Transversal Symposium on'Investment for the Future' projects in plant biology

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Transversal Symposium on 'Investment for the Future' projects in plant biology

GIS bV
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Summary

The 'Investment for the Future' projects labelled by the GIS BV

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Acknowledgments

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Preface

I Implemented by the General Secretariat for Investment (SGPI, formerly CGI) in 2011 as part of the 'Grand Emprunt' (a French government-funded investment programme), and managed by the National Research Agency (ANR), the PIA provided the framework for a massive and targeted investment in research and innovation.

The 9 projects labelled by the GIS BV concern 8 'Biotechnologies and Bioresources' projects: AKER, AMAIZING, Biomass For the Future, BREEDWHEAT, GENIUS, PeaMUST, RAPSODYN, SUNRISE, and an 'Infrastructure' project: PHENOME. These long-term projects (2011/2012-2020) were structured around large-scale public-private partnerships, which cover research, development and training. They are fully in line with the ambitions of the GIS BV to foster new technologies and skills, and to gain the knowledge needed to provide innovative plant varieties for more efficient and sustainable agricultures.

Started in 2011/2012, these ongoing PIA projects have generated a wealth of knowledge on genome structure and function, created new genetic material through the exploration of hundreds of thousands of accessions, and implemented innovative technologies and powerful tools to address the current and future structural challenges and scientific themes identified as priorities by the GIS BV for the plant biology scientific community.

The GIS BV Symposium 2019 is the opportunity to present the achievements of each of the 9 projects with a transversal vision, illustrating their contributions to common objectives. The program will highlight both (i) technological advances in the areas of biotechnology, plant breeding methodology, big data management and phenotyping, and (ii) the generation of novel genetic material at the pre-breeding stage for efficient use of biomass, reduction of pesticides and other inputs, and adaptation to climate change, including drought tolerance. A prospective session on the future of plant breeding at national and international levels will close the Symposium.

This booklet contains first of all the Symposium programme as well as the abstracts of all talks on PIA project results. In its second part, it presents to you the key highlights, main results and success stories of each project.

We are proud of the major achievements made so far, and very pleased to share some of them with stakeholders and government officials during this major event for our public-private plant research community.

We wish you a very good Symposium!

Peter Rogowsky,
president of the GIS BV managing board

Pascual Perez,
vice-president of the GIS BV managing board

Pascal PEREZ

\\ As supervisor of applied research, aiming to set up plants better adapted to tomorrow's agriculture issues, I particularly notice that these long lasting PIAs established excellent collaborations between public research and different private contributors, a huge transversality and a fair complementarity.

Peter ROGOWSKY

\\ PIAs kept their promises. Their moved ahead plant breeding and allow to accommodate social aspirations with modern agriculture needs, like promoting biodiversity, lowering pesticides use, developing varieties climate resilient and reinforcing nutritional quality of food.

Programme

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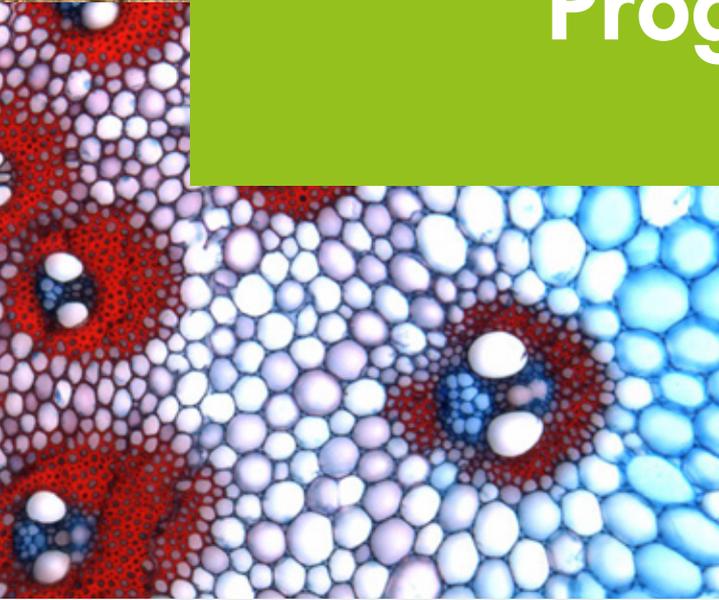
Introductive speeches

14:00 – 14:30 GIS BV presentation and PIAs projects key facts - *Peter Rogowsky (GIS BV Managing Board)*
14:30 – 14:45 The Biotechnology & Bioresources initiative within the "Investments For the Future Program" – *Emmanuelle Simon (ANR)*

Towards new insights in "omics" and data

Chairman: *Henning Hermjakob (EMBL-EBI Cambridge, GIS BV Scientific Advisory Board)*

14:45 – 15:10 Plant Phenomics: Current status and major challenges in relation to breeding – *François Tardieu (INRA)*
15:10 – 15:35 Metabolomics and system biology – *Yves Gibon (INRA)*
15:35 – 16:00 Current and future major issues on genomics – *Peter Westhoff (University of Düsseldorff)*
16:00 – 16:25 Big data and data analysis– *Pascal Neveu (INRA)*

16:25 – 17:00 Coffee break and poster session

Success stories by young scientists

Chairman: *Ian Graham (University of York, GIS BV Scientific Advisory Board)*

17:00 – 17:05 Increasing the genetic variability of sugar beets with interesting new alleles from exotic resources around the world – *Prune Pegot-Espagnet (INRA, AKER)*
17:05 – 17:10 Systems genetics of drought related traits in maize – *Mélisande Blein-Nicolas (INRA, AMAIZING)*
17:10 – 17:15 Integration of genetic and ecophysiological modeling to explore ideotypes: the case of biomass growth and its regulation by water deficit in sorghum – *Florian Larue (Cirad, BFF)*
17:15 – 17:20 Drought tolerance of winter bread wheat in France: from varietal characterization to the identification of the allelic effects in different water stress scenarios – *Gaëtan Touzy (RAGT, BREEDWHEAT)*
17:20 – 17:25 Gene and base editing to confer agronomic traits in Potato: example of the GBSSI gene – *Florian Veillet (INRA, GENIUS)*
17:25 – 17:30 Bruchid resistance in pulses – *Estephania Carrillo-Perdomo (INRA, PeaMUST)*
17:30 – 17:35 Dealing with multi-source and multi-scale information in Plant Phenomics: the PHIS ontology-driven Information System – *Llorenç Cabrera-Bosquet (INRA, PHENOME)*
17:35 – 17:40 Temperature and radiation stresses explained most of the environmental variations of seed yield across a French experimental network, and allowed to tackle the G×E interaction issues in WOSR – *Erwan Corlouer (INRA, RAPSODYN)*
17:40 – 17:45 Development of new sunflower ideotypes by combining quantitative genetics approach and crop modelling – *Florie Gosseau (INRA, SUNRISE)*
17:45 – 18:00 Questions

18:30 – 19:30 Afterwork drink at FIAP Jean Monnet

Highlights and scientific breakthroughs of PIAs projects for sustainable agriculture

Chairmen: *Roberto Tuberosa (University of Bologna, GIS BV Scientific Advisory Board) & Rod Snowdon (Justus Liebig University-Giessen, GIS BV Scientific Advisory Board)*

⅏ Drought resilience and climate change

09:00 – 09:15 Predicting the impact of traits / alleles in current and future European drought scenarios – *Boris Parent (INRA, AMAIZING & PHENOME)*
09:15 – 09:30 Predicting sunflower yield from traits to fields: application to assessment and recommendation of cultivars – *Pierre Casadebaig (INRA, SUNRISE)*
09:30 – 09:40 Questions

⅏ Plant resistance to pathogens

09:40 – 09:55 Plant resistance and architecture for protection of pulses against pathogens – *Marie-Laure Pilet-Nayel (INRA, PeaMUST)*
09:55 – 10:10 Targeted gene modifications in tomato for the development of virus resistance – *Marianne Mazier (INRA, GENIUS)*

10:10 – 10:20 Questions

⅏ Fostering Biomass Value chains development

10:20 – 10:40 Merging biobased material and energy production value chains development, with OMICS, modelling and value chain assessment – *Maryse Brancourt (INRA, BFF) & David Pot (Cirad, BFF)*
10:40 – 10:45 Questions

10:45 – 11:15 Coffee break

⅏ Low inputs and nitrogen availability response

11:15 – 11:30 Integrative approaches to investigate Nitrogen Use Efficiency in oilseed rape and plant functioning under low N input – *Nathalie Nesi (INRA, RAPSODYN)*
11:30 – 11:45 Improving Nitrogen Use Efficiency in Wheat by Genome Wide and Candidate Genes Targeted Association Studies – *Stéphane Lafarge (Biogemma, BREEDWHEAT)*
11:45 – 12:00 Root System Architecture, Nodulation & Nitrogen nutrition in pea – *Virginie Bourion (INRA, PeaMUST)*
12:00 – 12:10 Questions

Innovative tools for plant breeding

Chairman: *Chris-Carolin Schoen (Technical University of Munich, GIS BV Scientific Advisory Board)*

⅏ New breeding technologies
12:10 – 12:25 New tools for plant genome editing: Examples from rice – *Christophe Perin (Cirad, GENIUS)*

12:25 – 12:40 Efficient targeted mutagenesis of a perennial crop with vegetative propagation Efficient targeted mutagenesis of apple, a vegetatively propagated perennial crop – *Elisabeth Chevreau (INRA, GENIUS)*

12:40 – 12:50 Questions

13:00 – 14:15 Lunch

⠕ Discovering and integrating species diversity

14:15 – 14:30 Improving the diversity of *Brassica napus* using doubled haploids (DH) derived from a panel of newly created semi-synthetic lines – *Sébastien Faure (Innolea, RAPSODYN)*
14:30 – 14:45 Worldwide phylogeography and history of wheat genetic diversity – *Etienne Paux (INRA, BREEDWHEAT)*
14:45 – 15:00 An innovative and ambitious approach to identifying and integrating genetic resources into Elite material (Sugar Beet as an example) – *Pierre Devaux (Florimond Desprez, AKER)*
15:00 – 15:15 Discovering, characterizing and exploiting structural variation in maize – *Johann Joets (INRA, AMAIZING)*
15:15 – 15:30 Questions

⠕ Genomic selection

15:30 – 15:45 Genomic selection in a broad cooperative maize panel: impact of population structure and identification of diversity sources for variety development – *Alain Charcosset (INRA, AMAIZING)*
15:45 – 16:00 Elaboration of a genomic calibration tool to predict performance under limited N supply – *Laurent Hanneton (Limagrain, RAPSODYN)*
16:00 – 16:15 Multiscale modeling to predict sunflower tolerance to abiotic stresses – *Nicolas Langlade (INRA, SUNRISE)*
16:15 – 16:25 Questions

16:25 – 16:50 Coffee break

Chairman: *Pere Arús (IRTA, GIS BV Scientific Advisory Board)*

Socio-economic studies of PIAs projects

16:50 – 17:10 Socio-economic analysis of the impact of agricultural biotechnology – *Stéphane Lemarié (INRA)*
17:10 – 17:15 Questions

Data management & information systems

⠕ Data management & information systems

17:15 – 17:35 Management of the data sets using GnpIS following the FAIR principles – *Anne-Françoise Adam-Blondon (INRA, interPIA)*
17:35 – 17:50 Sunflower genome sequences: past, present, future – *Jérôme Gouzy (INRA, SUNRISE)*
17:50 – 18:00 Questions

The PIA experience: from scientific breakthroughs to societal impacts

Chairman: *Peter Westhoff (University of Düsseldorf, GIS BV Scientific Advisory Board)*

09:45 – 10:30 Delivering innovation to growers: how the PIA projects have improved the information provided to farmers on varieties – *Jean-Pierre Cohan (Arvalis Institut du Végétal), David Gouache (Terres Inovia), Fabienne Maupas (ITB), Xavier Pinochet (Terres Inovia)*
10:30 – 11:00 Ten years later: key facts of PIA projects – *Pascual Perez (GIS BV Managing board)*
11:00 – 11:15 Feedback and synthesis of scientific highlights of PIAs projects – *GIS BV Scientific Advisory Board*

11:15 – 11:35 Coffee break

Foreseeing the future of plant breeding

11:35 – 11:55 Which scenarios for the future of European agriculture: first results of CropBooster-P project – *Norbert Rolland (INRA)*
11:55 – 12:15 Foreseeing the future of plant breeding, in the current social, economic and environmental contexts – *Carole Caranta (INRA) & Jean-Christophe Gouache (Limagrain)*

Conclusion

12:15 – 12:30 Conclusion, acknowledgements and end of the meeting – *Fermin Azanza & Olivier Le Gall (GIS BV Strategic Committee)*

List of abstracts

Success stories by young scientists

Prune Pegot-Espagnet
UMR Laboratoire des Interactions Plantes-Microorganismes (CNRS-INRA), AKER

Increasing the genetic variability of sugar beets with interesting new alleles from exotic resources around the world

The selection of new stable sugar beet varieties producing more extractable sugar per hectare is the main target for sugar beet breeding. However, the genetic variability useful for genetic improvement of crop is increasingly narrow due to successive inbreeding crosses. AKER project (2012-2020) proposes to increase the genetic variability of sugar beets by searching for interesting new alleles from exotic resources around the world. During the project, 16 exotic accessions have been identified around the world as representing all the genetic diversity that is not already present in cultivated sugar beets.

Each of these accessions has been crossed with an elite sugar beet so that the genome of the exotic is fragmented into the elite germplasm. The effect of different schemes of crosses between the progenies of these different accessions on the root yield and on the genetic diversity will be simulated in silico to guide the production of a pre-breeding population. This pre-breeding population will represent a reservoir of genetic diversity useful for breeding programs. In order to simulate the evolution of root yield during crossings, the genetic architecture of this trait must be known. A QTL detection study was conducted and revealed several QTLs related to this trait. These results will be presented.

