Partnership

Nine public laboratories

INRA Rennes
UMR IGEPP (INRA, AgroCampus-Ouest, Univ. Rennes 1)

INRA Versailles-Grignon
UMR EGC (INRA, AgroParisTech)
UMR Agronomie (INRA, AgroParisTech)
UMR IJPB (INRA, AgroParisTech)
URGI (INRA)

INRA PACA
UMR GAEL (INRA, Univ. Pierre Mendès France)

Université de Caen Basse-Normandie
UMR EVA (Univ. Caen Basse Normandie, INRA)

CNRS
UMR IRISA (CNRS, ENS Rennes, INRIA, INSA Rennes, Institut Mines-Télécom, Supélec, UBS, Univ. Rennes 1)

IRSTEA
UR TERE

One technical institute

CETIOM

Six private companies

Biogemma
Euralis Semences
Limagrain Europe
Maïsadour Semences
RAGT 2n
Syngenta

Key figures

- ✓ Duration : 90 months (2012-2019)
- ✓ Total cost : 20.3 M€
- ✓ Funding : 6 M€ from the Investments for the Future program "Biotechnology and Bioresources"
- ✓ Complementary funding : 82 k€ from the Basse-Normandie Regional Council
- ✓ Partnership :
  - nine public partners / six industry partners / one technical institute
  - 24 full-time staff

For more information

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RAPSODYN project is labeled by the GIS Biotechnologies Vertes (GIS BV).

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RapsodyN

Optimization of the RAPeSeed Oil content anD Yield under low Nitrogen input

www.rapsodyn.fr

RAPSODYN: an ambitious long-term project designed to optimize NUE in rapeseed

A major oil crop facing future challenges

- ✓ 1st in France and in the EU-28, 3rd worldwide
- ✓ Increasing demand for edible oil
- ✓ Development of industrial uses (energy & green chemistry)
- ✓ Need for feed proteins

WP1 – Genomic resources

Aim: To obtain high throughput sequencing and genotyping data to support efficient genetic studies and breeding programs for improving NUE and yield.

Re-sequencing of rapeseed lines will boost marker discovery at the whole genome scale and the best candidate genes will be identified through whole exome sequencing. All genetic resources will be genotyped using *ad hoc* tools. Diagnostic markers will be developed at key loci for use in breeding programs.

WP2 – Rapeseed functioning under low N input

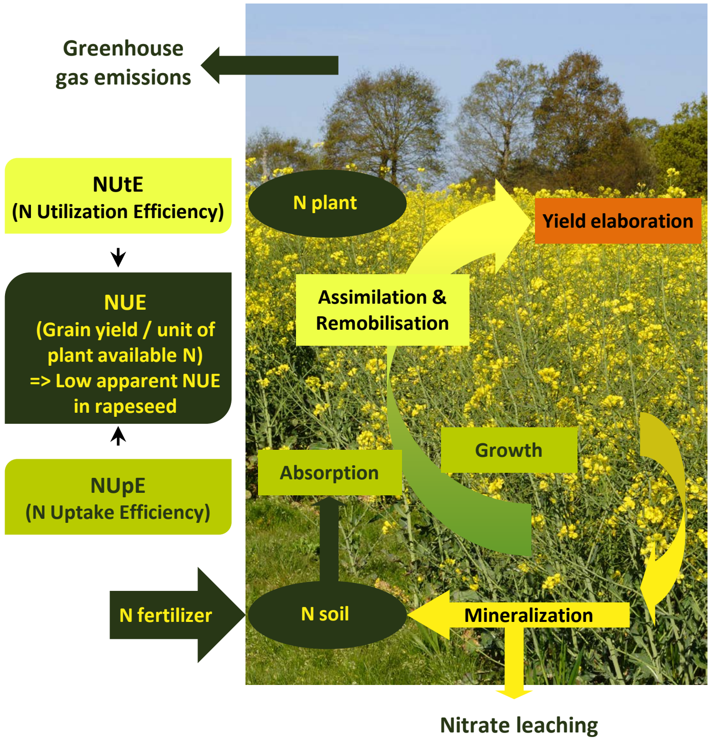
Aim: To decipher functional traits involved in NUE and develop novel tools for high throughput phenotyping of plant N status and crop NUE.

Predictive modeling of plant production under N limitation will be combined with genomics and post-genomics to identify the most promising functional traits associated with NUE. A challenge will be to connect models of plant or canopy functioning with models of resource flux allocation and to relate the contribution of these functional determinants to NUE. Efforts will also be devoted to the development of phenotyping tools for NUE (spectral reflectance-based technologies, NMR relaxometry devices, molecular tools …).

WP3 – Genetic architecture of rapeseed adaptation to N limitation

Aim: To unravel the genetic control of yield and NUE in the context of limited N inputs.

The genetic variability for yield will be explored using high resolutive populations trialed in a multi-location and multi-year phenotyping network (~ 50,000 plots). The most important regions identified in inbred lines will then be validated in Heterogeneous Inbred Families. Finally, new genetic variability at these loci will be investigated within the natural variability present in rapeseed populations.



Greenhouse gas emissions

NUtE
(N Utilization Efficiency)

NUE
(Grain yield / unit of plant available N)
=> Low apparent NUE in rapeseed

NUpE
(N Uptake Efficiency)

N plant

Yield elaboration

Assimilation & Remobilisation

Growth

Absorption

N fertilizer

N soil

Mineralization

Nitrate leaching

WP4 – Applications in breeding programs

Aim: To deliver NUE-improved varieties by introgressing new more efficient alleles into elite lines.

This will allow rapid delivery of NUE-improved varieties to markets as well as methods for germplasm characterization, gene discovery and breeding strategies. After being validated, tools and germplasms will be ready and available to develop adapted hybrid lines through new breeding strategies. Models and scenarios based on French and Canadian rapeseed breeding areas will be compared to determine the technical and economic conditions that would favor the development of NUE-improved rapeseed varieties.

WP5 – Bioinformatics

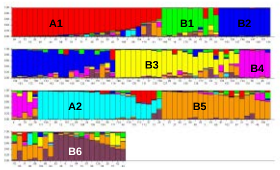
Aim: To develop a Rapsodyn Information System (RIS) designed with new tools for data storage and large scale analysis.

The RIS will enable data storage, integration and extraction through user-friendly interfaces. Advanced and innovative tools will be developed for genomics data computing. Throughout the project, advanced results will be added to the multispecies integrative information system being developed by INRA (GnpIS).

RAPSODYN goals

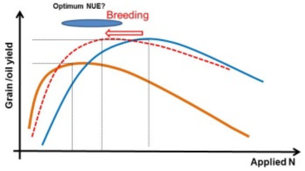
- ✓ Optimize rapeseed oil yield and content
- ✓ Improve Nitrogen Use Efficiency (NUE)
- ✓ Develop innovative breakthroughs in breeding methods and agricultural practices

Genotyping



Phenotyping / Modeling

New breeding methods



Economic evaluations

Data management

- ✓ Communication tools
- ✓ Training
- ✓ International conferences

- ✓ QTL and genes
- ✓ Allele mining
- ✓ Diagnostic markers
- ✓ Improved modeling

- ❖ Innovative varieties
- ❖ Integration of G×E×N interactions
- ❖ Optimized N fertilization strategies

Deliver the right nutrient rate at the right time to the right variety adapted to fully characterized environments