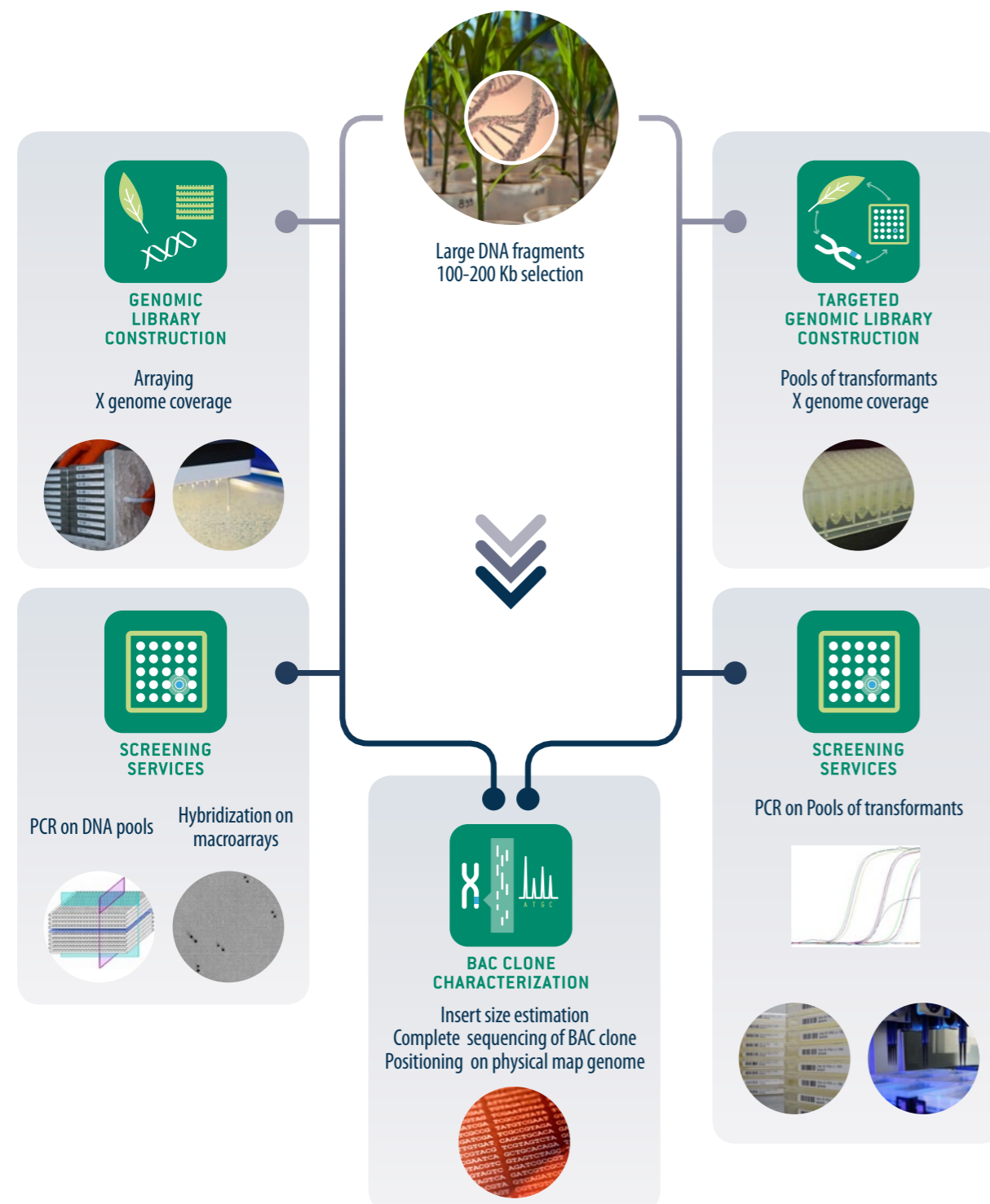
IBSC\*\* - International Barley Sequencing Consortium - funding by U.S. Department of Agriculture - Cooperative State Research, Education, and Extension Service (USDA/CSREES) - coordinated by Nils Stein, IPK-Gatersleben, Germany.

International Tomato Genome Sequencing Project\*\*\* - funding by Solanaceae Genome Network - coordinated by, Monder Bouzayen, UMR990 Génétique et Biotechnologies des Fruits (GBF), Castanet-Tolosan, France.

Genomics of Sunflowers\*\*\*\* - funding by INRA - Genome CANADA - coordinated by Loren Rieseberg, Botany Department University of British Columbia, Canada / Patrick Vincourt, UMR0441 Laboratoire des Interactions Plantes-Microorganismes (LIPM), Castanet-Tolosan, France / Steven J. Knapp, Institute of Plant Breeding, Genetics, and Genomics - Center for Applied Genetic Technologies, Athens, USA.

# Genome analysis for enhanced plant breeding

Deciphering plant agronomic traits to understand their molecular bases and improve plant varieties



With climatic pressure ever-increasing and arable land becoming a rare commodity, agriculture is faced with the challenge of sustainably feeding 9 billion people in 2050. One way of facing up to this challenge is through the creation of new plant varieties that are more productive and robust.

Plant development requires the identification of interesting characteristics (high yields, disease resistant, drought resistant) as well as the identification of genes and molecular mechanisms that govern them. This process requires a broad range of disciplines including phenotyping, genetics, molecular biology and genomic resources management. With this multidisciplinary aim in mind, the CNRGV provides genomic resources and expertise, through varied dimensional projects, to public laboratories and private companies.

The CNRGV is a partner in 4 “Biotechnology and Bioresources” projects, within the framework of the Investments for the Future program. These projects aim to develop biotechnologies to promote technological advances that will facilitate plant selection. Projects BREEDWHEAT\*, AMAIZING\*\*, PeaMUST\*\*\* and SUNRISE\*\*\*\* respectively cover wheat, corn, peas and sunflower. They will enable public laboratories and companies to collaborate over several years with the objective of identifying genes and their interaction networks that influence production stability and to select alleles of interest within cultivated and wild genetic resources for genetic improvement. The CNRGV provides these projects with access to its genomic resources, as well as the possibility of creating new ones in response to emerging questions. The BREEDWHEAT project for example, represents a total investment of more than €34M over a 9 year period. It involves 26 partners, 11 of which are industrial, including the best French wheat research and selection teams, from both the public and private sector. This group of players in the sectors aims to improve agronomical traits and to provide basis to create new varieties able to sustainably feed humans and animals alike in terms of quantity and quality, whilst ensuring farm competitiveness. Project success is based around several axes, including development of genetic markers and the isolation of genes involved in the characters of interest; the study of wheat adaptation to biotic and abiotic stresses; the characterization and exploitation of genetic diversity, as well as the development and implementation of new selection strategies.

