

**French Plant Genomic Resource Center (CNRGV)** is a non-for-profit service centre dedicated to plant genomics.

The objectives of the CNRGV are to gather, to **conserve and to manage genomic** libraries but also to **provide high throughput molecular tools** to the scientific community.

The CNRGV is already in charge of more than 7 millions unique samples among more than 50 plant genomic libraries of model and crop plant.

- Because cloning of genomes into bacterial artificial chromosome (BAC) libraries constitutes an invaluable tool for genomic analysis, CNRGV offers to construct plant BAC libraries.

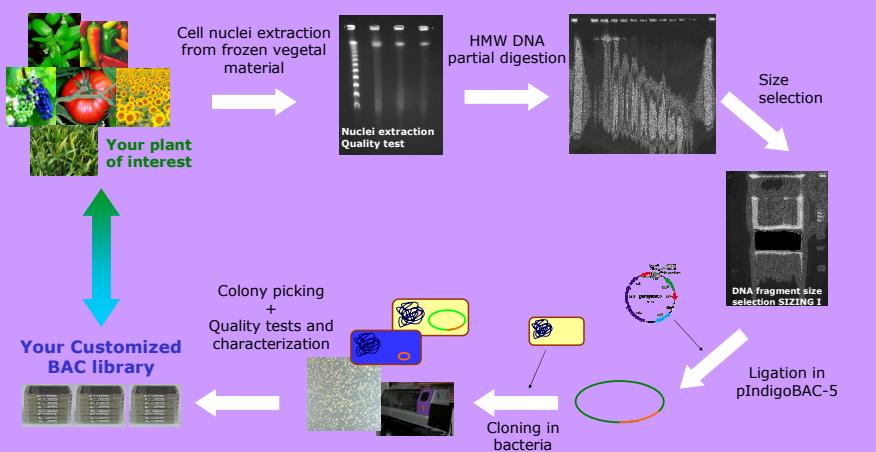
BAC library construction can be associated to our efficient **3D-pools** production and screening methods. All this steps can be carried out at CNRGV. This "**3D-pools screening pipeline**" has been developed and validated at CNRGV.

- Fast identification of large DNA regions of interest based on **Non Gridded BAC Libraries** method is set-up at CNRGV. It allows easier access to genetic diversity.

**Plant BAC library construction service**

BAC library constructions carried out in 2010 :

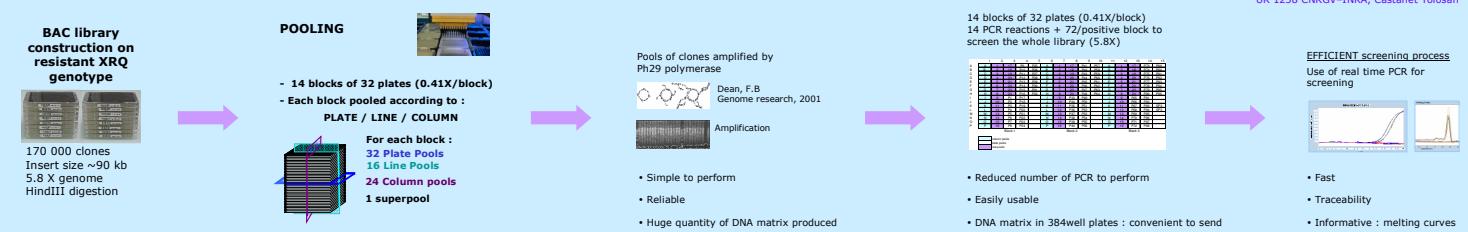
Species	Genotype	Library name	Enzyme	Mean insert size (kb)	Clone number
Medicago truncatula	F83	Mtr-B-F83	Hind III	65	55296
Arabidopsis thaliana	Ita-o	Ath-B-Ita0	Hind III	96	15360
Arabidopsis lyrata	03A7/1	Aly-B-03A7	Hind III	73	15360
Arabidopsis lyrata	05B17/1	Aly-B-05B17	Hind III	89	15360
Arabidopsis lyrata	05B37/3	Aly-B-05B37	Hind III	102	9984
Arabidopsis halleri	05B8/1	Aha-B-05B8	Hind III	110	13824
Arabidopsis halleri	L406	Aha-B-L406	Hind III	115	13440
Arabidopsis halleri	HF11-4	Aha-B-HF11	Hind III	92	14592
Arabidopsis halleri	PL22-138	Aha-B-PL22-138	Hind III	84	16512
Arabidopsis halleri	Bulk 19	Aha-B-19	Hind III	94	44544
Helianthus annus	XRQ	Han-B-XRQ	Hind III	92	162000
Cichorium intybus	S1	Cin-B-S1	Hind III	120	81408
Cichorium intybus	S2	Cin-B-S2	Hind III	90	89088
Phytophthora parasitica		Ppa-B-1	Hind III	134	11520
Passiflora edulis	Flavicarpa	Pev-B-Flav	Hind III	140	142080
Quercus suberis	HDL	Qsu-B-HDL	Hind III	115	41472
Helianthus annus	HA 412	Han-B-412b	Bam HI	114	86400
Helianthus annus	HA 412	Han-B-412e	EcoRI	93	81792
Helianthus annus	HA 412	Han-B-412h	Hind III	121	96000
Hordeum vulgare	Bison H1H4HS	Hvu-B-H145	Hind III	89	56064
Quercus robur	3P	Qro-B-3P	Hind III	115	98304
Helianthus annus	XRQ	Han-B-XRQ	Hind III	84	169344
Spartina maritima	Sma-B-MOB	Hind III / Bam HI		108	44544
Oidemelidia affinis	Oaf-B-UQh	Hind III		100	128640
26 libraries		101		1502928	