Mélisande Blein-Nicolas
UMR de Génétique Quantitative et Evolution (INRA-UPS-CNRS-AgroParisTech), AMAIZING

Systems genetics of drought related traits in maize

The evolution of maize yields under drought is of particular concern in the context of climate change and human population growth. To better understand the mechanisms associated with the genetic polymorphisms underlying the variations of traits related to drought tolerance, we used a systems genetics approach integrating high-throughput phenotypic, proteomics and genomics data acquired on 254 maize hybrids grown under well-watered and water deficit conditions. We show that water deficit, even mild, induced a strong proteome remodeling and a reprogramming of the genetic control of the abundance of many proteins. We identify close co-localizations between QTLs and pQTLs, thus highlighting environment-specific pleiotropic loci associated to the co-expression of drought-responsive proteins and to the variations of phenotypic traits. These findings bring several lines of evidence supporting candidate genes at many loci and provide novel insight into the molecular mechanisms of drought tolerance.

Florian Larue
UMR Amélioration Génétique et Amélioration des Plantes (Cirad-INRA-Montpellier SupAgro-MUSE), BFF

Integration of genetic and ecophysiological modeling to explore ideotypes: the case of biomass growth and its regulation by water deficit in sorghum

Crop models describe the process-based traits (equation parameters) contributing dynamically to plant growth, adaptation and crop performance in response to the environment. They are increasingly expected to model the genetic value of plant parameters in order to predict crop ideotypes as optimal trait and allelic value combinations. Predicting sorghum ideotypes relies on a multi-criteria approach modulated by breeding objectives (biomass and/or grain; rain-fed and/or irrigated). This implies to model water and carbon source/sink relationships and their interactions, and the numerous underlying plant parameters. This PhD works aims at providing an ecophysiological model dedicated to sorghum ideotyping and its integration in a computational pipeline enabling to estimate heuristically model parameters, their genetic value and crop ideotypes.

Gaëtan Touzy
RAGT, BREEDWHEAT

Drought tolerance of winter bread wheat in France: from varietal characterization to the identification of the allelic effects in different water stress scenarios

Drought is one of the main abiotic stresses limiting winter bread wheat growth and productivity around the world. Breeding for new high-yielding and stress-tolerant varieties is therefore necessary. Markers linked to favourable alleles identified in precisely defined environments can help to achieve this goal.
A panel of 210 elite European varieties was evaluated in 35 field trials. These varieties were registered from 1992 to 2011 and genotyped using a 280K SNP chip, which allowed evaluating the genetic progress and performing a genome-wide association study (GWAS).
Four main water stress scenarios were identified in the field trials network. The performance of varieties, the genetic progress and the identification of allelic effects from the GWAS depended on these water stress scenarios. These results will facilitate breeding for improved drought tolerance to specific environmental scenarios and sustain genetic progress for future environments, *i.e.* drought stress environments.

Florian Veillet
UMR Institut de Génétique, Environnement et Protection des Plantes (INRA-Agrocampus-Ouest-Université Rennes 1), GENIUS

Gene and base editing to confer agronomic traits in Potato: example of the *GBSSI* gene

Genome editing has recently become a method of choice for basic research and functional genomics, and holds great potential for molecular plant-breeding applications. The powerful CRISPR/Cas9 system can be used to generate knockout mutants through the classical gene editing strategy. Recently, a CRISPR/Cas9-derived base editing strategy has been developed, allowing precise and predictable nucleotide substitution(s) in the target locus. As a proof-of-concept in potato (*Solanum tuberosum*) for these two editing strategies, we targeted the *StGBSSI* gene that is responsible for amylose biosynthesis. We delivered the CRISPR/Cas9 components using stable or transient expression, followed by tissue culture steps and molecular characterization of regenerated plants.

We successfully produced tetra-allelic mutants with impaired amylose biosynthesis, confirming the loss of function of the *StGBSSI* protein. These results in the tetraploid potato open up new avenues for genome engineering in this species, especially for the identification of genes conferring resistance towards pathogens.

Estephania Carrillo-Perdomo
UMR Agroécologie (AgroSup Dijon-CNRS-INRA-Université de Bourgogne), PeaMUST

Bruchid resistance in pulses

Seed weevils (Bruchus spp.) are major pests of pulses, causing yield losses and affecting marketability 1,2. Available insecticides have low efficiency and important negative impacts on the environment, humans and non-target organisms. Therefore, breeding resistant varieties represent the most promising strategy to overcome seed weevils. The pyramiding of several resistance genes in cultivars is an important objective because this will make the resistance more durable and suitable for sustainable agriculture. The PeaMUST project (ANR-11-BTBR-0002) aims at discovering the mechanisms of tolerance and resistance to bruchids in pea (Pisum sativum L.) and faba bean (Vicia faba L.) crops and identifying the functional candidate genes for future implementation in Genomics-Assisted Breeding (GAB). A multidisciplinary approach that includes Genome-Wide Association Studies (GWAS), Quantitative trait locus (QTLs) mapping, RNA sequencing (RNA-Seq), shotgun proteomics and Volatile Organic Compounds (VOCs) analysis has been used to identify potential candidate genes for resistance to bruchids. The results will provide (i) original basic knowledge about resistance strategies in pea and faba bean, the candidate genes underlying quantitative resistance to bruchids and its conservation in other legume species, as well as, (ii) innovative applied knowledge and tools for breeding pea and faba bean varieties resistant to bruchids, which will be useful in future strategies of durable resistance management.

Llorenç Cabrera-Bosquet
UMR Laboratoire d'Ecophysiologie des Plantes sous Stress Environnementaux (INRA, SupAgro Montpellier), PHENOME

Dealing with multi-source and multi-scale information in Plant Phenomics: the PHIS ontology-driven Information System

A major challenge in plant phenomics is to design information systems able to store and organize heterogeneous datasets originating from multiple sources, and taking into account spatial and temporal relationships between objects (i.e. plants, organs, sensors, phenotyping facilities). The challenge is still larger if information systems aim to organize data originating from different groups, different scales and different infrastructures with FAIR requirements (Findable, Accessible, Interoperable and Reusable).
Here we present PHIS, an open-source information system designed for plant phenotyping experiments for various categories of installations (field, greenhouse). It non-ambiguously identifies all objects and traits in an experiment and establishes their relations via ontologies and semantics that apply to both field and controlled conditions. Events such as successive plant positions, anomalies and annotations are associated to objects so they can be easily retrieved.
Its ontology-driven architecture is a powerful tool for integrating and managing data from multiple experiments and platforms, for creating relationships between objects and enriching datasets with knowledge and metadata. It interoperates with external resources via Web services, thereby allowing data integration into other systems such as modelling platforms or external databases. It has the potential for rapid diffusion among phenomic infrastructures because of its ability to

integrate, manage and visualise multi-source and multi-scale data, but also because it is based on ten years of trial and error in our groups.

Erwan Corlouer
UMR Institut de Génétique, Environnement et Protection des Plantes (INRA-Agrocampus-Ouest-Université Rennes 1), RAPSODYN

Temperature and radiation stresses explained most of the environmental variations of seed yield across a French experimental network, and allowed to tackle the G×E interaction issues in WOSR

A major challenge in plant breeding is to ensure optimized and stable production under fluctuating environments while reducing the environmental impacts of agriculture. Thus, the offering of new rapeseed varieties should be adapted to a wide range of pedoclimatic conditions and constraints. Addressing this issue requires a better knowledge of the effects of the environment and the genotype by environment (G×E) interaction that will help identifying the critical factors limiting crop production. The goal of the present work was to characterize the effects of environment and G×E interaction that affect seed yield of winter oilseed rape grown over a large field network representing main cultivation areas in France. The first step consisted of defining a pedoclimatic indicator set able to highlight the potential limiting factors along the whole crop cycle. This analysis was run with two probe genotypes (Aviso and Montego) characterized over 20 'year by location' combinations across the field network. Out of the 84 pedoclimatic indicators, 10 were identified as limiting for seed yield after a Partial Least Square (PLS) regression analysis and 5 envirotypes were built. Using a subset of 11 environments with a larger genetic diversity, the G×E were tested inside clusters and the ranking of genotype were analysed. These results were discussed in light of field network management issues and plant breeding purposes.

Florie Gosseau
UMR Laboratoire des Interactions Plantes-Microorganismes (CNRS-INRA), SUNRISE

Development of new sunflower ideotypes by combining quantitative genetics approach and crop modeling

Direct selection for yield continues to be implemented and improved, but there is a widening gap between potential yields and those observed in agricultural parcels. Indeed, the joint effect of climate change and practice change, such as the reduction of inputs, impacts growth and increases genotype - environment interactions. In this context, it seems necessary to develop predictive biology approaches that combine quantitative genetics and functional crop modeling to predict complex traits such as performance. This approach makes it possible to predict unobserved hybrids under varied crop conditions and to identify sets of traits suitable for characterized environmental conditions.

Highlights and scientific breakthroughs of PIAs projects for sustainable agriculture

Boris Parent, Francois Tardieu, Claude Welcker
UMR Laboratoire d'Ecophysiologie des Plantes sous Stress Environnementaux (INRA, SupAgro Montpellier), AMAIZING / PHENOME

Predicting the impact of traits / alleles in current and future European drought scenarios

Retrospective analyses of the genetic progress suggest that the allelic diversity that governs adaptive traits conferring drought tolerance was largely unexploited by breeding because it results in positive or negative effects on yield depending on drought scenarios. We propose a probabilistic approach of drought tolerance that estimates the benefits and risks of combination of alleles in the most likely drought scenarios in each region, with current or future climates and different management practices. For that, we (i) use phenotyping platforms and field networks to identify genotype-dependent parameters of crop models (e.g. responses of grain number to intercepted light and soil water potential). (ii) Those parameters can in turn be predicted based on allelic values for new genotypes, (iii) allowing yield prediction in new fields and climates based on crop model simulations. This strategy may allow exploiting new sources of allelic diversity for yield in drought-prone regions, by explicitly taking into account the alleles that optimize adaptive responses in expected environmental scenarios for each region.

Pierre Casadebaig
UMR AGroécologie, Innovations et TeRritoires (INRA-ENSAT), SUNRISE

Predicting sunflower yield from traits to fields: application to assessment and recommendation of cultivars

Plant breeding programs design new crop varieties which, while adapted to distinct population of environments, are nevertheless grown over large areas.
In this study, our aim is to assess how a finer spatial management of genetic resources could reduce the genotype-phenotype mismatch in farming environments and ultimately improve the efficiency and stability of crop production. We designed a computational experiment that evaluated the performance of a collection of commercial sunflower cultivars in a realistic target population of cropping environments in France, build from agricultural surveys. Optimization methods were then used to search for cultivars $\times$ environments combinations that lead to increased yield expectations.
Results showed that a single cultivar choice adapted to the most frequent cropping environments is a robust strategy even if the fit of cultivars in specific environments is gradually increasing with the knowledge of pedo-climatic conditions. At the national scale, tuning the choice of cultivar impacted crop performance the same magnitude as the effect of yearly genetic progress made by breeding.

Marie-Laure Pilet-Nayel
UMR Institut de Génétique, Environnement et Protection des Plantes (INRA-Agrocampus-Ouest-Université Rennes 1), PeaMUST

Plant resistance and architecture for protection of pulses against pathogens

Major diseases, such as Aphanomyces root rot, are limiting factors to cool season pulse production in many countries worldwide, especially in France. In the context of pesticide reduction, plant genetic resistance and architecture are main traits that can be mobilised in breeding for disease management.

Fine mapping and sequencing of major resistance QTL, whole genome RNA sequencing, as well as Genome-Wide Association Study (GWAS), have been developed to identify and compare loci and candidate genes for resistance to Aphanomyces root rot in pea and faba bean. Comparative GWAS of root system architecture (RSA) and Aphanomyces root rot resistance identified co-segregating loci/alleles controlling both traits, as well as some pea lines with large RSA having a higher potential of tolerance to Aphanomyces root rot. Combining plant resistance and architecture traits unfavourable to diseases will be a key strategy for durable crop protection.

Perrot Laura, Veillet Florian, Botton Emmanuel, Thenault Christina, Lebaron Caroline, Nogue Fabien, Gallois Jean-Luc, Mazier Marianne
UE Génétique et Amélioration des Fruits et Légumes (INRA), GENIUS

Targeted gene modifications in tomato for the development of virus resistance

Plant resistance to pathogens is a major concern for the development of a sustainable and healthy agriculture in the context of climate change. Recently developed new gene targeting tools such as Crispr-Cas9 provide the opportunity to perform targeted and precise base modifications directly in crop genomes when favourable alleles are not available in the genetic variability. Altering key host susceptibility factors indispensable to pathogens is a strategy of choice to obtain resistance especially for viruses. As a proof of concept in the GENIUS project, we targeted the susceptibility gene eIF4E in tomato. Besides the mastering of different editing tools to expand the breeding toolbox, an output of this work was the creation of original tomato prototypes carrying new resistances against viruses that will reinforce our knowledge in eIF4E-mediated resistance to viruses.

Maryse Brancourt & David Pot
UR AgroImpact (INRA) & UMR Amélioration Génétique et Amélioration des Plantes (Cirad-INRA-Montpellier SupAgro-MUSE), BFF

Merging bio-based material and energy production value chains development, with OMICS, modelling and value chain assessment

The objectives of the project Biomass For the Future (BFF) are: 1) the development of biomass production and valorization chains of local miscanthus and sorghum, focused on bio-based materials and energy production, 2) the creation of new varieties and cropping systems for miscanthus and fiber sorghum with improved lingo-cellulosic biomass yield, reduced environmental footprint and a composition tailored for industrial uses. For this purpose, the project originally triggered and merged scientific, technological, economic and territorial breakthroughs: development of new technologies for the production of ligno-cellulosic biomass-based materials, high throughput anatomical and chemical phenotyping, advances in OMICS in support of the monitoring of biomass production and quality, crop modelling and finally the definition of the optimal feedstock/value chain combination

through the association of multidisciplinary scientists and economic actors covering the entire value chain.