Apart from these national projects, the CNRGV is willing to partner any plant genomic project. Such projects could be based on already existing resources or might include the creation of new libraries. For example, the CNRGV was partner of a project developed by the University of Lille, led by Dr Delbreil with the aim of characterizing cold resistance mechanisms of the pea. Access to the sequencing of gene candidates was carried out in the CNRGV by screening BAC pea and *Medicago truncatula* libraries. If the resources on hand are unable to provide the necessary answers, the CNRGV produces specific libraries of the most pertinent varieties. This has enabled the CNRGV to participate in a project co-financed by the Promais association that regroups the industrial players in the field and within INRA. As part of this collaboration, which aims to explain a QTL of maize digestibility, two corresponding libraries of parental lines were built. The screening then sequencing of BAC clones of a region of interest will enable the identification of the genes involved in the composition of the plant cell walls.

The CNRGV is willing to support any interested team, regardless of project size, with their resources and expertise.

**BREEDWHEAT\***, Developing new wheat varieties for sustainable agriculture – funding by the ANR (The French National Research Agency) “Future Investments Program”, coordinated by Jacques Le Gouis, UMR1095 Génétique, Diversité et Ecophysiologie des Céréales (GDEC), Clermont-Ferrand, France.

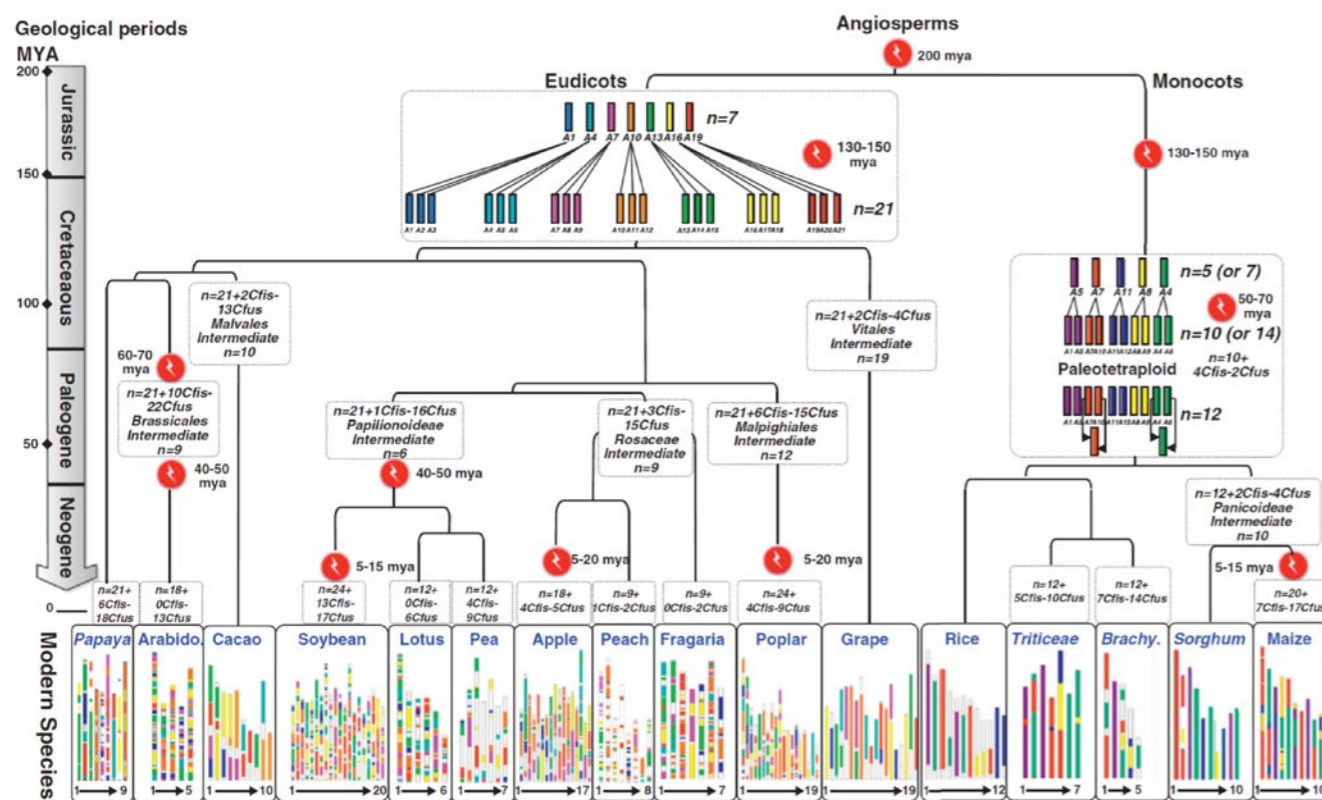
**AMAIZING\*\***, Developing new maize varieties for sustainable agriculture funding by the ANR (The French National Research Agency) - coordinated by Alain Charcosset, UMR de Génétique végétale, Moulon, France.

**PeaMUST\*\*\***, Pea Multi-Stress adaptation and biological regulations for yield improvement and stability - funding by French ANR “Future Investments Program”, coordinated by Judith Burstin, UMR AgroEcologie, Dijon, France.

**SUNRISE\*\*\*\***, SUNflower Resources to Improve yield Stability in a changing Environment - funding by ANR Biotechnologies et Bioressources coordinated by Patrick Vincourt, UMR041 Laboratoire des Interactions Plantes-Microorganismes (LIPM), Castanet-Tolosan, France.

# Plant genomics serving basic research projects

CNRGV's expertise on genomic approaches helps to understand plant biology



Salse J (2012). In silico archeogenomics unveils modern plant genome organisation, regulation and evolution. *Curr Opin Plant Biol.* 15: 122-130.

Basic research aims at increasing the scientific knowledge and the understanding of the biological processes. The CNRGV's innovation and efficacy plays a key role in assisting such projects based on genomic libraries which are invaluable tools to assist in the understanding of molecular mechanisms at the genomic level. Thereby a wide variety of scientific questions can be addressed thanks to the expertise and resources developed at the CNRGV.

For example, preparation and screening of genomic libraries were the starting point of the BRASSIDOM ANR project\*. The aim of this project is to understand the molecular mechanism of the classical genetic dominance/recessivity interaction in *Arabidopsis* multi-allele self-incompatibility system. The dominance/recessivity relationship was shown to be controlled by a small hairpin RNA (hpRNA) produced within the genomic cluster controlling self-incompatibility, and acting

in trans through de-novo methylation of the promoter of recessive alleles. In the framework of the project, the CNRGV's team has identified and sequenced BAC clones carrying the S-locus (self-incompatibility locus) from different genotypes. The annotation of genomic sequence produced, combined with transcriptomic analysis highlights miRNA presence and its targets elucidating the dominance/recessivity network (Castric et al, 2012, Castric et al, 2014).

