



Sunflower Biological Resource Center

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BRCA staff

- Scientific management

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- Operational responsibility
 - Maintenance accessions
 - Creation new accessions
- Institutional relations
 - Diffusion accessions
 - Phytosanitary agreements

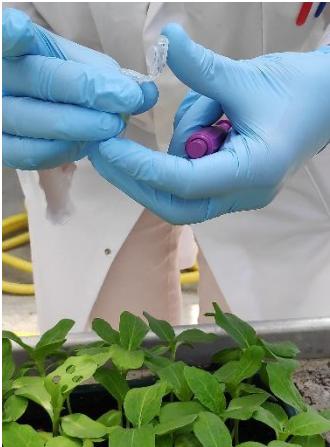
Marie-Claude Boniface
&
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What is the BRC

- Molecular characterization
- Phenotypic characterization
- Material development





Historical perspective Sunflower genetic resources at INRAE

- **INRAE Clermont-Ferrand (1960-2010)**
 - GMS Leclercq 1966
 - CMS PET1 Leclercq 1969, restoration gene 1971
 - Pathogen resistance 1970-2010 (Downy mildew, sclerotinia...)
- **INRAE Montpellier (1980-2010)**
 - Wild *H. annuus* and relative species
 - Interspecific crosses
- **INRAE Toulouse (since 2007)**
 - Drought tolerance, downy mildew and orobanche



GRC sunflower created in 2013



INRAE collections

Over 6600 accessions

	Nature	#
Traditional GR	Cultivated lines	2600
	Cultivated population and genetic pools	400
	Wild ecotypes*	760
Scientific GR	RILs	590
	TILLING EMS mutant populations (M2 families)	2100
	Interspecific lines	170



* Includes 137 *H. tuberosus* UE Diascope, INRA Montpellier



Helianthus network

- Public-private consortium to maintain strategic GR
 - Helianthus Network Started in 2017
 - Corteva, MAS Seeds, RAGT2n, Soltis, Syngenta

	Sterility status	Helianthus network	National collection
Populations		115	5
Lines	cmsPET1 A+B	253	10
	cmsPET1 B	472	
	cmsPET1 R	259	
GMS lines	GMS	58	
Alloplasmic lines	cms non-PET1	122	6
RILs		638	
TOTAL		1917	21





GR distribution

	2014	2015	2016	2017
INRAE laboratories		20		
Public research labs	3		96	95
French (except INRAE)				
European and international	3		96	95
Private companies	162	74	106	169
French	161	74	91	152
European and interantional			15	17
TOTAL	165	94	202	264





Characterization

- Passport data on *Helianthus* network collection

Height, branching, flowering time, oil content, TKW, seed color

- SIREGAL web portal (URGI, INRAE Versailles) currently 2170 accession (201901)



<https://urgi.versailles.inra.fr/siregal/siregal/card.do?id=33&dbName=siregal&className=genres.admistration.Grclmpl>

The screenshot shows the SIREGAL web portal interface. At the top, there's a logo for EURGI and another for GnpIS (Genetic and Genomic Information System). The main menu includes 'Log in', 'Preferences' (with dropdowns for 'All species' and 'Select one...'), 'Main' (with links to 'HOME' and 'Documentation'), 'Documentation' (with links to 'USER GUIDE', 'HOW TO ORDER', 'DATA SUBMISSION', 'FAQ', 'GENETIC RESOURCES', 'MODULE NEWS', and 'RELEASE NOTES'), 'Other GnpIS data' (with links to 'DATA SUBMISSION', 'GNPIS PORTAL', 'GENOMES', 'SEQUENCES', 'GENETIC MAPS', 'POLYMORPHISMS', 'PHENOTYPES', 'ASSOCIATION', 'GENETIC RESOURCES', 'PLANT SYNTENY', and 'TRANSCRIPTOMIC'), and 'Miscellaneous' (with a link to 'EXTERNAL LINKS'). The 'Main' menu also has a 'HOME' link. Below the menu, there's a section titled 'Siregal Genetic resources' with a sub-section for 'Siregal Genetic resources'. It describes Siregal as the Plant Genetic Resources Information System of the National Institut for Agronomical Research (INRA), France, which presents accessions managed by INRA Biological Resource Centers (BRC) and some of the French networks for crop genetic resources. It notes that the BRC are not commercial suppliers of plant material and distribute in general small amounts of plant materials mainly for research, development and biodiversity preservation activities. It also mentions that the main data associated to accessions are of two types: multicrop passport descriptors (common to all plant species) and specific data (may be different for each species group). It provides links to the project web page and the GnpIS module. The bottom part of the screenshot shows a grid of images representing various fruit, model, vegetable, and crop species, each with a name and a BRC link.

Fruit species	Model species	Vegetable species	Crop species
arabidopsis Citrus fruits Cherry BRC	Arabidopsis Medicago truncatula BRC	Yam BRC Allium BRC	Maize BRC Grain legumes BRC



Use in research programs

- Molecular characterization

- HQ genome : 8 lines (Sunrise + Helior + ICSG)
- Re-Seq 57 public lines (Sunrise) + ~1000 lines (ICSG)
- AXIOM 50k SNP (5 populations + ~2500 lines HeliaDiv + Sunrise)
- 384 SNP 115 pop 1000 lines

- Phenotypic characterization

- Drought tolerance 57 public lines (Sunrise)
- Disease resistance (ResODiv, MilVarSunRes)

- Material development

- ~500 wild *H. annuus* IL (Oleosol, Sunrise)
- 18x100 NAM RIL (Sunrise)
- Branching studies
- Mutant EMS production (300 M2 families)





Perspectives

- Maintenance
 - Duplicate the collection at -20°C on another site (Montpellier)
- Diffusion
 - Cost estimation (with LIPME Gestion)
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- Characterization
 - Consolidation of historical data in Siregal
 - Development of phenotyping archiving





Thank for your attention



Thanks to sunflower INRAE teams ; ASTR and SPI
Thanks to all national and international partners