Nathalie Nesi
UMR Institut de Génétique, Environnement et Protection des Plantes (INRA-Agrocampus-Ouest-Université Rennes 1), RAPSODYN

Integrative approaches to investigate Nitrogen Use Efficiency in oilseed rape and plant functioning under low N input

Oilseed production has to face an increasing worldwide demand in oil and proteins. In a context of stable cultivated land surfaces, a significant increase in seed yield is needed, while a reduction of synthetic nitrogen inputs is imposed. Oilseed rape (OSR) is the third main oil crop worldwide and can partly fulfill this challenge. However, despite its outstanding economical importance, OSR has a negative image in terms of sustainability due to its high dependence on inorganic nitrogen (N) combined with low nitrogen use efficiency (NUE). The main ambition of the project is to deliver the right nutrient rate at the right time on the right variety grown under the right environment. The RAPSODYN project was mainly centered on the development and application of smart methods to decipher the relationships between molecular polymorphisms and fine N-phenotypic traits related to agronomical targets. Therefore it aimed at 1) identifying favorable alleles at loci contributing to phenotypic variation, 2) characterizing N-traits at the functional level (from molecular determinants to crop integrative processes) and 3) providing robust multilocus SNP-based predictors of the breeding value of agronomical traits under polygenic control. Moreover, it allowed identifying new genetic variability for trait improvement. The current presentation will provide a scheme of the integrative approaches used to investigate NUE and plant functioning under low N input.

The BREEDWHEAT Consortium, <u>Stéphane Lafarge</u>
Biogemma, BREEDWHEAT

Improving Nitrogen Use Efficiency in Wheat by Genome Wide and Candidate Genes Targeted Association Studies

Breeding new varieties adapted to limited nitrogen application and with an improved Nitrogen Use Efficiency (NUE) is a crucial challenge in a context of limitation of inputs, especially fertilizers, for ecological and financial issues. The main objectives of our study were to identify varieties of interest and markers associated to NUE traits to help breeders selecting and developing varieties able to answer farmers' demand in the future. To do so, BreedWheat develop a field trials networks to evaluate an elite and a diversity panel at different contrasted nitrogen applications. A classification based on an environmental characterization allowed to determine nitrogen stress duration and intensity in each experiment. GWAS was performed on a set of traits linked to NUE to select interesting genetic areas, among them, five were selected for SNP densification and field validation. Candidate genes produced in the project using RNASeq data were also analyzed by association studies using specific SNPs develop in their sequences and linked to previous results by colocalization.
In fine, we developed a set of markers associated with traits of interest and also identified varieties with contrasted behaviors regarding different types of nitrogen stresses. These tools will help breeders perform a selection of varieties with a better NUE in the future.

Virginie Bourion, **Aurélien Barbe, Christophe Lecomte, Anthony Klein, Gérard Duc, Marc Lepetit, Marion Prudent Julie Cullimore, Judith Burstin**
UMR Agroécologie (AgroSup Dijon-INRA), PeaMUST

Root System Architecture, Nodulation & Nitrogen Nutrition in pea

To meet the challenge of food security and sustainable agriculture, the PeaMUST project searches solutions for the development of pea legume crop, in France. Thanks to their symbiotic association with soil rhizobia that fix atmospheric nitrogen (N), legume crops allow better N management at the rotation level by reducing the need for N fertiliser. However, their yield instability contributes to farmers' lack of confidence in their income and hinders their development. One of the PeaMUST project aims is to improve the pea N nutrition, a major factor affecting grain yield and protein content, by: (i) identifying root architecture accessions or mutants with increased root size and sustained nodule number; (ii) evaluating the impact of rhizobia, arbuscular mycorrhizal fungi or lipochitooligosaccharides, which are signals produced by these microbiotes, on root architecture and nodulation, particularly under stress conditions.

Innovative tools for plant breeding

Périn Christophe, **Meunier Anne Cécile, Herbert Léo, Bes Martine, Vernet Aurore, Portefaix Murielle, Guiderdoni Emmanuel**
UMR Amélioration Génétique et Amélioration des Plantes (Cirad-INRA-Montpellier SupAgro-MUSE), GENIUS

New tools for plant genome editing: Examples from rice

When the grand emprunt project GENUIS started, the only technologies available for targeted mutagenesis were TALEN and meganucleases. Quickly, during the first demonstration of the effectiveness of CRISPR/CAS9 technology in eukaryotic cells in 2012, our efforts in GENIUS were redirected towards the use of this technology for genome editing. CRISPR/CAS9 technologies, and their evolutions, are now routinely used in our laboratory with great efficiency in the GENIUS project and through new projects, with the hope of using them as new Breeding Tools (NBT). The discovery of other nucleases with properties complementary to CAS9 (CPF1), the development of base editor (BE) to introduce specific mutations and single nucleotide polymorphism reinforce the interest of these technologies for plant breeding and functional analysis. We have therefore developed an approach combining ddPCR and protoplasts to facilitate the evaluation of these new technologies quickly and quantitatively. This approach allows not only to compare the effectiveness of these technologies with each other, but also to prototype constructions before their use for plant species for which genetic transformation is difficult. We are also seeking, within the framework of the AGROPOLIS GENERICE project, to demonstrate that these technologies, primarily BE and CRISPR/CAS9 technology, have an interest in improving traits of agronomic interest for the south, through the editing of genes intervening in the nitrogen use efficiency (NUE) for a south variety, CHHD. I will illustrate all these aspects through examples to illustrate the limitations and technical pitfalls that we have highlighted.

Emilie Vergne, Aurélie Charrier, Nicolas Dousset, Andréa Richer, Aurélien Petiteau, <u>Elisabeth Chevreau</u>
UMR Institut de Recherche en Horticulture et Semences (INRA-AgroCampus Ouest-Université d'Angers), GENIUS

Efficient targeted mutagenesis of apple, a vegetatively propagated perennial crop

Apple tree is a vegetatively propagated perennial crop whose genome editing is complex. The stable transformation efficiency of this species is low and highly variable and the transgenic lines have a multicellular origin. Also, the apple tree has a long juvenile period and is self-incompatible, which does not allow the analysis of edition events on the T1 generation. We developed a CRISPR-targeted mutagenesis method that allowed the highly efficient editing of two marker genes: the phytoene desaturase gene conferring an albino KO phenotype and the Terminal Flower 1 gene conferring a KO phenotype of early flowering. Molecular analysis of the T0 line edits indicated a majority of biallelic chimeric situations. In addition, transient transformation with the CRISPR-PDS construct produced two T-DNA free edited apple lines. Our overall results indicate that the CRISPR/Cas 9 system is a powerful and precise method to induce targeted mutagenesis in the first generation of apple lines.

Sébastien Faure
Innolea, RAPSODYN

Improving the diversity of Brassica napus using doubled haploids (DH) derived from a panel of newly created semi-synthetic lines

Oilseed rape (*Brassica napus*) has a very narrow genetic diversity among cultivated lines. It is an allo-tetraploid species derived from the hybridization of *B. rapa* and *B. oleracea* which have both a much wider genetic diversity. Thus, exploiting the *B.rapa* and *B.oleracea* genepools could be of much help for *B. napus* improvement, both for biotic and abiotic stress response. However, interspecific crosses can be tricky and generate high genomic instability. Based on semi-synthetic BC1F1I1 materials derived from the cross between one *B. napus* variety (AVISO) and 10 *B. rapa* or 9 *B.oleracea* accessions, the Rapsodyn project developed DH individuals capturing a high percentage of the diversity available in these crosses. For this, the original BC1F1I1 lines were genotyped with a 15k SNP array, a selection of 100 mother plants based on the non-AVISO allele representation was done and DH were produced. We thus obtained 385 DH lines, 137 of which were observed in the field in 2018-19 for morphological traits as well as behavior under N stress.

François Balfourier, Sophie Bouchet, Sandra Robert, Romain De Oliveira, Hélène Rimbert, Jonathan Kitt, Frédéric Choulet, International Wheat Genome Sequencing Consortium, BreedWheat Consortium, <u>Etienne Paux</u>
UMR Génétique Diversité Ecophysiologie des Céréales (INRA-UCA), BREEDWHEAT

Worldwide phylogeography and history of wheat genetic diversity

Since its domestication in the Fertile Crescent ~8,000 to 10,000 years ago, wheat has undergone a complex history of spread, adaptation and selection. To get better insights into the wheat phylogeography and genetic diversity, we describe allele distribution through time using a set of 4,506 landraces and cultivars originating from 105 different countries genotyped with a high-density SNP array. Although the genetic structure of landraces is collinear to ancient human migration roads, we observe a reshuffling through time, related to breeding programs, with the apparition of new

alleles enriched with structural variations that may be the signature of introgressions from wild relatives after 1960.

Pierre Devaux, Christian Huyghe, Vincent Laudinat, Karine Henry, Fabienne Maupas, Bruno F. Desprez
Florimond Desprez, AKER

An innovative and ambitious approach to identifying and integrating genetic resources into Elite material (Sugar Beet as an example)

Sugar beet must be competitive ahead of cane. The AKER challenge was to increase the rate of sugar yield (around 2% at present), and, as a more global challenge, creating varieties that are high quality, safe and are agriculturally sustainable.

Global diversity availability and its management to answer these questions are critical. Considering the 'funnel' effect of breeding, AKER's project aims to widen this limitation by exploring and maximizing genetic resources, as well as shortening time to improved elite material.

After genotyping all germplasm available in the 50 world Gene banks consulted, we estimated that a core collection of as low as 15 plants was enough to carry all the allelic variability which is not present so far into the elite germplasm. After eight years of backcrossing these into an elite background, choosing the right complementary ones, we have produced 3,000 plants representing all variability. The remaining two years within the AKER program has been dedicated to phenotyping this final collection, bringing a value for each of these small sources of genomic variation, resulting in desirable or undesirable results for useful traits. By the way, we brought up high-throughput, non-destructive, accurate and dynamic phenotyping.

Johann Joets
UMR Génétique Quantitative et Evolution (INRA-UPS-CNRS-AgroParisTech), AMAIZING

Discovering, characterizing and exploiting structural variation in maize

Plant genomes exhibit a high level of structural variation (SV). Pairwise genotypes comparisons usually reveal hundreds of thousands of SVs including presence/absence of a thousand of genes. The contribution of these SVs to phenotype variation was shown to be major in maize. However, as it is still little characterized, a significant part of these genetic variation is poorly captured by present genotyping experiments preventing its valorization in breeding. To overcome these limitations, we addressed the challenging task of building a pan-genome assembly in maize to describe as exhaustively as possible the structural diversity of this species. Starting from a pilot assembly including two genotypes (B73 and F2), we have shifted to the assembly of a pan-genome sequence made from 19 high quality whole genome sequences of maize, 7 of which were produced in the frame of the Amaizing project. We have also developed SVs typing methods based either on low-to-medium depth resequencing of panels, or on an Illumina Array dedicated to SV typing. These results have provided many insights about 1/The extent of SVs in maize genome, especially in gene space, 2/ The specific structural features, expression patterns and functions of present/absent genes and 3/ The frequency of SVs in population and their impact on historical linkage disequilibrium. Altogether these resources will provide the community with invaluable tools to work with SVs in breeding as well as to fuel basic research in genome structure dynamics and evolution.

Laurence Moreau, Simon Rio, Antoine Allier, Alain Charcosset
UMR Génétique Quantitative et Evolution (INRA-UPS-CNRS-AgroParisTech), AMAIZING

Genomic selection in a broad cooperative maize panel: impact of population structure and identification of diversity sources for variety development

Amaizing consortium assembled an original cooperative inbred line panel of 389 lines, which represents the diversity of the dent maize genetic pool with a continuum from first cycle inbred lines extracted from traditional landraces to 49 recent elite lines contributed by the 7 breeding companies participating to the project. This panel was evaluated in a total of 24 environmental conditions. We investigated the impact of population structure on genomic prediction, using different scenarios including within- or across-group predictions. For a given training set size, the best accuracies were achieved when predicting individuals using a model calibrated on the same genetic group. Nevertheless, a diverse training set representing all the groups had a certain predictive efficiency for all the validation sets, and adding extra-group individuals was almost always beneficial. Relevant predictive abilities were observed on a large independent population of private elite materials of RAGT, which supports the interest of such a collaborative panel for diversity management perspectives. We evaluated different criteria to identify within the panel a donor to improve a given elite recipient line for grain yield, or a set of donors complementing an elite population, and to define a crossing plan between identified donors and elite recipients. The approach appears promising in view of a more efficient integration of genetic resources in elite breeding.

Laurent Hanneton
Limagrain, RAPSODYN

Elaboration of a genomic calibration tool to predict performance under limited N supply

Using the Rapsodyn phenodataset gathering 2 years/ 7 locations under 2 highly contrasted N supply levels on a panel of 154 lines genotyped by a 15k chip array, a GBLUP model was built to predict the performance of 5 new different elite panels observed in 2018 on 2 to 4 locations under low supply low N supply (N- condition). The model was trained by 3 different calibration sets to test the effect of diversity on the prediction results. Correlation rate between observed and predicted value did not show effect of the diversity level of the training population but extreme phenotypes of the training population seem to help the model. For SY and SN traits, important variation of correlation rate are observed pending on the elite panels. Furthermore, GxE interactions seem to be significant enough to disturb the predictive model.

The SUNRISE Consortium, Nicolas Langlade
UMR Laboratoire des Interactions Plantes-Microorganisms (CNRS-INRA), SUNRISE

Multiscale modeling to predict sunflower tolerance to abiotic stresses

As the result of climate changes, more variability is expected from location to location in the timing and quantity of water availability for crop production. On the long term period, the competitiveness of sunflower chain - seeds, farmers, coops, oil seed industry,... - is highly depending on the stability of oil yield across years and locations.
Since 10 years, we develop in the frame of public-private partnership, interdisciplinary projects (SUNYFUEL, OLEOSOL, SUNRISE) at the interface between genetics, systems biology and agronomy to identify the genetic basis of yield plasticity in response to abiotic stresses such as drought. Our goals are to understand the molecular and physiological processes involved in drought, identify novel

genetic material to improve the elite germplasm tolerance and being able to predict performance in different climatic scenarios and therefore tolerance based on genomic information.