Another fundamental aspect to investigate to understand plant evolution is the polyploidization phenomenon. Contemporary plant's genomes result from several cycles of whole genome duplications followed by both gene losses and gains of functions. We are partners of the DUPLIC ANR project\*\* that aims to improve the understanding of gene evolution involved in meiotic recombination following polyploidy events. One of the research objective is to determine the patterns of duplicated copy retention/loss for recombination genes in two complementary polyploid crops, oilseed rape (*Brassica napus*) and bread wheat (*Triticum aestivum*) using genomic resources available at the CNRGV.

Additionally, bread wheat is an important worldwide crop but is also a very comprehensive plant model for polyploid genome evolution study. *Triticum aestivum* hexaploid genome has been shaped by old and recent polyploidization events followed by dramatic genome reorganization such as chromosome fusion. Genomic analysis of this plant will give answers to chromosome fusion processes and gene losses / gains during evolution after whole genome duplication. Deciphering the chromosome fusion mechanism at the genomic level and how the duplicated regions behave during *Triticum aestivum* evolution is one of the goals of the PAGE ANR project\*\*\*. Based on specific genomic resources at its disposal, the CNRGV will identify the genomic breakpoint of an ancient chromosome fusion and also characterize a duplicated region present in chromosome 1 and 3.

The CNRGV has shown its ability to support basic research projects. In order to do so the CNRGV relies on genomic libraries available for more than 45 species and on its expertise on genomic library production. But beyond these resources we strive to listen to scientists' requirements and to meet their needs to help them to improve fundamental knowledge.

\* BRASSIDOM ANR coordinated by Vincent Castric, Lille University, France.

\*\*DUPLIC ANR coordinated by Eric Jenczewski, INRA - Versailles - Grignon, France.

\*\*\*PAGE ANR coordinated by Jerome Salse, INRA Clermont-Ferrand, France.

# Information System

Ensuring safety and accessibility to data associated with genomic resources

Within the context of high-throughput data management, the CNRGV has built an Information System (IS) that is crucial to its effective functioning and service quality.

Our IS is divided into 3 main sectors:

## Genomic resources management

GenoLIMS, an essential IT tool in high-throughput data management, is the result of 10 years of development and is instrumental in our laboratory work. It assists in the analysis and traceability of around 200 genomic libraries of nearly 30 million clones preserved in CNRGV freezers at -80°C. Various pipelines are associated with this tool ensuring the automation of data processing from data traceability to analysis to entry in public databases.

## Project management and communication with our collaborators

Key to our business activity is the effective management of various projects that involve numerous collaborators. eZPublish, a content management tool, enables the effective administration of these aspects. We implement our own project monitoring modules, customer satisfaction surveys, newsletters and will even share results with our partners. We are working on developing links on other web sites with the aim of improving services and resource visibility.

## Laboratory management

Effective laboratory functioning and management requires the maintenance of high technology robots and consumable stocks to be monitored as closely as possible. With this in mind, the IS includes the GIMACO tool, which ensures the overall management of laboratory materials. It is also an essential tool in our quality system within the framework of non-conformity monitoring or implemented action plans. These tools are linked together to share common data, thus providing an original and effective laboratory management system.

We continue to develop and improve our information tools to better meet the demands of the technological changes and methodologies within a laboratory environment. This is done focusing specifically on service quality, reliability, robustness, performance and data security.

# Quality Management System

Rely on quality standards to ensure the safety of genomic resources  
and provide best possible services



Biological resources are crucial to life science research. Genomic resources in particular constitute a starting point for all genomic programs. This significance and the interest to mutualize costs have led to the appearance of Biological Resource Centers (BRCs) as an essential part of the infrastructure of science and technology. Thus BRCs provide the scientific community infrastructures that are able to respect high quality standards for such resources and associated data. In this context the CNRGV has set up quality procedures to manage plant genome libraries including protocols for their multiplication, storage, referencing and dissemination.

As a producer and distributor of resources and services for genome research programs, we decided to rely on a Quality Management System (QMS) in compliance with ISO 9001 quality standards. The ISO 9001 standard which is published by the International Organization for Standardization (ISO) is internationally recognized. It sets out the requirements for the organization of laboratory activities to meet needs of our customers and partners. Our quality management system is a set of processes and procedures that are established to guarantee the quality of genomic resources that we maintain and distribute and to implement conditions to provide the best possible service.

We maintain continuously our quality management system in order to improve its efficiency in compliance with the requirements of the standard.

Our QMS is certified ISO 9001 since September 2005.

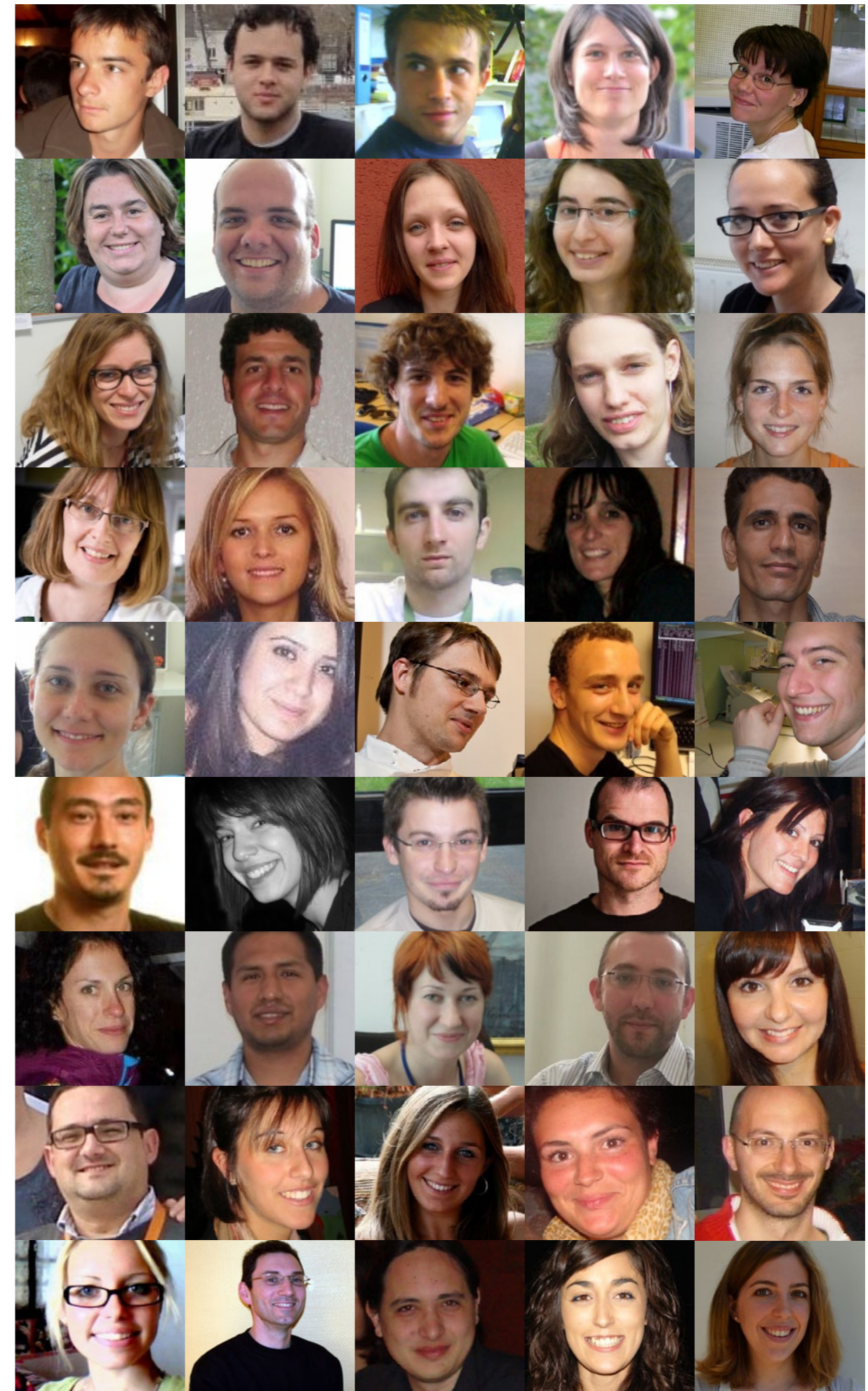
# Collaboration and training at PLANT GENOMIC CENTER