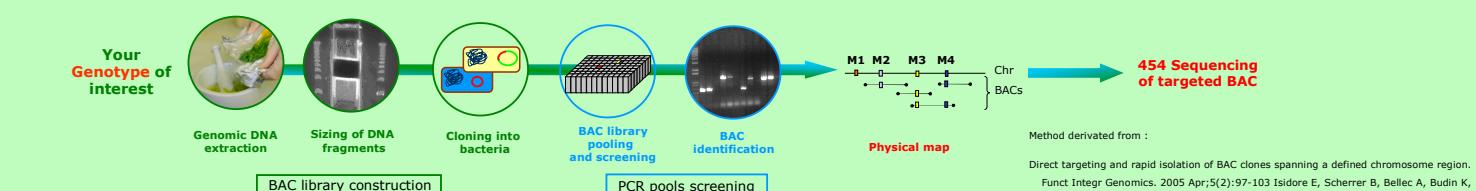
**3D-pools : efficient tool for high-throughput BAC library screening**

Schema of 3D-pools produced for the characterization of a quantitative resistance to Downy Mildew (*Plasmopara halstedii*) in cultivated Sunflower

**PROMOSOL Mildew project**  
 Laboratoire Interactions Plantes Microorganismes, UMR 441-2594 INRA/CNRS, Castanet Tolosan  
 UMR 1095 Amélioration et Santé des Plantes INRA/ Université Blaise Pascal, Clermont Ferrand  
 UMR 1065 Snat des plantes INRA/ENITA, Bordeaux  
 UR 1258 CNRGV-INRA, Castanet Tolosan



**Fast BAC clones isolation in genotypes of interest : Non Gridded BAC Libraries strategy**



Our aim is to **avoid time and cost expensive steps** of BAC clones organization in microplates in order to **access efficiently the diversity** among plant cultivars.

Various projects regarding wheat, barley, coffee, pepper cultivars are already in progress through collaboration with INRA Clermont-Ferrand and CSIRO Canberra.  
 e.g. Mapping of the Gene SKr gene in Courtot wheat line

We propose the **fast BAC clones isolation method associated to BAC's sequencing services using the 454 technology** available at PlaGe, INRA, Toulouse.

CNRGV is involved in numerous projects on various model and crop species including :

- Wheat and barley improvement: TriticeaeGenome FP7 (1)
- Tomato: Physical mapping for sequencing of chromosome 7 (2)
- Sunflower: SunFuel et Mildew (3)
- Medicago: Various projects as Medicago Stock Center (4)
- Eucalyptus : Eucalyptus BAC Libraries as tools to identify and characterize genomic sequences involved in wood formation (5)
- Pepper : Positional cloning and confirmation of candidate genes for a broad-spectrum resistance QTL against Phytophthora in Solanaceae (6)
- Rapeseed improvement (7)
- Chicory Genetic and physical mapping of the S-locus (Asteraceae) (8)
- Sugarcane genome sequencing (9)
- Towards the positional cloning of 4HL stripe rust resistance quantitative trait loci in barley (10)
- Construction of a BAC library of the tetraploid species *T. dicoccoides* (11)

CNRGV's collaborators:

- (1) ETGJ / ITMB / Triticeae Genome partners
- (2) Génétique, diversité et évolution des plantes et champignons UMR 1095 Clermont-Ferrand
- (3) Laboratoire d'Amélioration et d'amélioration des fruits INRA/INRA/CNRS Toulouse - France
- (3,4) Laboratoire des Interactions Plantes Micro-organismes INRA/CNRS Toulouse - France
- (5) Centro das Florestas e Produtos Florestais Lisboa - Portugal
- (6) Caractérisation Fonctionnelle des interactions Plantes/Bioagresseurs INRA-UR1052-AFAL Avignon - France
- (7) INRA/ENITA/INRA/CNRS Toulouse - France
- (7) Amélioration des Plantes et Biotechnologies Végétales UMR118 INRA/AgroCampusOuest/Université de Rennes - France
- (8) Stress abiotique et différenciation des végétaux cultivés, UMR USTL/INRA/281/SADIV Lille - France
- (9) Développement de Botânica-IBUSP São Paulo, Brasil
- (10) Structure et évolution des génomes CIRAD, UMR 1095 Montpellier, France
- (10) Universidad Peruana Cayetano Heredia, Departamento de Bioquímica, Biología molecular y Farmacología Lima - Peru
- (11) Institute of cytology and Genetics of Novosibirsk, Russia

The libraries, tools and techniques presented above as well as similar tools produced on numerous plant species are available for scientific community  
 See more information and make your own request for specific genomic tool or service - or set up of collaborative project - on our web site

<http://cnrgv.toulouse.inra.fr/>