I will present our strategy combining different modeling approaches and up-to-date results including the identification of a genomic region involved in drought tolerance for grain yield, its physiological effect and its potential use in elite hybrids.

Anne-Françoise Adam-Blondon
UR Génomique Info (INRA), interPIA

Management of the data sets using GnpIS following the FAIR principles

Six of the « Bioressources » projects (Breedwheat, Amaizing, Aker, BFF, Peamust and Rapsodyn) have used the information system developped at INRA-URGI, GnpIS, to store and publish all or part of the data sets produced by their consortia. It allowed to generate common workflows and to mutualize the developments necessary in GnpIS and for the data workflows but also to disseminate from one project to another good practices in the domain of the data management. In 2014-2015, several projects in which INRA-URGI was involved have greatly influenced these activities : the two infrastructure projects Phenome and IFB and the international Wheat Initiative. These three projects have started to develop resources and guidelines for aligning data management practices to the FAIR principles, which have been implemented in the six projects.

Jérôme Gouzy
UMR Laboratoire des Interactions Plantes-Microorganismes (CNRS-INRA), SUNRISE

Sunflower genome sequences: past, present, future

Assembling the sunflower genome using short-reads data proved impossible because of the large size of the genome (> 3Gb) and a very large number of highly conserved transposable elements. Early 2015, the breakthrough of the single-molecule real-time sequencing technology (PacBio) combined with the integration of four genetic maps made possible to obtain the first sunflower genome sequence, in the frame of the SUNRISE project (Badouin *et al.* Nature 2017). Today, long-reads based sequence assemblies are coupled with the latest generation of optical maps, or HiC data, allowing reconstructing almost all chromosomes in a single scaffold. These improvements, combined with the optimization of bioinformatics protocols, make it possible to switch from a genetic resolution to a very precise physical resolution and to obtain a new annotated genome in less than two months. The current challenge is to assemble heterozygous wild sunflower genomes to precisely explore the diversity of the species. These new genomes will be assembled as part of the international consortium ICSG by developing bioinformatics protocols to take benefit of the recent advances in PacBio technology. Bioinformatics and genomics issues, results and perspectives will be presented.

Project's fact sheets

Project's fact sheets Summary

AKER — P.27

AMAIZING — P.33

Biomass For the Future (BFF) — P.38

BREEDWHEAT — P.44

GENIUS — P.51

PeaMUST — P.58

PHENOME — P.64

RAPSODYN — P.68

SUNRISE — P.75

Description

Project title	*Betterave 2020 - L'innovation compétitive* (Sugar Beet 2020 – for a competitive innovation)
ACRONYM (+ logo)	AKER
Website	www.aker-betterave.fr
Coordinator	Bruno DESPREZ (Florimond Desprez)
Project manager	Christian HUYGHE (INRA - Scientific Directorate Agriculture)
Number of researchers involved	60
Public/private ratio (%)	60/40
Number of trainees	12
Number of PhDs	1
Number of post-doc fellows	1
Project summary	AKER aims to improve the competitiveness of sugarbeet by 2020, doubling the annual productivity rate (t of sugar/ha). AKER, making a vital contribution to a dynamic sector. AKER is supported by eleven public and private partners representing the French sugarbeet industry. AKER is an original and innovative program in research, development and training. It establishes sugarbeet as a leader crop for research and innovation.
Project aims	The AKER program represents a paradigm shift in the field of sugarbeet research and selection, underpinned by two original approaches: AKER makes predictions — AKER manages variability. AKER will bring new and sustainable genetic material, meeting the sugar sector competitiveness wishes, together with the ones from the consumers/Society (e.g. environnemental benefits). The AKER program is also a source of knowledge, new tools and methods that will lead to transfers of technology with an impact far beyond the sugarbeet industry.
In figures	11 partners – of which only one is private 60 researchers 15 reference plants 40 million molecular data points 3,000 selected genotypes 63,000 phenotyping plots (2018)

Results

TRL (Technology Readiness Level) Reference - 1 to 9

Most significant results achieved	1. **Choice of 15 reference plants representative of the total genetic variability of cultivated and wild beet not yet used in breeding selection**
	At the start of the AKER program, 15 exotic plants were selected from 3,000 of 10,000 plants from international genetic resource centres (gene banks), representing the wide genetic diversity of sugarbeet and related wild species (crossing compatible). With these 15 exotic reference plants, the AKER program covers 100% of the allelic variability available, and potentially useful, within this *Beta* genus complex, and not already used into the elite germplasm. The 15 reference plants constitute after backcrossed into an elite background, a perfect core collection, source of new potential useful variability. TRL: 1 to 7
	2. **Sequencing and molecular marking of reference plant genomes**
	Researchers in the AKER project have sequenced the genomes of the 15 reference plants and of the elite material used for recurrent backcrosses. Molecular markers have been defined to differentiate these genomes. These markers were used to control the quality of back-crosses. The research team then identified more than 40 million SNP variations in the genetic code of the studied material (1 over 20 SNPs in average). Extensive bioinformatic analysis resulted in the retention of 200,000 Single Nucleotide Polymorphisms (SNPs) amenable for use as reliable and robust molecular markers (DNA chips). Molecular labelling makes it possible to locate chromosome fragments of each of the 15 reference plants distributed within the elite genome, without *a priori* knowing what kind of effects these will produce – this being the aim of the phenotyping stage. TRL: 4
	3. **Genomic selection for the prediction of yield components**
	The AKER program also applies genomic selection to sugarbeet plants. The interest lies in the saving time and costs in selection programs, while increasing the rate and performance of selection. The genomic selection of sugarbeet *in situ* gives prediction accuracies ranging from 65% (root yield) to 85% (sugar content). For example, a training population of 1,300 sugarbeet lines has been tested during three years providing an average predictive ability (correlation) of 0.775 for the trait "white sugar yield." This is already in use in the breeding programmes. At the end of the program, the AKER population resulting from crosses between an elite parent and wild accessions will be also taken as a training population, and genomic selection can be applied for the prediction and selection of individuals from post-AKER crosses. TRL: 3 to 9

Prominent tools developed	**1. X-ray 3D tomograph for seed phenotyping** The Laboratory of Seed Physics of the SNES (GEVES) was equipped with a tomograph in 2013, thanks to AKER/PIA funding. This X-ray imaging tool photographs slices, which are then assembled into a 3D image for processing and interpretation. It makes the study of the internal morphology of seeds possible, for example imaging the surfaces and volumes of the various components such as the nucellus, the embryo and envelope. TRL: 5 to 7 **2. Non-destructive NIR probe for root phenotyping** Researchers at Irstea have recommended the use of a (non-invasive) contact probe that measures sucrose and dry matter in the first few millimetres of the root, at the collar. After determining the wavelengths of interest with a laboratory spectroradiometer, more compact tools for field use were tested. The ITB recommends the SCIO miniaturised root probe. TRL: 9 **3. An ontology for the referencing of sugarbeet criteria** The AKER program has represented an opportunity to develop an ontology for sugarbeet. An universal vocabulary and a structured information database, the ontology makes it possible to share data acquired by different researchers and to carry out automated searches. It is a dictionary, a lexicon, a tree structure, and a map of relations between terms, working to a cascading logic. The sugarbeet ontology is intended to be applied to the phenotyping data generated by the AKER program, and to become an International reference. TRL: 7
Scientific and technical success stories	**1. 15 reference plants, representative of the genetic variability of wild and cultivated sugarbeet** At the start of the AKER program, 15 exotic plants were selected from 3,000 of 10,000 plants from international genetic resource centres, representing the wide genetic diversity of beet. With these 15 reference plants, the AKER program covers 100% of the allelic variability available within the *Beta* genus, in complementarity to the genetic resources already used today. TRL: 1 to 7 **2. Phenotyping of the leaf by camera installed on a drone** Researchers of Irstea and ITB have experimented with different tools and methods for measuring the architecture and biochemical content of the canopy. An hyperspectral camera used in proxi-detection mode allowed methods to be developed during the first years of the project. These technologies developed progressively towards the use of RGB and multispectral cameras embarked on a drone. The measurements made concern the dynamics of the rate of ground coverage, the foliage surface area, as well as the chlorophyll and nitrogen content of the leaves. Diseases are detected too, sometimes before visual appearance. ITB, Florimond Desprez and Hiphen are pursuing their work on this project.

	TRL: 8
Non-scientific success stories	The AKER program has created a true public-private scientific community at the service of the sugarbeet industry in France. AKER is a partnership a collaborative, multidisciplinary and transversal program with an international dimension. It also associates research and development with training and education opportunities.

Partnerships and transfers

Role and importance of the public-private partnership in the project	The public-private partnership of the AKER program is also relevant by the newly research implement of INRA into the sugarbeet sector in France. AKER has mobilised the entire sugarbeet sector with the Beet Technical Institute (*Institut Technique de la Betterave* - ITB), representing both planters and sugar refineries. The AKER program was made possible by to the dedicated involvement of a private breeder: Florimond Desprez.
External collaborations on results at the national and international levels	5 collaborations: - Selkit - Adapt - Be Domino - Phenaufol - Taker
Most significant collaborations showing the added value of project results	1. Selkit - Using AKER genetic/selection results and simulation 2. Adapt - Using AKER results for landscape genetics 3. Be Domino - Using AKER results to track domestication - USDA preselection and selection - search for new lines of research based on the variability already detected 4. Taker is the use of AKER's data for red table beet
Types of results transferred for use outside the project	Beet Sequences for the USDA in the TAKER project
External partners having benefited from the results of the project	Research organisations: USDA, University of Padova-Italy

Economic benefits/impacts

Current and future impacts of the project for the sector concerned and for French agriculture	AKER brings a positive and innovative scientific contribution to productive agriculture, respecting public health and the environment of our fellow citizens. AKER offers society all the passion of its sixty researchers, who have learned to work together with a strongly collaborative approach. AKER calls upon the highest technologies (genetics, digital, bioinformatics) at the service of agriculture, in compliance with all current regulations (non-GM) and with an eye on necessary future developments (genetic vs. phytosanitary). AKER offers an edge in improving the competitiveness of the

	French sugarbeet industry. The methodologies developed are applicable far beyond the sugarbeet industry, with positive impacts in the management of genetic tools and resources, the evaluation of germination and knowledge of diseases.
Impact of the project on the positioning of the scientific community at the international level	In the international context, sugarbeet is in competition with sugar cane, which accounts for 80% of sugar supplies, especially since the quota system came to an end in 2017. While sugarbeet yields are higher than cane yields, and e.g. using less water supply, production costs remain higher and need to be further reduced. Higher growth in yield and greater stability of these yields should result in significant savings and greater competitiveness for sugarbeet.
Economic benefits for the project partners (at term)	AKER will contribute to the improvement of sugarbeet performance by obtaining high quality genetic material, but it will also provide publications, references and models to all prescribers, collaborators at the ITB and technicians in the agronomic departments of sugar refineries. AKER will provide sugarbeet farmers with personalised advice and agronomic support in order for the new genetic material proposed to best express its potential. It will also provide them with decision-making tools.

Publications

Number of publications in peer-reviewed journals	20 in 2018
Notable publications	1. Mangin B., Sandron F., Henry K., Devaux B., Willems G., Devaux P., Desprez B., Goudemand E. (2015). Breeding patterns and cultivated beets origins by genetic diversity and linkage disequilibrium analyses. Theor Appl Genet. vol. 128, pp. 2255-2271 (2015). 2. Andrello M., Henry K., Devaux P., Desprez B., Manel S. (2016) Taxonomic, spatial and adaptive genetic variation of *Beta* section *Beta*. Theor Appl Genet, vol. 129, pp. 257-271 (2016). 3. Belin E., Douarre C., Gillard N., Franconi F., Rojas-Varela J., Chapeau-Blondeau F., Demilly D., Adrien J., Maire E., Rousseau D. (2018) "Evaluation of 3D/2D imaging and image processing techniques for the monitoring of seed imbibition"; *Journal of Imaging* 4, 83,1-16 .