**CNRGV welcomes researchers and students to share their knowledge and expertise in plant genomics.**

The CNRGV team supports researchers worldwide by providing training in plant genomics techniques. They provide expertise to successfully carrying out projects by sharing their knowledge of different laboratory activities. Their project is developed in the laboratory using existing libraries or by building new genomic libraries of particular genotypes. These projects aim to skillfully identify and characterize a targeted genomic zone thanks to specific resources.

The laboratory equally welcomes and trains numerous students from 2nd year in university (BAC+2) to Masters Level in university (BAC+5). Students wishing to specialize in plant biotechnology are integrated into projects that the laboratory collaborates in. We offer them an experience in plant genomics using high-throughput robotized stations. Students interested in specializing in computer science, have the opportunity to train on the different applications allowing for the traceability of data collected in CNRGV genomic libraries or exploitation of data from sequencing projects.

Visits to the CNRGV are regularly organized for different publics to provide the opportunity to discover a unique centre, at the heart of plant genomics technology used for numerous research projects on plants or plant models of agronomic interest.





# List of genomics libraries available at the PLANT GENOMIC CENTER

Species	Library Name	Library type	Ecotype	Coverage
<i>Acyrtosiphon pisum</i>	Api-B-LSR1	BAC	LSR1	6.6 X
<i>Aphanomyces euteiches</i>	Aeu INT	EST	souche ATCC 201684	
<i>Aphanomyces euteiches</i>	Aeu MYC	EST	souche ATCC 201684	
<i>Arabidopsis halleri</i>	Aha-B-HF11	BAC	HF11	5.5 X
<i>Arabidopsis halleri</i>	Aha-B-H25	BAC	H25	4.3 X
<i>Arabidopsis halleri</i>	Aha-B-I9	BAC	bulk I9	16.7 X
<i>Arabidopsis halleri</i>	Aha-B-L406	BAC	L406	5.6 X
<i>Arabidopsis halleri</i>	Aha-B-PL22_138	BAC	PL22_138	5.1 X
<i>Arabidopsis lyrata</i>	Aly-B-03A7	BAC	03A7	4.9 X
<i>Arabidopsis lyrata</i>	Aly-B-05B17	BAC	05B17	5.9 X
<i>Arabidopsis lyrata</i>	Aly-B-05B37_3	BAC	05B37_3	4.3 X
<i>Arabidopsis lyrata</i>	Aly-B-05B8	BAC	05B8	5.1 X
<i>Arabidopsis thaliana</i>	Ath-B-ITA	BAC	ITA	11.8 X
<i>Arabidopsis thaliana</i>	GSLTFB	EST	Col 0	
<i>Arabidopsis thaliana</i>	GSLTLS	EST	Col 0	
<i>Arabidopsis thaliana</i>	GSLTPGH	EST	Col 0	
<i>Arabidopsis thaliana</i>	GSLTSIL	EST	Col 0	
<i>Arabidopsis thaliana</i>	AGRONATOME	ORFEOME	Col-0	
<i>Arabidopsis thaliana</i>	ATOME1	ORFEOME	accession Col 0	
<i>Arabidopsis thaliana</i>	ATOME2	ORFEOME	accession Col	
<i>Arabidopsis thaliana</i>	TRANSPORTOME	ORFEOME	Col-0	
<i>Brassica napus</i>	Bna-B-DarmorBZH	BAC	Darmor-bzh	13.0 X
<i>Brassica napus</i>	Unigene set GOPT6	EST		
<i>Brassica napus</i>	Unigene set RF02	EST		
<i>Capsicum annuum</i>	Can-B-HD208	BAC	HD208	10.9 X
<i>Cichorium intybus</i>	Cin-B-S1	BAC	S1	6.0 X
<i>Cichorium intybus</i>	Cin-B-S2	BAC	S2	6.0 X
<i>Cucumis melo</i>	Cme-B-PI161375	BAC	PI161375	12.3 X
<i>Cucumis melo</i>	LIBEST_027112 DFLP2	EST	Dulce	
<i>Cucumis melo</i>	LIBEST_027110 DFTP2	EST	Dulce	
<i>Cucumis melo</i>	LIBEST_027115 MNCP2	EST	Piel de Sapo T-111	
<i>Cucumis melo</i>	LIBEST_027117 MNFG2	EST	Piel de Sapo T-111	



Species	Library Name	Library type	Ecotype	Coverage
<i>Cucumis melo</i>	LIBEST_027116 MNRP2	EST	Piel de Sapo T-111	
<i>Cucumis melo</i>	LIBEST_027111 PFLP2	EST	PI161375	
<i>Cucumis melo</i>	LIBEST_027109 PFTP2	EST	PI161375	
<i>Cucumis melo</i>	LIBEST_027113 SFLP2	EST	Piel de Sapo T-111	
<i>Cucumis melo</i>	LIBEST_027107 SFTP2	EST	Piel de Sapo T-111	
<i>Cucumis melo</i>	LIBEST_027114 VFLP2	EST	Vedrantais	
<i>Cucumis melo</i>	LIBEST_027108 VFTP2	EST	Vedrantais	
<i>Fragaria vesca f. semperflorens</i>	CUFvAB	BAC	Ali Baba	6.6 X
<i>Fragaria x ananassa</i>	Fragaria x ananassa	BAC	Capitola	5.8 X
<i>Gerbillus nigeriae</i>	Gni-B-CBGP07060h	BAC	CBGP07-060	1.0 X
<i>Helianthus annuus</i>	Han-B-Genoplante-YDQ	BAC	YDQ dérivé de HA335	4.8 X
<i>Helianthus annuus</i>	Han-INP-Ha 821	BAC	Ha 821	2.6 X
<i>Helianthus annuus</i>	Han-B-XRQ	BAC	XRQ	4.3 X
<i>Helianthus annuus</i>	Han-B-412b	BAC	HA412	2.7 X
<i>Helianthus annuus</i>	Han-B-412e	BAC	HA412	2.1 X
<i>Helianthus annuus</i>	Han-B-412h	BAC	HA412	8.7 X
<i>Hordeum vulgare</i>	HVVMRXALLhA	BAC	Morex	2.3 X
<i>Hordeum vulgare</i>	HVVMRXALLhB	BAC	Morex	1.5 X
<i>Hordeum vulgare</i>	HVVMRXALLrA	BAC	Morex	4.8 X
<i>Hordeum vulgare</i>	HVVMRXALLmA	BAC	Morex	6.4 X
<i>Hordeum vulgare</i>	HVVMRXALLeA	BAC	Morex	3.7 X
<i>Hordeum vulgare</i>	HVVMRXALLhB_MTP	BAC	Morex	0.2 X
<i>Hordeum vulgare</i>	HVVMRX83KhA	BAC	Morex	1.6 X
<i>Hordeum vulgare</i>	Hvu-B-H145	BAC	Bison H1H4H5	0.9 X
<i>Hordeum vulgare</i>	HVVMRX_MTPs	BAC	Morex	1.0 X
<i>Hordeum vulgare</i>	HVVMRX_MTP0	BAC	Morex	1.0 X
<i>Hordeum vulgare</i>	HVVMRX_MTP1	BAC	Morex	0.8 X
<i>Hordeum vulgare</i>	HVVMRX_MTP2	BAC	Morex	1.5 X
<i>Hordeum vulgare</i>	HVVMRX_MTP3	BAC	Morex	0.8 X
<i>Hordeum vulgare</i>	HVVMRX_MTP4	BAC	Morex	0.7 X
<i>Hordeum vulgare</i>	HVVMRX_MTP5	BAC	Morex	0.7 X
<i>Hordeum vulgare</i>	HVVMRX_MTP6	BAC	Morex	0.8 X

Species	Library Name	Library type	Ecotype	Coverage
<i>Hordeum vulgare</i>	HVVMRX_MTP7	BAC	Morex	0.8 X
<i>Medicago truncatula</i>	Mtr-B-F83	BAC	F83	6.8 X
<i>Medicago truncatula</i>	Mtr-B- mte1	BAC	A17	7.2 X
<i>Medicago truncatula</i>	Mtr-B- mth2	BAC	A17	22.8 X
<i>Medicago truncatula</i>	Mtr-B- mth4	BAC	A17	24.0 X
<i>Medicago truncatula</i>	MtA17_B_random_shear	BAC	A17	12.4 X
<i>Medicago truncatula</i>	WTSI_1018	BAC	A17	5.5 X
<i>Medicago truncatula</i>	MtBA-Dvt	EST	A17	
<i>Medicago truncatula</i>	MtBB-Dvt	EST	A17	
<i>Medicago truncatula</i>	MtBC-DvT	EST	A17	
<i>Nicotiana tabacum</i>	Nta-B-BB16NN	BAC	BB16NN	5.1 X
<i>Nicotiana tabacum</i>	LIBEST_019510 BL12	EST	K326, Burley 21, TN86	
<i>Nicotiana tabacum</i>	LIBEST_019511 KF8	EST	K326, Burley 21, TN86	
<i>Nicotiana tabacum</i>	LIBEST_018153 KG9B	EST	K326, Burley 21, TN86	
<i>Nicotiana tabacum</i>	LIBEST_018782 KL4B	EST	K326, Burley 21, TN86	
<i>Nicotiana tabacum</i>	LIBEST_019512 KL5B	EST	K326, Burley 21, TN86	
<i>Nicotiana tabacum</i>	LIBEST_019513 KN6B	EST	K326, Burley 21, TN86	
<i>Nicotiana tabacum</i>	LIBEST_018173 KP1B	EST	K326, Burley 21, TN86	
<i>Nicotiana tabacum</i>	LIBEST_019514 KR2B	EST	K326, Burley 21, TN86	
<i>Nicotiana tabacum</i>	LIBEST_018783 KR3B	EST	K326, Burley 21, TN86	
<i>Nicotiana tabacum</i>	LIBEST_019515 KT7	EST	K326, Burley 21, TN86	
<i>Nicotiana tabacum</i>	LIBEST_019516 TL13	EST	K326, Burley 21, TN86	
<i>Oldenlandia affinis</i>	Oaf-B-UQh	BAC	Affinis	3.3 X
<i>Passiflora edulis</i>	Ped-B-Flav	BAC	f. flavicarpa	6.0 X
<i>Pastinaca sativa</i>	Pas-B-Dlg	BAC	Demi-long de Guernesey	3.6 X
<i>Pisum sativum</i>	Psa-B-Cam	BAC	Caméor	8.0 X
<i>Quercus robur</i>	Qro-B- EnglishOak 3P	BAC	3P	12.0 X
<i>Quercus robur</i>	Qro-B-3Ph	BAC	3P	11.3 X
<i>Quercus suber</i>	Qsu-B-HDL	BAC	Herdade dos Leitoes	5.0 X
<i>Raphanus sativus</i>	Rsa-B	BAC		
<i>Saccharum hybrid</i>	SHCRBa	BAC	CultivarR570	1.3 X
<i>Saccharum hybrid</i>	Shy-B-80_3280	BAC	SP80_3280	2.3 X