Communications

Training organised during the project	Annual sessions organised for students by the University of Lille, AgroCampus Ouest and Florimond Desprez on topics related to sugarbeet genomics.
Number of scientific posters	23
Number of oral communications at scientific conferences	67
Number of symposia (French	- 1 at the launch of the program in 2012

and international) organised	- 1 at the end of the program in June 2020
Newsletters and public communications	- Multi-year programming: each year, one theme is developed and one partner is highlighted - 4 participations in works - Numerous articles and researcher profiles on the website - More than 60 interventions with professional audiences and students - 12 newsletters, 2 leaflets, 10+ videos
Other communication tools	- AKER in brief, public posters, kakemonos - 8 press releases and 8 press kits - 57 training participations - Twitter account (400 subscribers) - A book published at the end of the program (to be confirmed)
Notable communication actions	1. Press trip to Angers on the subject of phenotyping seeds and seedlings (2014) 2. Interactive animation at the Betteravenir Congress (2016) 3. Press trip to the Somme on the subject of field phenotyping (2018)

Description

Project title	Developing new maize varieties for sustainable agriculture: an integrated approach from genomics to breeding
ACRONYM (+ logo)	AMAIZING
Website	www.amaizing.fr
Coordinator	Alain CHARCOSSET (INRA UMR GQE, Le Moulon - Versailles-Grignon)
Project manager	Agathe RENARD (Inra Transfert)
Number of researchers involved	150
Public/private ratio (%)	60/40
Number of trainees	35
Number of PhDs	8
Number of post-doc fellows	14
Project summary	The aim of the AMAIZING project is to develop the knowledge, breeding methods and farming practices that will be required to develop high yield varieties under a wide variety of abiotic stress factors, with improved environmental qualities. The project is based on a broad partnership between the key actors in the French maize industry with, in particular, a strong partnership with private enterprise. This collaboration facilitates the transfer and use of knowledge, resources and methods issuing from the project, in order to obtain new varieties and products, support the competitiveness of maize producers and benefit the maize sector in France.
Project aims	This ambitious project aims to gain improved knowledge of the organisation of the genome, its plasticity and the mechanisms of environmental adaptation. It also enables effective selection on a molecular basis to reduce the time between the discovery of a trait and the marketing of a variety. The project calls upon strong investment in human resources with and financial means and technical partnerships allowing, for the first time, genetic resources, methods and tools of interest to breeders to be to developed and used in the same project.
Achievements of objectives	The project has met or exceeded all planned objectives. Objectives in terms of development of genetic material and phenotyping were achieved, as were association studies and the calibration of genomic prediction models. All tools and methods planned have been developed, alongside a new R package for faster mixed

	model analysis. Seven genomes have been sequenced de novo rather than the five originally planned. The only exception is the discontinuation of the mutagenesis by tilling approach, following the cessation of activity of the partner AELRED.
In figures	- De novo sequencing and annotation of 7 new genomes -> 4,600 new genes discovered - Resequencing 7 to 15X of 100 lines, with discovery of more than 15M SNPs, showing admixture phenomena (Brandenbourg et al., 2017) - Combination of technologies - GBS (2,000 lines analysed) and Affymetrix (1000 lines) to obtain a genotyping of more than 1M SNPs, application directly in GWAS or after imputation to approximately 3,000 lines (1,200 Flint lines, 500 Dent lines and 1,000 new lines created in the project to break the structuring into groups) - Development of 75 BC5-S1 introgression populations of more than 150 individuals each, for the rapid validation of associations - 20,000 experimental plots for evaluation of the yield, its components and environmental characterisation, 5,400 plants analysed in the platform with measurements of architecture, growth, development, transpiration and stomatal control

Results

TRL (Technology Readiness Level) reference - 1 to 9

Most striking results	1. Analysis of the diversity of a collection of genetic resources by resequencing (Brandenbourg et al., 2017) and GBS (Gouesnard et al., 2017), TRL: 4/5 2. Evaluation of the stability of the genomic prediction equation and models taking into account structure/admixture, TRL: 5/6 3. Large scale genetic analysis of protein expression (proteomics) in contrasted water status conditions Proteomics , TRL:5/6 4. Validation of GWAS/QTL zones by introgression: positive results for certain zones - precocity, cold, drought and yield, TRL: 3/4
Prominent tools developed	1. Transformation of recalcitrant genotypes, TRL: 4/5 2. Gene Machine, TRL 4/5 3. Gene Atlas (transcriptome by sequencing of 13 tissues, including 5 with and without water stress) on 7 genotypes, TRL: 4/5 4. Development of the MM4LMM R package allowing the rapid implementation of the mixed models required for GWAS and GS at the hybrid level, TRL: 6/7 5. BioMercator: QTL and Gwas meta-analysis, genome visualisation and genetic maps, TRL: 5/6
Scientific and technical success stories	1. ***Analysis and prediction of the effect of genetic diversity on yields in Europe***. The yields of 256 hybrids were studied in 41 field trials in Europe, with environmental conditions evaluated

	in each field and phenotypic characteristics of each hybrid analysed in 4 phenotyping platform assays. Statistical or dynamic models have been used to extend the results to other situations, including climate change (i) Any yield QTL may have a positive or negative effect on yield, depending on the environmental scenario measured in the field considered (ii) The yield of thousands of genotypes in hundreds of fields can be predicted from the genotype of the plants, from a fine phenotyping on the platform and from the environmental conditions in the field under consideration. (iii) The effects of climate change can be counterbalanced by an appropriate choice of cycle duration, following rules currently being applied by farmers.
	TRL: 6/7
	2. Construction of a maize pangenome from the genome sequences of 19 lines, of which 7 produced by Amaizing. This pangenome comprises more than 4,600 new genes, absent from the American reference line and present in at least one of the 18 other lines. The Gene Atlas will provide a better understanding of the role of these genes and the many molecular markers produced (SNPs and SVs) and will allow these new genes to be included in breeding programs in which they are so far largely excluded.
	TRL: 5/6
Non-scientific success stories	Development of the link between the French and international maize communities through the organisation of the Maize Meeting in 2018 (500 international participants).

Partnerships and transfers

Role and importance of the public-private partnership in the project	Co-construction of research questions: - Private: possibility of developing new populations, in order to characterise them finely in extended networks - Public: capacity for development in modelling, advanced data analysis
External collaborations on results at the national and international levels	2 at the national level: - Collaboration with the SMH Maïs experimental unit (Saint-Martin-de-Hinx, INRA Nouvelle-Aquitaine site). This unit hosts tests of the research program within the framework of the AMAIZING project. - TranscriptOmic Platform iPS2 (POPS, Paris-Saclay University). Development of transcriptome analysis in plants using high throughput RNA sequencing 3 at the international level: - Cornell for GBS analysis of diversity and GWAS - CIMMYT for comparison of methods of population diversity analysis - WUR on the modelling of G/E interactions in GS and GWAS
Most significant collaborations showing the	- Evolution of the iPS2 service in a research collaboration - University of Bologna (analysis of Gaspé Flint)

added value of project results	- Implementation of a new collaborative pre-breeding programme within Promaïs (ValRG), using sources of diversity identified in the project
	- Participation in the SeqOccin consortium on genome analysis methodologies (mixed plant-animal project)
	- Maike Stam (Amsterdam), Maud Fanny (Sweden)
Types of results transferred for use outside the project	- Genomic sequences
	- Genotyping data from the Dent panel
	- Phenotyping data
	- Genotypic characterisation of genetic resources
	- Bioinformatic tools (GWAS pipelines, genomic selection scripts, Thalia database)
External partners having benefited from the results of the project	Cornell University, Catholic University of Louvain, Meiogenix and Monsanto/Bayer (collaboration), INRA UMR Mistea (Montpellier), CIMMYT

Economic benefits/impacts

Current and future impacts of the project for the sector concerned and for French agriculture	- Criteria for selection for environmental adaptation
	- Anticipation of the phenology of varieties that will be needed after climate change
	- Characterization of genetic resources to enrich the diversity of breeding programs
Impact of the project on the positioning of the scientific community at the international level	- Position of international leadership in phenotyping and enhanced drought modelling
	- International positioning now reached on comparative analysis of genomes and epigenomics
	- International positioning enhanced on the characterisation of genetic diversity
	- International positioning enhanced in quantitative genetics and selection methodology
Economic benefits for the project partners (at term)	- Targeting of traits of interest and training in phenotyping protocols/modelling methods (currently in use)
	- Identification of original genetic resources for use in pre-breeding (currently in use)
	- Selection methods (currently in use)
	- Genomic and genetic reference data for the study of genetic diversity in each partner's material (currently in use)
	- Diagnostic markers of strong effect alleles (validation by partners in 2020)

Publications

Number of publications in peer-reviewed journals	- 30 in October 2019
	- 15 more expected by end 2020
Themes of publications expected end 2020	- Comparative genomics, structural and epigenomic variation
	- System genomics papers
	- Admixture for GWAS and GS
	- Fine ecophysiological characterisation of the factors at play in

	genetic progress in Europe
Themes of publications expected 2 years after the end of the project	In the process of definition
Notable publication coming soon	- Blein-Nicolas et al. Proteomics - Maize pangenome and structural variation

Communications

Training organised during the project	- Phenotyping-modelling (LEPSE) - Association genetics (GWAS) - Genomic selection (twice) - Mapping and application in selection - Information system training - Nine 90 minute webinars were also organised on specific topics
Number of scientific posters	52
Number of oral communications at scientific conferences	79
Number of symposia (French and international) organised	2 - Eucarpia Maïs et Sorgho (maize and sorghum) 2015 - Maize Genetics conference 2018
Newsletters and public communications	- 5 newsletters - 1 website - 1 information leaflet
Other communication tools	New website in 2017
Notable communication actions	1. Organization of the Eucarpia Maïs Sorgho (maize and sorghum) conference (2015) 2. Launch of the new website in 2017 3. Organization of the 60th International Maize Genetics Conference

Description

Project title	Biomass For The Future
ACRONYM (+ logo)	BFF
Website	http://www.biomassforthefuture.org
Coordinator	Herman HÖFTE (INRA IJPB)
Project manager	Laure Trannoy (Inra Transfert)
Number of researchers involved	30 each year on average
Public/private ratio (%)	84/16
Number of trainees	80
Number of PhDs	3
Number of post-doc fellows	6
Project summary	Biomass For The Future is a multidisciplinary project with public and private partners working around the development of local value chains for miscanthus and sorghum biomass. This implies: (1) the development of new energy sectors (combustion, anaerobic digestion) and new uses of biomass in biosourced materials (polymer composites, building materials), (2) the use of genomics to accelerate the domestication of sorghum and miscanthus for the sustainable production of lignocellulosic biomass, (3) evaluation of the economic and environmental impact of these new industries.
Project aims	Biomass For The Future aims to contribute to the establishment of local value chains for miscanthus and sorghum biomass for energy purposes (combustion and anaerobic digestion), polymer composites and building materials. Biomass For The Future aims to exploit plant genomics in maize, sorghum and miscanthus for the creation of new dedicated varieties and cropping systems for the sustainable production of lignocellulosic biomass. These new varieties will combine improved yield, a limited ecological footprint and a composition suitable for industrial uses.
Achievement of objectives	Concerning the development of value chains : a new polypropylene-miscanthus composite with a favorable life cycle analysis has been validated by PSA for the production of automobile parts. A miscanthus-based concrete bloc has been conceived and improved. The utilisation of sorghum biomass for methane production has been evaluated and agronomic and logistic hurdles for the production and transformation of miscanthus have been overcome. The commercialisation of these products is now in the hands of the industrial partners. BFF has

	also contributed to the development of comparative genomics among the three species studied in the project (maize, sorghum and miscanthus), for instance with the identification of QTLs for the GxE interactions governing the chemical composition and histology of the biomass and in particular the favorable impact of drought stress on biomass digestibility. New sorghum and (sterile, triploïd) miscanthus hybrids are being evaluated.
In figures	- **Collection and multiplication of a collection of 800 wild miscanthus** - **200 measurements of the Biomass Methane Potential of genotypes of sorghum or miscanthus** - **18 dry discontinuous codigestion reactors** - 500 plots of maize and sorghum cultivars cultivated for 3 years in different locations and with varying irrigation conditions - 3,500 powders stored of maize and sorghum samples harvested from mapping populations, selected lines or mutants

Results

TRL (Technology Readiness Level) Reference - 1 to 9

Most significant results achieved	1. **Miscanthus-carrying concrete blocks** A one-step method for producing miscanthus-based concrete blocks with excellent mechanical properties TRL: 4 2. **Predicting miscanthus yield** After three years of field trials, an agronomic model to predict miscanthus yield is available TRL: 3 3. **Genes controlling biomass composition identified:** Genomic regions (QTLs) controlling the composition and the digestibility of biomass have been mapped in maize and sorghum. The cloning of these QTLs should facilitate the introduction of their traits into elite lines for these species, and allow the selection of the same traits in miscanthus, which is closely related to maize and sorghum. TRL: 3
Prominent tools developed	1. **Analysis of the composition and histology of the biomass produced.** High throughput methods for analysis of the composition, digestibility and histology of the biomass. TRL: 3 2. **Simulation of sorghum growth** A new ecophysiological model to simulate the growth and yield of the lignocellulosic biomass of sorghum according to the effects of genotype and environmental variability.

	TRL: 3
	3. **Management of data** Bioinformatics platforms for the storage and analysis of genomic and phenotypic data for maize, sorghum and miscanthus. Gateways "Grass Genome Hub" (CIRAD) and GNPIS (INRA). TRL: 3
Scientific and technical success stories	1. **Development of miscanthus-polypropylene composites for automotive parts at the laboratory scale** These composites have mechanical properties comparable to other, more expensive biosourced products — key factors for improving product performance and scaling up production have been identified. TRL: 4-5 2. **Lignin content and digestibility of biomass in dry conditions** Under drought conditions, the lignin content decreases and the digestibility increases in both sorghum and maize. Depending on the variety, the extent of this response to drought varies considerably. This offers a key for the selection of varieties combining good yield and good industrial quality for uses in 2G biofuels, green chemistry and animal feed. TRL: 3
Non-scientific success stories	**Creation of a vibrant multidisciplinary community** (materials science, plant genomics, ecophysiology, agronomy, LCA), a fully inter-sectorial (public, private and local communities) network, based on maize, sorghum and miscanthus biomass in an industrial context.