Species	Library Name	Library type	Ecotype	Coverage
<i>Saccharum hybrid</i>	Shy-B-93_3046	BAC	IAC-SP93-3046	1.7 X
<i>Secale cereale L.</i>	Sce-B-FRG Blanco	BAC	Blanco	5.4 X
<i>Solanum lycopersicum</i>	LE_Hba - Heinz1706	BAC	Heinz 1706	15.8 X
<i>Solanum lycopersicum</i>	SL_Mbol - Heinz1706	BAC	Heinz 1706	7.5 X
<i>Solanum lycopersicum</i>	SL_EcoRI - Heinz1706	BAC	Heinz 1706	8.0 X
<i>Solanum lycopersicum</i>	SL_FOS	FOSMIDE	Heinz 1706	6.1 X
<i>Spartina maritima</i>	Sma-B-MOB	BAC		1.3 X
<i>Spartina maritima</i>	Sma-B-MOBb	BAC		0.9 X
<i>Spodoptera frugiperda</i>	Sfr-B-SFB MC	BAC	Guadeloupe	10.0 X
<i>Spodoptera frugiperda</i>	Sfr-E-RGOBAC	EST		
<i>Spodoptera frugiperda</i>	Sfr-E-Sf1H	EST		
<i>Spodoptera frugiperda</i>	Sfr-E-Sf1P	EST		
<i>Spodoptera frugiperda</i>	Sfr-E-Sf2M	EST		
<i>Spodoptera frugiperda</i>	Sfr-E-Sf9L	EST		
<i>Triticum aestivum</i>	Tae-B-Chinese spring	BAC	Chinese Spring	9.0 X
<i>Triticum aestivum</i>	Tae-B-CsE	BAC	Chinese Spring	2.0 X
<i>Triticum aestivum</i>	Tae-B-Renan	BAC	renan	5.6 X
<i>Triticum aestivum</i>	TaaCsp1ALhA	BAC	Chinese Spring	8.0 X
<i>Triticum aestivum</i>	TaaCsp1ALhB	BAC	Chinese spring	7.7 X
<i>Triticum aestivum</i>	TaaCsp1ALhMTP	BAC	Chinese spring	1.0 X
<i>Triticum aestivum</i>	TaaCsp1AShA	BAC	Chinese spring	11.8 X
<i>Triticum aestivum</i>	TaaCsp1AShMTP	BAC	Chinese spring	1.0 X
<i>Triticum aestivum</i>	TaaCsp1BLhA	BAC	Chinese Spring	15.4 X
<i>Triticum aestivum</i>	TaaCsp1BLhAMTPv1	BAC	Chinese Spring	1.0 X
<i>Triticum aestivum</i>	TaaCsp1BShA	BAC	Chinese Spring	15.7 X
<i>Triticum aestivum</i>	TaaCsp1BShMTP	BAC	Chinese Spring	1.8 X
<i>Triticum aestivum</i>	TaaCsp2BLhA	BAC	Chinese spring	15.1 X
<i>Triticum aestivum</i>	TaaCsp2BShA	BAC	Chinese spring	15.6 X
<i>Triticum aestivum</i>	TaaCsp2DLhA	BAC	Chinese Spring	15.3 X
<i>Triticum aestivum</i>	TaaCsp2DSHA	BAC	Chinese Spring	15.6 X
<i>Triticum aestivum</i>	TaaCsp3BFhA	BAC	Chinese Spring	7.0 X
<i>Triticum aestivum</i>	TaaCsp3BFhB	BAC	Chinese Spring	10.5 X

Species	Library Name	Library type	Ecotype	Coverage
<i>Triticum aestivum</i>	TaaCsp3BFhA_MTP	BAC	Chinese Spring	1.0 X
<i>Triticum aestivum</i>	TaaCsp3BFh_MTPv2	BAC	Chinese spring	1.0 X
<i>Triticum aestivum</i>	TaaCsp3DLhA	BAC	Chinese Spring	11.2 X
<i>Triticum aestivum</i>	TaaCsp3DLhA MTP	BAC	Chinese Spring	1.0 X
<i>Triticum aestivum</i>	TaaCsp3DSHA	BAC	Chinese Spring	11.0 X
<i>Triticum aestivum</i>	TaaCsp3DSHA MTP	BAC	Chinese Spring	1.0 X
<i>Triticum aestivum</i>	TaaCsp4BLhA	BAC	Chinese spring	15.0 X
<i>Triticum aestivum</i>	TaaCsp4BShA	BAC	Chinese spring	15.4 X
<i>Triticum aestivum</i>	TaaCsp5ALhA	BAC	Chinese spring	18.3 X
<i>Triticum aestivum</i>	TaaCsp5ALMTP	BAC	Chinese spring	1.0 X
<i>Triticum aestivum</i>	TaaCsp5AShA	BAC	Chinese spring	16.5 X
<i>Triticum aestivum</i>	TaaCsp5ASMTMTP	BAC	Chinese spring	1.6 X
<i>Triticum aestivum</i>	TaaCsp5DLhA	BAC	chinese spring	16.5 X
<i>Triticum aestivum</i>	TaaCsp5DSHA	BAC	chinese spring	17.0 X
<i>Triticum aestivum</i>	TaaCsp6ALhA	BAC	Chinese Spring	15.7 X
<i>Triticum aestivum</i>	TaaCsp6AShA	BAC		16.0 X
<i>Triticum turgidum</i>	Ttu-B-LDN65	BAC	Langdon	5.0 X
<i>Triticum turgidum</i>	Ttu-B-TTD140	BAC	TTD140	3.3 X
<i>Vitis vinifera</i>	VVCS - CabernetSauv	BAC	Cabernet Sauvignon clone 412	13.0 X
<i>Vitis vinifera</i>	VVPN40024 -PinotNoir	BAC	Pinot Noir 40024	16.1 X
<i>Vitis vinifera</i>	VVPN777	BAC	PN777	14.8 X
<i>Vitis vinifera</i>	VVSyrENTAV73	BAC	Syrah clone ENTAV 73	7.7 X
<i>Zea mays</i>	Zma-B-EP1h	BAC	EP1	1.0 X
<i>Zea mays</i>	Biogemma F2 BAC	BAC	flint inbred line F2	3.2 X
<i>Zea mays</i>	Zma-B-F331h	BAC	F331	1.0 X
<i>Zea mays</i>	Zma-B-KUI3h	BAC	KUI3	1.0 X
<i>Zea mays</i>	Zma-B-MO17h	BAC	Mo17	1.0 X
<i>Zea mays</i>	ZMS1P8 cdna	EST	Lignee F2 ou mat exotiq trop	

# List of collaborating projects

CNRGV believes that collaboration is essential to modern research. Thus since its inception in 2004 CNRGV is partner of projects in collaboration with public and private laboratories and is involved in many international consortia.

The table below gives an overview of the various projects in which the CNRGV is involved. This list shows the diversity of the scientific questions that can be addressed using the resources and services provided by the CNRGV

Species	Project Name and Coordinator	Partners
<i>Arabidopsis</i>	Evolutionary dynamics and genetic basis of dominance: sporophytic self-incompatibility in the Brassicaceae as a case study- Vincent Castric	Laboratory of Genetics and Evolution of Plant Populations-Ville-neuve d'Ascq-France
		Laboratory for Theoretical Computer Science - Lille- France
		ENS Lyon CNRS-laboratory of Plant Reproduction and Development- Lyon - FRANCE
		INRA-CNRGV-France
<i>Barley</i>	Ger4 locus characterization in 8 barley varieties and its relation with powdery mildew resistance - Patrick Schweizer	IPK-Gatersleben-Germany
		INRA-CNRGV-France
<i>Barley</i>	Towards the positional cloning of 4HL stripe rust resistance quantitative trait loci in barley. Development of a BAC library - Gisella Orjeda	Peruvian University Cayetano Heredia-Lima- Peru INRA-CNRGV-France
<i>Barley</i>	IBSC - International Barley Sequencing Consortium - Nils Stein	IPK - Gatersleben - Germany
		University of Minnesota - USA
		Carlsberg Laboratory - CITY - Denmark
		Australian Centre for Plant Functional Genomics -CITY- Australia
		National Institute of Agrobiological Sciences-CITY - Japan
		Research Institute for Bioresources - Okayama University - Japan
		Plant Genomics Laboratory - MTT Agrifood Research and University of Helsinki - Finland
		Scottish Crop Research Institute - Scotland
		Department of Plant Pathology - Iowa State University - Ames - USA
Zhejiang University - China		
<i>Coffee</i>	Isolation of SH3 coffee tree gene(s) conferring the resistance to leaf rust using a non gridded BAC library strategy - Philippe Lashermes	UMR RPB-Defense Mechanisms of plants to bioagressors-Montpellier-France INRA-CNRGV-France
<i>Eucalyptus</i>	Eucalyptus BAC libraries as tools to identify and characterize genomic sequences involved in wood formation - Jorge Paiva	IBET-Oeiras-Portugal
		UMR 5546 - Cell Surfaces and signaling in plants -Toulouse-France
		INRA-CNRGV-France
<i>Gerbil</i>	Inside the Gerbil's Genome - Philippe Gauthier	UMR IRD-INRA-Cirad-SupAgro - Center for biology and management of populations- Montpellier - FRANCE INRA-CNRGV-France
<i>Maize</i>	Genomic structure and variation of coding and non-coding region in maize varieties - Clémentine Vitte	Plant genetics station-Paris - France
		INRA-CNRGV-France
<i>Maize</i>	Physical map of the major QTL loci affecting cell wall digestibility - Yves Barrière	INRA - Lusignan- France
		ProMaïs association - France
		UMR5546-LRSV- Toulouse - France
		INRA-CNRGV-France

Species	Project Name and Coordinator	Partners
<i>Multispecies</i>	Plant and Animal Genome Evolution - Jérôme Salse	INRA-GDEC-Clermont Ferrand-France
		INRA - URGI -Versailles-France
		INRA - LGC -Toulouse-France
		CNRS-LGDP-Pepignan-France
		CNRS - UMR8541-Paris-France
		INRA-CNRGV - France
<i>Oldenlandia</i>	<i>Oldenlandia affinis</i> BAC library construction - Joshua S. Mylne	Chemistry & Structural Biology Division-Institute for Molecular Bioscience-The University of Queensland-St Lucia-Australia
		INRA-CNRGV-France
<i>Parsnip</i>	Characterization of genes involved in the biosynthesis of furanocoumarins - Frédéric Bourgaud	UMR1121 - INRA - Agronomy and environnement - Nancy-France INRA-CNRGV-France
<i>Passiflora</i>	Passiflora BAC library construction - Maria Lucia Carneiro Vieira	University of São Paulo-Laboratory of Cellular and Molecular Biology of Plants-Piracicaba- Brasil
		INRA-CNRGV-France
<i>Pea</i>	Towards the understanding of the mechanisms involved in frost tolerance in pea - Bruno Delbreil	UMR USTL-INRA - Abiotic stress and differentiation of cultivated plants - Villeneuve d'Ascq-France
		INRA-CNRGV-France

Species	Project Name and Coordinator	Partners
<i>Pea</i>	PeaMUST: Pea MUlti-STress adaptation and biological regulations for yield improvement and stability	INRA-AgroSup - AgroEcology- Dijon-France
		INRA- AgroParisTech – Agronomy-France
		INRA-Agrocampus-Ouest- IGEPP - Univ. Rennes1-France
		BIOPI- Université Picardie Jules Verne-France
		GAEL- Université Pierre Mendès France-France
		IBP- CNRS-Université Paris Sud- Orsay-France
		INRA –IJPB- AgroParisTech-France
		INRA-CNRS –LIPM Toulouse-France
		IRD - LSTM- Montpellier-France
		INRA - PISC - Versailles-France
		INRA-SADV- Université Lille1-France
		INRA-URGI – Versailles-France
		INRA-URGV-Toulouse-France
		Agri-Obtentions-France
		ARVALIS – Institut du végétal-France
		BIOGEMMA-France
		WELIENCE-France
		GEVES-France
		LIMAGRAIN Europe-France
		MOMONT -France
		NOVOZYMES-France
		RAGT 2n-France
		ROQUETTE-France
UNIP-France		
UNISIGMA-France		
VITAGORA-France		
INRA-CNRGV-France		
<i>Pepper</i>	Screening the pepper BAC library in order to identify all the members of the eIF4E multigenic family - Carole Caranta	INRA - Genetics and Improvement of Fruits and Vegetables Research Unit-Montfavet-France
		INRA-CNRGV-France
<i>Pepper</i>	Functional confirmation of candidate genes for a broad-spectrum resistance QTL against Phytophthora in Solanaceae - Véronique Lefebvre	INRA- GAFL-Functional characterization of interactions Plants - Pathogens- Montfavet-France INRA-CNRGV-France
<i>Rapeseed</i>	Evolutionary dynamics of genes controlling meiotic recombination in polyploid crop plants (DUPLIC) - Eric Jenczewski	Institut Jean-Pierre Bourgin -INRA-Versailles-France
		INRA - GDEC - Clermont Ferrand-France
		INRA-CNRGV-France
<i>Strawberry</i>	Using BAC libraries to isolate the allele responsible for the perpetual flowering trait in <i>Fragaria x ananassa</i> - Beatrice Denoyes-Rothan	INRA - University of Bordeaux - Fruit biology and pathology - Villenave d'Ornon-France
		INRA-CNRGV-France

Species	Project Name and Coordinator	Partners
<i>Sugarcane</i>	Identification of allelic copies of loci that control traits of economic importance and analysis of its variation between hom(e)ologous chromosomes in sugarcane ( <i>Saccharum</i> spp.) - Anete Pereira de Souza	Institute of Biology (IB), Univ. East of Campinas (UNICAMP)-Campinas-Brazil INRA-CNRGV-France
<i>Sugarcane</i>	The Sugarcane Genome Sequencing Initiative (SUGESI): Strategies for Sequencing a Highly Complex Genome - Glauca Souza	Botanic Department - IBUSP-São Paulo- BRASIL São Paulo University - BIOEN -Sao Paulo-Brazil CIRAD- Structure and evolution of genomes - Montpellier -FRANCE Plant Genome Mapping Laboratory Center for Applied Genetic Technologies- Athens -Greece University of Illinois at Urbana-Champaign-USA Southern Cross University-Centre for Plant Conservation Genetics Bioenergy Research Institute-Lismore - Australia Queensland Bioscience Precinct -St Lucia-Australia South African Sugarcane Research Institute-South Africa INRA-CNRGV -France
<i>Sugarcane</i>	Screening the R570 sugarcane BAC library to identify BAC clones that underlie QTL of agronomic importance - Karen Aitken	CSIRO Plant Industry-St Lucia-Australia INRA-CNRGV-France
<i>Sunflower</i>	SUNRISE: SUNflower Resources to Improve yield Stability in a changing Environment - Patrick Vincourt	INRA-CNRS - LIPM- Toulouse-France INRA - Agrosystems-Resource Management-Innovation and Ruralities - France INRA - Biometry and Artificial Intelligence-Toulouse-France  INRA - EPGV- Evry - France University Pierre and Marie Curie- Cellular Physiology and Plant Molecular - Paris- France INRA - Plant genetics- Le Moulon- France INRA - Applied Mathematics and Informatics - Paris -France ENFA - Laboratory for study and research on Economy-Policies and Social Systems- Toulouse - France INRA - Fruit biology and pathology- Bordeaux - France CETIOM-The Technical Center for Oilseed Crops and Industrial Hemp- Paris- France BIOGEMMA-France CAUSSADE Semences-France MAISADOUR Semences-France RAGT 2n-France SOLTIS-France SYNGENTA-France INRA-CNRGV-France