Partnerships and transfers

Role and importance of the public-private partnership in the project	The public-private partnership is essential for the concerted development of research priorities, based on the identification of the needs of biomass producers and users and the bottlenecks in the different steps of each value chain and in line with the scientific and technological skills of each partner.
External collaborations on results at the national and international levels	13 external collaborations
Most significant collaborations showing the added value of project results	1. Collaborations between geneticists, materials scientists (CEMEF and Addiplast) and bioenergy researchers to develop varieties adapted for different uses. 2. Collaborations between geneticists, physiologists and private breeders towards an analysis of genetic determinism of the traits of interest (population development, inclusion in selection etc.). Collaboration between partners working on different species. 3. A multi-partner testing network (Phytorestore, Aelred, Axereal,

	INRA, CA GPS & O) which has led to the establishment of a multisite fieldtrial platform.
Types of results transferred for use outside the project	A Near Infra Red Spectroscopy method for estimating the digestibility of maize is being used in the framework of the Investment in the Future project AMAIZING.
External partners having benefited from the results of the project	RAGT, AMAIZING

Economic benefits/impacts

Current and future impacts of the project for the sector concerned and for French agriculture	Biomass For The Future has contributed to a growing interest for miscanthus in the agricultural world, with the cultivated area seeing an annual growth rate of 10% over the last 5 years. For the future, we can expect an increase in the areas under cultivation to meet the demands of biomass for energy use (combustion, anaerobic digestion) and following the emergence of new materials applications. The selection of new varieties of sorghum (biomass, silage, catch crops, cold resistant etc.) and miscanthus (new triploid clones, cultivars with improved drought resistance and saccharification) and of silage maize with better digestibility, should facilitate and secure the future production and use of biomass.
Impact of the project on the positioning of the scientific community at the international level	The publications are expected to promote the visibility of BFF in the fields of biosourced materials and plant genomics. The many invitations received by our researchers to participate in international conferences underscore the impact of BFF on the scientific community
Economic benefits for the project partners (at term)	The economic benefits of the Biomass For The Future project vary depending on the type of partner. For example: - Establishment of environmentally friendly alternative crops in water catchment areas (members of the Axereal cooperative) - Development of one or two ornamental miscanthus clones in the short-term (Agri-Obtentions) - Transfer of knowledge acquired in miscanthus for use in sorghum (Ragt2n) - Acquisition of LCA (Life Cycle Analysis) references in the agricultural field (A3i) - Valorisation of the knowledge acquired on biomass composition to improve the process of anaerobic digestion (Naskeo) - Launch of a new range of miscanthus-based thermoplastic compounds for the automotive market — potential of 1,000 tonnes/year, 3 years after the end of the project

Publications

Number of publications in peer-reviewed journals	- 18 - 30 expected end 2019

Themes of publications expected end 2019	- Analysis of the causes of variations in yield in *M. Giganteus* and *M. Sinensis* in the Greater Paris region (end of 2019) - Modelling the temporal evolution of yields in M. Giganteus and M. Sinensis - Soil carbon under a crop of M. Giganteus and M. Sinensis - ETM, PAHs, PCBs: Relationships between contaminants in soils and in crops of *M. Giganteus* and *M. Sinensis* - Genetic determinism of biomass production and biomass composition in *Miscanthus sinensis* (thesis by Raphael Raverdy) - Study of biomass production and nutrient recycling in two miscanthus species to explore ideotypes: ecophysiological and modelling approaches (thesis by Julie Leroy) - Discovery of new flowering alleles in *Miscanthus sinensis* (thesis by Wei Hou) - Bio Methane Potential (BMP)-phenotype relationships in sorghum - Pretreatment of sorghum with lime and soda: impact on BMPs and codigestion with cattle manure - Impact of genotypes and alkaline pretreatments on the methane potential of miscanthus - Pretreatment of miscanthus with lime impacts BMPs and codigestion with bovine manure - Understanding of the action of alkaline pretreatments on miscanthus and sorghum - "Grass Genome HUB" gateway, BFF genomic data gateway - "Rap-Green" package for analysis, exploration and visualisation of phylogenetic trees
Notable publications	1. L. CHUPIN, D. de RIEDER, S. JAFFUEL, A CLEMENT VIDAL, A. SOUTIRAS, E. GINEAU, G. MOUILLE, S. ARNOULT, M. BRANCOURT-HULMEL, C. LAPIERRE, D. POT, L. VINCENT, A. MIJA et P. NAVARD "Influence of the radial stem composition on the thermal behavior of miscanthus and sorghum genotypes for composite end-use", Carbohydrate Polymers, 167, 12-19 (2017) 2. Perrier L., Rouan L., Jaffuel S., Clément-Vidal A., Roques S., Soutiras A., Baptiste C., Bastianelli D., Fabre D., Dubois C., Pot D., Luquet D. 2017. Plasticity of sorghum stem biomass accumulation in response to water deficit: A multiscale analysis from internode tissue to plant level. Frontiers in Plant Science, 8 (1516) : 14 p. https://doi.org/10.3389/fpls.2017.01516
Notable publication coming soon	- Network of co-regulation to identify candidate genes for a QTL of cell wall digestibility in maize

Communications

Training organised during the project	- Modelling (2015) - Discussion on water stress for sorghum and maize, grinding, relationship between genotype and properties, pollutant life cycles, presentation of the sorghum sector (2017)

	- The challenges of structuring the plant fibre technical sector, Biosourced concretes, Reclaiming water quality (pesticides/nitrates), Prospects for the development of biomass markets for sorghum (energy, animal feed, Other uses) and constraints related to the management of a targeted biomass selection program, NIRS session and inter-species calibration, Impact of biomass quality on industrial properties (2018) - Bioinformatics, biochemical-histological phenotyping, LCA: State of progress and focus on the comparison of reinforcing an automotive plastic part with miscanthus and fibreglass, Market analysis "Sorghum and maize biomass": state of play and perspectives (2019)
Number of scientific posters	9
Number of oral communications at scientific conferences	75
Number of symposia (French and international) organised	7 annual meetings
Newsletters and public communications	- 2 newsletters per year - 10 communications for the general public
Other communication tools	- Written press and television
Notable communication actions	1. Agriculture Fair 2014, INRA stall with presentation of Biomass For The Future 2. France 3 National TV, 2014, report on miscanthus and biomaterials 3. Public Hearing at the Parliamentary Office for the Evaluation of Scientific and Technological Options (*Office parlementaire d'évaluation des choix scientifiques et technologiques* - OPECST): Current research on biomass at the INRA - state of play and perspectives. "The strategy for biomass in France: a step towards the bioeconomy? "

Description

Project title	Developing new wheat varieties for sustainable agriculture: an integrated approach from genomics to breeding
ACRONYM (+ logo)	BREEDWHEAT
Website	https://breedwheat.fr/
Coordinator	Jacques LE GOUIS (Inra GDEC)
Project manager	Marion BONDOUX (Inra Transfert)
Number of researchers involved	305 (472 persons/month)
Public/private ratio	45/55
Number of trainees	48 (150 persons/month)
Number of PhDs	19 (155 persons/month)
Number of post-doc fellows	4 (33 persons/month)
Project summary	The aim of the BREEDWHEAT project is to support the competitiveness of the French wheat breeding sector, responding to societal challenges for high quality sustainable production. This pre-competitive project belongs to a thematic continuum that includes the development of genetic tools, materials and methods. It aims to conduct genetic and ecophysiology studies on both yield and quality under biotic and abiotic stress conditions. It proposes also to evaluate new selection methods and creates original populations to be used in breeding programs.
Project aims	BREEDWHEAT aims to unite French research on bread wheat around a number of common objectives. It brings together 28 partners including public research teams and major breeding companies, conducting multidisciplinary studies in genomics, genetics, ecophysiology, agronomy and socio-economics. It also aims to position French research at the highest levels in international projects and consortia in the field.
Achievement of objectives	The objectives of BREEDWHEAT have so far all been met or exceeded. The project has structured the public and private research community at the national level and strengthened its position at the international level. New genotyping tools have been implemented and the objectives in data points have been greatly exceeded. A phenotyping experimentation trials network has been implemented. Genetic analyses were conducted, the raw data processed and the association results stored in the BREEDWHEAT information system (BWIS part of GnpIS), developed

	in collaboration with the other PIA Investment for the Future projects. New methods for modelling, constructing gene networks, characterising the environments and performing genomic selection have been developed and tested. Finally, panels and populations have been constructed in line with the aims of the program. This success was made possible through constructive discussions between the various partners and with the international scientific committee, allowing the program to adapt to evolutions in technologies, knowledge and context.
In figures	- A genotyping array of 423,000 SNP markers - A genetic map including more than 183,000 markers - More than two billion genotyping data points - Genotypic and phenotypic characterisation of 4,600 accessions, representing the world-wide diversity - Selection of a panel of 450 accessions - Phenotyping of approximately 70,000 experimental plots - Creation of 9 recombinant populations

Results

TRL (Technology Readiness Level) Reference - 1 to 9

Most significant results achieved	1. **Genotyping data** BREEDWHEAT has allowed the genotyping of approximately 8,000 bread wheat lines with over 260,000 SNP markers (about 40 times the number planned at the start of the project). These data form the basis of phylogeographical and genetic studies. TRL:7 2. **Phenotyping data** BREEDWHEAT has also allowed phenotyping a variety of genetic materials (a collection of 4,600 accessions from the genetic resources, an "elite" panel of 220 varieties, a "diversity" panel comprising 450 accessions, and nine recombinant populations) for the major constraints of global change (water, heat and nitrogen constraints, fusarium and septoria). TRL: 5 3. **Association data** The combination of genotyping and phenotyping data makes association genetic studies possible, in order to identify regions of the genome involved in stress tolerance. These data, as well as those that preceded them, are integrated into the BWIS database and are available to breeders. TRL: 5
Prominent tools developed	1. **The RulNet tool**, accessible via a web platform (rulnet.isima.fr), is dedicated to the inference and analysis of regulatory networks built from qualitative and quantitative -omic data using statistical techniques. TRL: 7

	2. **The ADEL-Wheat model**, an integrated ecophysiological model of wheat post-anthesis functioning, includes the acquisition of resources (photosynthesis, nitrogen uptake, transpiration) and the primary metabolism of carbon (C) and nitrogen (N). TRL: 4 3. **A chain of analyses for genomic selection** (GS) written in R, named the BREEDWHEAT Genomic Selection (BWGS) pipeline, consists of three modules allowing dataset reduction, imputation of missing data and estimation of the genetic values (GEBV) with a choice of several methods. TRL: 7
Scientific and technical success stories	1. **High-throughput genotyping chips** Two genotyping arrays, containing respectively 423,000 and 35,000 Single Nucleotide Polymorphism (SNP) markers, have been developed. They make it possible to establish "genetic identity cards" for wheat lines. By combining these data with phenotyping data, it is possible to identify the genomic regions involved in controlling traits of agronomic interest such as yield, disease resistance and drought tolerance. The 420K chip is one of the highest density arrays ever developed for wheat. 280K SNP of this chip, and the 35K chip, are available to the scientific community and are currently used for internal research and in several research collaborations. TRL: 9 2. **A diversity panel of 450 accessions** A panel representing world-wide wheat diversity was selected from the 11,960 bread wheats held at the Centre of Biological Resources at the UMR GDEC. This panel of 450 winter accessions covers the range of genetic diversity that is hardly present in European elite material. The panel was evaluated in the field by BREEDWHEAT partners to characterise its tolerance to major biotic and abiotic constraints such as diseases (Septoria and Fusarium), drought and nitrogen fertilisation deficiency. These data combined with the molecular data allows the identification of genomic regions involved in the tolerance, that can further be used in breeding programs. The list of accessions composing this panel is available on request to the wheat community, therefore allowing for its broader characterisation in the framework of other projects. TRL: 5
Non-scientific success stories	**Major player in global wheat research** Having made its genotyping arrays available to the scientific community, BREEDWHEAT has greatly strengthened its international visibility. The project also contributed to the production of the bread wheat reference genome sequence by the International Wheat Genome Sequencing Consortium (IWGSC), with sequencing of chromosome 1B, one of the 21 wheat chromosomes (IWGSC, Science, 2018), as well a strong involvement in the assembly of the whole genome reference

	sequence.

Partnerships and transfers

Role and importance of the public-private partnership in the project	The public-private partnership has so far resulted in a high level of complementarity, for example in the development of molecular markers, the conduct of field trials experiments to phenotype panels within a large network, as well as the construction of new genetic materials, discussed in depth between public and private researchers. It is also formalised by joint requests for complementary funding supported by all partners (funding from the FSOV).
External collaborations on results at the national and international levels	22 external collaborations: - 10 French research projects - 2 European projects H2020 - 9 international research institutes - 1 international consortium
Most significant collaborations showing the added value of the results of the project	1. FSOV Nitrogen Project (2010F). The genotyping produced by BREEDWHEAT with the TaBW420K chip allowed for the joint analysis of data from the BREEDWHEAT and FSOV project in order to characterise nitrogen stress tolerance for yield and protein concentration. 2. University of Wageningen (2016). In the context of the post-doc work of Renaud Rincent (UMR GDEC), access to the genotyping and phenotyping data of the "elite" BREEDWHEAT panel was granted to the team of F. van Eeuwijk. New approaches to take into account genotype × environment interactions have been tested in collaboration with this team, a leader in this field. 3. H2020 SolACE project (2017). A subset of the BREEDWHEAT "diversity" panel is being studied in the H2020 SolACE project. This project will also have access to the phenotyping and genotyping data essential for the analyses to be conducted on combined water/nitrogen constraints, complementary to those constraints tested in BREEDWHEAT.
Types of results transferred for use outside the project	These are primarily genotyping data, genetic maps, major gene genotyping data, phenotyping data, association data and chromosome 1B sequence data.
External partners having benefited from the results of the project	- 10 French research projects: ANR Phenoblé, FSOV Nitrogen, FSOV WEAB, FSOV B-Dul, Oséo ABBAH, FSOV HeatWheat, FSOV Yield, FSOV Septoria association, ANR Wheatamix, and ANR BacterBlé - 2 European projects H2020: SolACE, RustWatch - 9 international research institutes/breeders: Norwegian University of Life Sciences (UMB, Norway), Saaten Union Research (SUR, France), Institute of Experimental Botany (IEB, Czech Republic), Northwest A&F University (NWSUAF, China), University of Saskatchewan (USAK, Canada) , Murdoch University (Australia), Wageningen University (WUR,

	Netherlands), Penn State University (PSU, USA) and Michigan State University (MSU, USA) - 1 international consortium: International Wheat Genome Sequencing Consortium (IWGSC) - 5 PIA Investment for the Future projects (PeaMUST, Amaizing, RAPSODYN, AKER, PHENOME) also benefit from improvements in the GnpIS information system developed under BREEDWHEAT

Economic benefits/impacts

Current and future impacts of the project for the sector concerned and for French agriculture	The benefits of the BREEDWHEAT project is to provide innovative responses for the seed sector, helping to the creation of varieties that better meet the needs of tomorrow's agriculture, i.e. varieties that are more efficient in terms of input resources and best adapted to new environmental constraints. Varieties that are needed for the future will benefit from new genetic resources as well as molecular tools generated by the project. .
Impact of the project on the positioning of the scientific community at the international level	BREEDWHEAT has strengthened France's position in the international wheat sequencing initiative (IWGSC) and has participated to the publication of the reference sequence. It has also enhanced the position of our researchers in the Wheat Initiative (http://www.wheatinitiative.org/), and in particular within the expert working groups. The visibility of our research has been increased as a result of the organisation of two international congresses in collaboration with other foreign projects of the same size: Designing Future Wheat (UK BBSRC), proWeizen (German research and breeding alliance) and CRP Wheat (CGIAR challenge program). Finally, the results obtained have largely made it possible to support the studies on wheat within the European H2020 project SolACE.
Economic benefits for the project partners (at term)	Genotyping arrays, in particular the TaBW35K, allow breeders to better characterise their varieties (in progress). The partners will valorise the new germplasm produced during the project. This new genetic material will help developing innovative commercial varieties with increased disease resistance and resources use efficiency (water, fertiliser, pesticides etc.). On a 10-year perspective, we may see varieties listed in the French official catalogue deriving from the genetic material tested (included in the BWP3 panel) or created (AB-QTL populations) by BREEDWHEAT, for example concerning tolerance to water stress. The use of BWGS (BREEDWHEAT Genomic Selection) coupled with phenotypic selection may also improve the selection process for breeders (10-year perspective).