Species	Project Name and Coordinator	Partners
<i>Sunflower</i>	Genomics of Sunflower - Patrick Vincourt	Botany Department University of British Columbia-Canada INRA - LIPM-Toulouse - France Institute of Plant Breeding- Genetics- and Genomics-Center for Applied Genetic Technologies-Athens/Georgia-USA INRA-CNRGV-France
<i>Sunflower</i>	Improving sunflower yield and quality for biofuel production by genomics and genetics - Patrick Vincourt	UMR INRA-CNRS 441-2559-Toulouse-France UMR 1095 -INRA-Improvement and Plant Health-Clermont Ferrand-France UMR 1097-INRA-IRD-Montpellier Sup Agro-Univ. Montpellier II - Diversity and Evolution of Cultivated Plants -Montpellier-France UMR1248 - INRA-INPT/ENSAT - Agroecosystems and Territorial Development -Toulouse-France UMR1165 - INRA - CNRS- URGV- Evry-France INRA - EPGV -Evry-France INRA-BIA-Toulouse-France INRA-CNRGV-France
<i>Sunflower</i>	Durable resistance to downy mildew ( <i>Plasmopara halstedii</i> ) in sunflower	UMR 441-2559 - INRA-CNRS -Toulouse-France INRA-UMR 1095 " Amélioration et Santé des Plantes "-Clermont Ferrand-France UMR 1065 - INRA-ENITA - Plant Health- Bordeaux -France INRA-CNRGV- Toulouse -France
<i>Tomato</i>	Determining the minimum tilling path from the tomato BAC library in order to sequence chromosome 7 - Monder Bouzayen	UMR990-Laboratory of fruit genomics and biotechnology -Toulouse-France INRA-CNRGV-France
<i>Wheat</i>	Functional genomics of the wheat-Fusarium interaction - Hermann Bürstmayr	BOKU- University of Natural Resources and Life Sciences-Institute for Biotechnology in Plant Production-Tulln-Austria INRA-CNRGV- France

Species	Project Name and Coordinator	Partners
<i>Wheat</i>	Breedwheat : Developing new wheat varieties for sustainable agriculture - Catherine Feuillet - Jacques Le Gouis	INRA - GDEC - Clermont-Ferrand -France
		ARVALIS - Plant institute-Paris -France
		Study group and control Varieties And Seeds - GEVES-Beaucouzé-France
		RAGT 2n SAS -Rodez - France
		Florimond Desprez - France
		Biogemma - France
		LIMAGRAIN Europe - France
		Syngenta Seeds SAS - France
		Agri-Obtentions S.A.-GUYANCOURT - France
		SARL Adrien MOMONT & fils-MONS EN PEVELE - France
		Caussade Semences-Caussade-France
		Bayer CropScience - France
		Secobra Recherches SAS - France
		Céréales Vallée - Saint-Beauzire - France
		UMR INRA-AgroParisTech Agronomy - INRA Agronomie - Versailles-Grignon - France
		UMR INRA-UA Mediterranean Environmental Modelling and Agro-Hydrosystems - Avignon - France
		UMR INRA-AgroParisTech - Environment and Arable Crops (EGC) - Versailles - Grignon- France
		UMR INRA-UBI-UBII «Biologie du Fruit et Pathologie» (BFP) - INRA BFP - Bordeaux - France
		LIMOS UMR UPB - CNRS - Laboratory of Informatics, Modeling and Optimization - Clermont Ferrand - France
		UMR INRA-UPMF - GAEL - Saint Martin d'Hères - France
		INRA - Biology risk management in agriculture - plant pathogenic fungi -Versailles-Grignon - France
		INRA - Genomic-Computer science (GI) - Versailles-Grignon - France
		UMR INRA-UPS-CNRS - Plant genetics (GV) - Le Moulon - France
INRA - EPGV - Evry - France		
INRA - Biopolymers Interactions Assemblies - Nantes - France		
INRA-CNRCV - France		
<i>Wheat</i>	Identification of the genomic region responsible for the resistance to the leaf rust in the wheat variety Sinvalocho MA using non gridded BAC library - Maria-José Dieguez	Genetic Institute «Ewald A. Favret» - Buenos Aires – Argentina INRA-CNRCV - France
<i>Wheat</i>	Identification and sequencing of the asparagine synthetase genes in Durum Wheat - Gabriella Sonnante	Institute of Plant Genetics (IGV) – CNR-Bari-Italy INRA-CNRCV - France

Species	Project Name and Coordinator	Partners
<i>Wheat</i>	TriticaeGenome - Catherine Feuillet	INRA- GDEC -Clermont Ferrand-France
		IPK - Gatersleben Germany
		Institute of Experimental Botany - IEB - Czech Republic
		GSF- National Research Center for Environment and Health - GSF - Germany
		University of Milan - - Italy
		University of Haifa - HU - Israel
		MTT - Helsinki- Finland
		Scottish Crop Research Institute - SCRI - United Kingdom
		Sabancı University - SABA - Turkey
		National Institute of Agricultural Botany - NIAB - United Kingdom
		John Innes Centre - JIC - United Kingdom
		Universität Zürich - UZH - Switzerland
		INRA Transfert - IT - France
		Biogemma - BGA - France
Lochow-Petkus GmbH - LP - Germany		
Applied Genomic Institute- IGA - Udine - Italy		
University of Bologna -UNBO - Italy		
INRA-CNRCV-France		
<i>Wheat</i>	Construction of a BAC library of the tetraploid species <i>T. dicoccoides</i> - Elena Salina	Institute of Cytology and Genetics-Novosibirsk -Russia INRA-CNRCV-France
<i>Wheat</i>	IWGSC- International Wheat Genome Sequencing Consortium - K. Eversole - six co-chairs R. Appels (Australia)- J. Dvorak (USA)- C. Feuillet (France)- B. Gill (USA)- B. Keller (Switzerland)- Y. Ogihara (Japan) and K. Eversole (USA)	956 members of private and public laboratories
<i>Wheat</i>	Gap closing in the wheat variety -HOPE- using BAC libraries - Wolfgang Spielmeier	Commonwealth Scientific and Industrial Research Organisation (CSIRO)-Canberra - Australia INRA-CNRCV-France
<i>Wheat</i>	Identification of WRKY and DREB transcription factors involved in abiotic stress in durum wheat - Rim Mzid	Center of Biotechnology Ecopark of Borj Cedria (CBBC) -Tunis - Tunisia INRA-CNRCV-France

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