Publications

Number of publications in peer-reviewed journals	Number of publications (up to May 2019): 28 Number of additional publications expected by December 2020: 10
Themes of publications	- Analysis of structural variations in the bread wheat genome

expected end 2019	- Transcriptomic analysis of the heat stress response - Association genetic studies on biotic and abiotic constraints - Definition and validation of ideotypes for adaptation to global changes - The BWGS genomic selection tool
Themes of publications expected 2 years after the end of the project	- Comparison of genomic and phenotypic selection methods - Comparison of chromosome regions identified on "elite" and "diversity" association panels
Notable publications	1. F. Balfourier, S. Bouchet, S. Robert, R. De Oliveira, H. Rimbert, J. Kitt, F. Choulet, IWGSC, BreedWheat Consortium, E. Paux (2019). Worldwide phylogeography and history of wheat genetic diversity. Science Advances, Vol 5, No. 5, May 2019. 2. Julie Boudet, Marielle Merlino, Anne Plessis, Jean-Charles Gaudin, Mireille Dardevet, Sibille Perrochon, David Alvarez, Thierry Risacher, Pierre Martre, Catherine Ravel - Plant Journal (2019). The bZIP transcription factor SPA Heterodimerizing Protein represses glutenin synthesis in *Triticum aestivu*m. The Plant Journal, Volume97, Issue5. March 2019. 3. The International Wheat Genome Sequencing Consortium (2018). Shifting the limits in wheat research and breeding through a fully annotated and anchored reference Genome. Science, Vol 361, Issue 6403, August 2018.
Notable publication coming soon	BWGS: an R package for genomic selection and its application to a wheat breeding program. Submitted to PlosONE. Publications by BW are all listed on the website: https://breedwheat.fr/resultats/publications/

Communications

Training organised during the project	BREEDWHEAT has organised training sessions on various topics: in 2014 on genomic selection in partnership with the PeaMUST project, in 2016 on phenotyping, in 2015, 2017 and 2018 on the use of the BWIS. These are intended for partners but are also open to other PIA Investment for the Future project partners.
Number of scientific posters	23
Number of oral communications at scientific conferences	61
Number of symposia (French and international) organised	BREEDWHEAT has organised two international conferences in Clermont-Ferrand in close collaboration with the Design Future Wheat (UK BBSRC), ProWeizen (German research and breeding alliance) and CRP Wheat (CGIAR challenge program) programs: - 1st IWIW (International Wheat Innovation Workshop) in November 2015 (https://colloque.inra.fr/iwiw) - 2nd IWIW2 in March 2018 (https://symposium.inra.fr/eucarpia-cereal2018/IWIW2-Program)
Newsletters and public communications	Each year, BREEDWHEAT publishes a newsletter in French (intended for project partners, the general public, funding bodies and the institutional participants) on the theme of a milestone

	result of that year: - 2013: Characterisation and exploitation of genetic diversity - 2014: New markers to describe the wheat genome in response to the challenges of future variety improvement - 2015: Phenotyping the response of wheat to the major constraints of global change - 2016: Improving the effectiveness of breeding programs through genomic selection - 2017: Data management in the era of Big Data
Other communication tools	- Twitter account (290 subscribers) - Booklets for the international scientific community, covering the topics of each years' newsletters, with each theme further developed and published in English - Posters (French and English) presented at various events, such as scientific congresses - Brochures (French and English) presenting the project to a global audience
Notable communication actions	1. *Les Culturales* 2017 and 2019: presentation of BREEDWHEAT in the form of posters and cultural showcases to more than 250 visitors (including farmers and foreign delegations) (http://www.lesculturales.com/). 2. Two international conferences: 1st IWIW (International Wheat Innovation Workshop) November 2015 (https://colloque.inra.fr/iwiw) and 2nd IWIW2 March 2018 (https://symposium.inra.fr/eucarpia-cereal2018/IWIW2-Program). 3. Launch of the project in 2011 in Clermont-Ferrand in the presence of Laurent Wauquiez (Minister of Higher Education), Francis Lamy (Regional Prefect), Marion Guillou (CEO of INRA), Pierre Pagesse (Vice President of GIS BV), Xavier Beulin (President of the FNSEA) and Louis Giscard d'Estaing (parliamentary representative of the 3rd district of Puy-de-Dôme).

Description

Project title	**G**enome **EN**gineering **I**mprovement for **U**seful plants of a **S**ustainable agriculture
ACRONYM (+ logo)	GENIUS
Website	http://www.genius-project.fr/
Coordinator	Peter ROGOWSKY (INRA RDP)
Project manager	Laure Trannoy (Inra Transfert)
Number of researchers involved	28
Public/private ratio (%)	83/17
Number of trainees	40
Number of PhDs	4
Number of post-doc fellows	6
Project summary	GENIUS established in France genome editing technologies in 9 cultivated species (wheat, maize, rice, tomato, potato, oilseed rape, poplar, apple, rose) and 3 model species (Brachypodium, Physcomitrella, Arabidopsis). It also improved the efficiency of transgenesis in recalcitrant species (poplar, apple, rose) and for elite genotypes (maize, potato, apple, rose). Proofs of concept concerned disease resistance, salinity tolerance, early flowering, plant architecture and reproduction, favouring traits of interest for a more sustainable agriculture.
Project aims	- Giving access to genome editing technologies to French public and private research teams, for plant biology research in cultivated species - Testing developments or optimisations of genome editing technologies in model systems - Providing proof of concept in confined environments, illustrating the potential of genome editing technologies to provide traits for more sustainable agriculture - Federating a scientific community around a technology rather than a plant species
Achievement of objectives	- Different types of genome editing were achieved in partner labs: Targeted mutagenesis (12 species), base editing (6 species) and HR (3 species). - Guide RNA design, multiplexing, PAM modification and base editing were optimised in model species. - Proof of concept was provided for disease resistance, early flowering and plant architecture.

	- A proactive, strongly interacting genome editing community was established.
In figures	- 25 TALEN constructs (pairs) used in plant transformation
	- 266 guide RNAs used in plant transformation
	- 363 constructs (all types) used in plant transformation
	- 12,807 transformation events regenerated into plantlets
	- 2,557 edited plant lines obtained (events with modification)

Results

TRL (Technology Readiness Level) Reference - 1 to 9

Most significant results achieved	**1. polQ, a booster of homologous recombination?** GENIUS has shown that DNA polymerase Q (POLQ) involved in the NHEJ repair mechanism is essential for the random integration of transgenes and acts as a homologous recombination repair inhibitor. Thus, control of POLQ activity in plants may increase gene editing efficiency for plant breeding. TRL: 2 **2. Early flowering in perennial species** GENIUS has given rise to early flowering perennial plants (starting at the in vitro stage): CRISPR-directed mutagenesis of the MdTfl1.1 floral repressor in apple trees (standard and elite varieties) and overexpression of the flowering activator RoFT in rose bush (standard variety). TRL: 3 **3. Increase in the number of petals in rose bush** GENIUS has demonstrated the effectiveness of reducing the expression of a gene for the control of an ornamental trait of roses via an artificial micro-RNA ("amiRNA"). In "Old Blush," an ancestor of modern roses, the expression of an amiRNA targeting the floral gene *AGAMOUS* leads to a significant increase in the number of petals, from 25–30 to 50–80. TRL: 3
Prominent tools developed	**1. *In planta* transformation in poplar** GENIUS has developed an innovative genetic transformation protocol, based on the injection of *A. tumefaciens* into poplar flower buds. This protocol is effective on several genotypes of *Populus nigra*, an indigenous species recalcitrant to *in vitro* transformation. It paves the way for the use of transgenesis and genome editing in a wider panel of poplar genotypes. TRL: 4 **2. Transformation of elite lines** GENIUS has been successful in the genetic transformation of several elite genotypes of species not readily amenable to transformation, by optimising the protocols for the production of mother plants, transformation by *A. tumefaciens* and/or plant regeneration in maize (1 line), rose (2 varieties) and apple tree (1

	variety and 1 rootstock) TRL: 4
	3. DFR - a visible marker for targeted insertion A method for obtaining targeted insertions of transgenes into the plant genome, an event known to be very rare and which requires expensive molecular analyses, has been developed and validated experimentally in tomato. It is based on the exploitation of the *DFR* gene, involved in the synthesis of anthocyanins. Obtaining targeted insertions at the *DFR* site in plants previously mutated in this gene is associated with repair of the *DFR* gene. Seedlings bearing targeted insertions are visually recognisable by their characteristic red colour as soon as they appear during *in vitro* culture. TRL: 4
Scientific and technical success stories	**1. Resistance of tomato to potyvirus** Original tomato genotypes were obtained by making two targeted modifications in the *eIF4E* gene, required by many potyviruses affecting tomato crops to carry out their infectious cycle. GENIUS seeks to make this gene unusable by these viruses while keeping it perfectly functional for plant development and growth. Phenotyping work is underway to confirm that these tomato plants have a new spectrum of resistances to different potyviruses, thus broadening the genetic variability for virus resistance in this species. TRL: 3 **2. Reduction of amylose content in potatoes** In potato, a single enzyme (GBSS - Granule-Bound Starch Synthase) governs the amylose content of the starch stored in tubers. Its inactivation leads to a particularly sought-after starch quality used in certain industrial processes. In 1987 mutants were obtained by inactivation of the *gbss* gene by irradiation. This same gene was inactivated in potato standard and elite lines by the use of two types of site-specific nucleases: TALEN and CRISPR/Cas9. Due to a particular protocol the action of the nucleases was limited in time, with no integration of transgenes into the plants. This approach resulted in plants with mutations at the targeted site, accompanied by a significant reduction in amylose content. TRL: 6
Non-scientific success stories	**A technology-focused community** While France has always possessed excellent know-how in cellular engineering, this expertise had hitherto remained partitioned at the local level at the service of research focused on the biology or improvement of a given species. GENIUS has taken the various players out of their isolation and federated them around a major challenge, the implementation of plant genome editing in France. The establishment of common tools, mutual training, calling upon international experts, a dialogue between basic and applied research and exchanges on the problems encountered, have greatly accelerated the advancement of this challenge, and meetings with researchers in human and social sciences were

	helpful to position the technological advances made in a societal context.

Partnerships and transfers

Role and importance of the public-private partnership in the project	The public-private relationship was quite different depending on the profile of the private partner, either active in biotechnology or in plant breeding. An example of the first case is the world-renowned know-how of Cellectis in the design and production of meganucleases and TALEN, which in the first years of the project was indispensable to public partners for the effective implementation of these tools in the different species. In the second case, it was rather the skills and know-how of the public partners in the cellular engineering of laboratory lines, which allowed the breeders Germicopa and Delbard to progress in the transformation of elite lines.
External collaborations on results at the national and international levels	The collaborations concerned essentially the know-how and experience gained in the project (the technology), rather than the proofs of concept (traits). National (5) + International (7): - Tomato: 0 + 1 - Maize: 1 + 1 - Rice: 2 + 3 - Potato: 1 + 0 - Apple tree: 0 + 1 - Physcomitrella: 1 + 1
Most significant collaborations showing the added value of project results	- P5a and Turkey on CRISPR-Cas9 in trees - P1a and Italy on CIRSPR-Cas9 in maize - P3a and Taiwan on CRISPR-Cas9 in potato
Types of results transferred for use outside the project	- Apple tree: optimised protocol for genetic transformation of the apple tree - Apple tree: CRISPR-Cas9 directed mutagenesis protocol - Tomato: distribution of the CRISPR-Cas9 protocol for genome editing - Tomato: transformation and regeneration protocols - Rice: protocol for the transient transformation of protoplasts - Potato: direct protoplast transformation techniques without transgene integration - Physcomitrella: distribution of the CRISPR-Cas9 module for genome editing
External partners having benefited from the results of the project	**Apple tree:** - Fernando Andres et Joan Estevan, INRA Montpellier (France) - Michela Dall'Agata, University of Bologne (Italy) - Nicat Cebrailoglu, Technical University of Gebze (Turkey) **Tomato:** - Ben Field, BIAM, Aix-Marseille (France) - Marc Valls/Nuria Sanchez-Coll, CRAG, Barcelona (Spain) **Rice:** - Anne-Aliénor Véry, INRA Montpellier (France) - Mathias Lorieux, CIAT (Colombia) - Adam Price, University of Aberdeen (UK)

	- Thibault Mounier, University of Shanghai (China)
	Potato:
	- Xavier Bailly, CNRS Roscoff (France)
	- Nicolas Szydlowski University of Lille (Belgium)
	Physcomitrella:
	- Yoan Coudert, ENS Lyon (France)
	- Mark Estelle, UCSD La Jolla (USA)
	- Stuart McDaniel, University of Florida (USA)
	- Kaye Peterman, Wellesley College (USA)
	- Karen Hicks, Kenyon College (USA)
	- Luis Vidali, Worcester Polytechnic Institute (USA)
	- Tomomichi Fijita, Hokkaido University (Japan)
	- Gohta Goshima, Nagoya University (Japan)
	- Yuji Hiwatashi, Miyagi University (Japan)
	- Mitsuyasu Hasebe, NIBB Okazaki (Japan)
	- Keiko Sakakibara, Rikkyo University (Japan)
	- Daisuke Takezawa, Saitama University (Japan)
	- Jon Hughes, Giessen University (Germany)
	- Gabriel Iturriaga, Instituto Tecnológico de Roque (Mexico)
	- Miguel Angel Villalobos, IPN (Mexico)
	- Andrey Knyazev, Russian Academy of Sciences, (Russia)
	- Ann-Cathrin Lindner, Instituto Gulbenkian (Portugal)
	- Kun Wang, Wuhan University, (China)
	- Jiang, Chen-Kun, Beijing University (China)
	- Lihong Xiao, Shanghai Center for Plant Stress Biology (China)
	- Mauricio Lopez Obando, University of Agricultural Sciences, Uppsala (Sweden)
	- Ulla Rasmussen, Stockholm University (Sweden)
	- Laura Saavedra, Universidad Nacional de Córdoba (Argentina)
	- Peter Szovenyi, University of Zurich (Switzerland)

Economic benefits/impacts

Current and future impacts of the project for the sector concerned and for French agriculture	GENIUS is a transversal project in plant biotechnology. Its technological developments and results will be applicable to a multitude of traits (agronomic, quality and technological) in a large number of cultivated species, and therefore concern many different sectors. Blocked by a strong uncertainty around regulation in the European Union, the benefits are highly limited at present.
Impact of the project on the positioning of the scientific community at the international level	Although the GENIUS project has served as an example for calls for tender and for the emergence of dedicated platforms in the field of genome editing at the European level, there is no formal link between GENIUS and these other European activities. Its impact is therefore more visible at the level of the GENIUS partners, using the new knowledge gained to establish bilateral collaborations and new projects. For the private partners involved, the acquisition of knowledge concerning new breeding techniques is crucial for strengthening their position in markets open to genome editing products.
Economic benefits for the	The economic benefits of the project will depend primarily on the

project partners (at term)	evolution of the regulatory framework in the European Union. The only patent filed to date will probably not see any return in the short term as it concerns a tool of interest in basic research/for the creation of new GM organisms. In the short term, GENIUS has made it possible to develop techniques to improve transgenesis in several species, some of which are little studied or used. The project has also harnessed genome editing - a technique that was virtually unknown at its outset- and produced several proofs of concept. In the medium term (5 to 12 years), the skills acquired in the GENIUS project will serve as a basis for maintaining competitive know-how in a fast-moving field (genome editing) the contours of which remain blurred and which will undoubtedly have far wider implications than are clear today. If reasonable European Union regulation is put in place, the possibilities for development are open-ended. Seed companies might innovate by creating original genetic variability on the species they select, gain or simply maintain market share, both at European and global level for those who have undertaken to position themselves in other markets. Start-ups might be set up simultaneously to exploit niches, notably with regard to diversification and quality criteria, recreating a diversity of companies, as existed two or three decades ago.

Publications

Number of publications in peer-reviewed journals	- 19 - 30 expected end 2019
Themes of publications expected end 2019	- Tomato, *eIF4E* editing, potyvirus resistance - Rice, SHR1/SHR2 site-directed mutagenesis, functional analysis - Rice, SAP9 directed mutagenesis, functional analysis - Rice, replacement of *OsSAP9* with *AlSAP*, salt tolerance - Rose bush, transformation by organogenesis - Apple tree, proof of concept amiRNA with *PDS* - Apple/pear, *PDS* (proof of concept) and *Tfl1* (early flowering) mutagenesis - Maize, site-directed mutagenesis *OSD1*, non-reduced gametes
Notable publications	1. Veillet, F.; Perrot, L.; Chauvin, L.; Kermarrec, M.-P.; Guyon-Debast, A.; Chauvin, J.-E.; Nogué, F.; Mazier, M. (2019) Transgene-Free Genome Editing in Tomato and Potato Plants Using Agrobacterium-Mediated Delivery of a CRISPR/Cas9 Cytidine Base Editor. Int. J. Mol. Sci. 2019, 20, 402. 2. Charrier A., Vergne E., Dousset N., Richer A., Petiteau A., Chevreau E. (2019) Efficient targeted mutagenesis in apple and pear using the CRISPR/Cas9 system. Frontiers in Plant Science (doi: 10.3389/fpls.2019.00040) 3. Collonnier C, Epert A, Mara K, Maclot F, Guyon Debast A, Charlot F, White C, Schaefer DG, Nogué F (2017) CRISPR-Cas9-mediated efficient directed mutagenesis and RAD51-dependent and RAD51-independent gene targeting in the moss

	Physcomitrella patens. Plant Biotech J 15: 122-131.
Notable publication coming soon	- Gallois J-L. and Chauvin J-E. (2019) The Solanum tuberosum GBSSI gene: a target for assessing geneand base editing in tetraploid potato. Plant Cell Reports (under review).

Communications

Training organised during the project	In 2018: - 1 workshop "plant transformation, regeneration and genome editing" - 4 interventions in M2 (2 in France, 2 in Taiwan)
Number of scientific posters	7
Number of oral communications at scientific conferences	- Scientific conferences: 57 - General public communications: 26
Number of symposia (French and international) organised	- 2014, International Symposium on Genome Editing, Paris, France - 2016, International Symposium on Genome Editing, Paris, France
Newsletters and public communications	- Consumer brochure (in French) - Poster for the general public (in French) - Consumer data sheets (in French) => website - Consumer technical dictionary (in French) => website - Editing the Genome, file on the internet site http://www.inra.fr/Chercheurs-etudiants/Biotechnologies/Tous-les-dossiers/Modifications-ciblees-des-genes-l-ere-post-OGM
Other communication tools	- Scientific brochure (in English) - Scientific poster (in English) => 5 international conferences - Participation in the feature film "*Les semences du futur*" (The seeds of the future) by Honorine Périno (2017) - Contribution to the TV show "*Le blogueur*" (The Blogger) on ARTE TV: "*OGM, on en est où ?*" (GM products, where are we?) (2013) - Contribution to the organisation of two public debates on GM products in Angers (2013) - Educational game teaching CRISPR-Cas9 developed as part of the CULTIVAR project - Presentation of the GENIUS project at scientific conferences, competitiveness clusters and societies in the breeding world
Notable communication actions	1. Press release from Limagrain, following the occupation of Biogemma by the activist group *Faucheurs Volontaires* (2014) 2. Participation in the feature film "*Les semences du futur*" (The seeds of the future) by Honorine Périno (2017) 3. Presentation of the project at the OECD conference on genome editing (2018)

Description

Project title	PEA MUlti-STress adaptation and biological regulations for yield improvement and stability
ACRONYM (+ logo)	PeaMUST
Website	https://peamust-project.fr/
Coordinator	Judith BURSTIN (INRA Agroecology)
Project manager	Amandine REMY (INRA Agroecology)
Number of researchers involved **Public/private ratio (%)**	380 Nearly 1250 person-months of permanent staff (approximately 21% from private organisations/79% in public bodies) Nearly 750 person-months of non-permanent staff (of which around 12% from private organisations and 88% in public bodies)
Number of trainees	18
Number of PhDs	4
Number of post-doc fellows	5
Project summary	The instability of yields severely limits the surface area dedicated to pea and fava bean cultivation, which are otherwise highly interesting from an environmental and nutritional point of view. Faced with the numerous biological and climatic stresses responsible for this instability, the PeaMUST project seeks to allow the selection of new pea varieties and to optimise symbiotic interactions in order to obtain stabilised yield and seed quality. With a multidisciplinary approach, and relying on high throughput sequencing, genotyping and phenotyping technologies, PeaMUST aims to provide innovative solutions and tools for studying multi-stress resistance mechanisms.
Project aims	By developing new varieties of pea, ensuring stabilised yield and seed quality, the PeaMUST project aims to increase yields by 5–7 quintals/ha and increase the gross margin of farms from 90 to 130 €/Ha. This improvement could then lead to an increase in the surface area under pea cultivation and a reintroduction of pulses into European cropping systems, thus acting for a more sustainable, more energy-efficient and higher quality food crop.
Achievement of objectives	In 8 years, most of the objectives of the PeaMUST project have been achieved. Thanks to the exploitation of large collections of genetic resources and the creation of specific plant material (TILLING population, architecture mutants, recombinant lines, breeding populations), the project has made great progress on the resistance of peas to biotic and abiotic stresses, including the

	validation and / or identification of many markers associated with QTL resistance to root rot, frost, and bruchids. Complementary approaches such as the study of architecture, transcriptomics or VOC analyses (Volatile Organic Compounds) have identified genes potentially involved in resistance, and the effect of the inoculation strategy on tolerance to stress has been studied. The deployment of genomic breeding programs on winter and spring peas has also made it possible to measure the genetic and economic gain of this selection method compared to more conventional selection strategies. Finally, the development of gene function validation tools, such as the VIGS technique on pea, now makes it possible to have a validation technique for previously identified candidate genes. Thanks to the high throughput genotyping and phenotyping strategies exploited throughout the project, a large body of biological, genetic and genomic resources will have been produced within the PeaMUST project, boosting the continued search for genetic levers of resistance to the different combined stresses in peas.
In figures	- More than 7,000 pea lines and nearly 600 fava bean lines have been used and/or created - Nearly 2.3 million SNPs identified in 982 pea genotypes and more than 1.7 million SNPs discovered in 248 fava bean genotypes - 3,100 mutant lines available

Results

TRL (Technology Readiness Level) Reference - 1 to 9

Most significant results achieved	1. **Trait markers of interest for selection** Calling upon numerous experimental tests, along with the genotyping and phenotyping data generated, the PeaMUST project seeks to identify markers of resistance to certain biotic stress (aphanomyces, ascochytosis, bruchus weevil) and abiotic stress (frost, drought). Different SNP markers associated with resistance to different stresses have been identified, and the routine use of these markers is ongoing. TRL: 6 2. **Genetic advances for resistance to *Aphanomyces euteiches*** The validation of QTL combinations in quasi-isogenic pea lines, the fine mapping of a major resistance QTL and the study of the association of this QTL with root architecture are some of the approaches that have allowed genetic levers of interest for resistance to *Aphanomyces euteiches* to be identified within the framework of the PeaMUST project. TRL: 5-6 3. **Genetic advances for frost tolerance** Within the framework of the PeaMUST project, an association genetic study (GWAS) has permitted the validation and reduction

	of QTL confidence intervals for frost tolerance. Haplotypes favourable to tolerance QTLs have been identified. TRL: 5-6
Prominent tools developed	**1. VIGS (Virus-induced Gene Silencing)** VIGS is a functional validation technology that makes it possible to test the effect of a given gene by voluntarily decreasing its expression, introducing into the plant a virus specifically modified for the gene under study. Within the framework of the PeaMUST project, this technology has been adapted to the pea, and appears to be a tool of interest for the validation of candidate genes identified by other researchers working in the project. TRL: 3 **2. Whole genome SNP resources for peas and fava beans** The PeaMUST project has analysed the DNA of 982 pea genotypes, using the capture exome genotyping technique, highlighting more than 2.3 million SNPs. Nearly 3,200 genotypes have been genotyped by capture on 5,000 SNPs selected from exome capture results. In fava beans, the same genotyping technique has identified more than 1.7 million SNPs in a collection of 248 genotypes. This constitutes an unprecedented resource for both of these species, in terms of the size of the discovery panels and by the number of SNPs identified and usable in subsequent studies. TRL: 5 **3. TILLING population for winter peas** The TILLING method was used to create a population of 3,100 mutant lines of winter pea, Hr336/11. This population is available for the screening of lines mutated for each gene of interest in the pea. The selected genotype allows the analysis of traits in the phenological context of a winter pea. TRL: 4
Scientific and technical success stories	**1. Implementing genomic selection for the pea** One of the components of the PeaMUST project was to develop genomic selection programs on spring pea and winter pea varieties, to test the implementation and potential benefits of this selection method in relation to classical phenotypic selection. By allowing the selection of interesting varieties simply from knowledge of their genome, genomic selection may allow a saving of time and efficiency/precision compared to classic phenotypic selection where the interesting varieties are selected on phenotypic criteria observed in whole plants. TRL: 5-6 **2. Phenotyping of bruchus weevil damage by tomography** Within the framework of the PeaMUST project, the SNES physical analysis laboratory (GEVES) adapted the X-ray tomography imaging technique to the specific study of bruchus (weevil) damage in pea seeds and fava beans. This technology makes it possible to accurately quantify the damage caused to seeds by these insects,

	in order to compare between genotypes and with genomic results obtained elsewhere. TRL: 5
Non-scientific success stories	**An engaged and structured community** Bringing together the principal breeders and researchers working on peas and fava beans, the PeaMUST project has created a community based around the study of these two protein crops. Also integrating the technical institute and the inter-professional organisation within the consortium, the PeaMUST project brings together participants in the protein sector as a whole, which represents real added value.

Partnerships and transfers

Role and importance of the public-private partnership in the project	The scope of the public-private partnership in the PeaMUST project allows a wide diversity and complementarity of skills. The partnership also offers, above all, a meeting point between research activities and the applied results expected by selection companies. PeaMUST brings together an inter-professional organisation, a technical institute and industries downstream of scientific research in a consortium, helping to clarify and prioritise the objectives of selection and breeding.
External collaborations on results at the national and international levels	Collaboration is ongoing with the international project NORFAB, a project aiming to improve fava beans, coordinated by the University of Aarhus. A second PeaMUST-NORFAB collaboration for the production of a fava bean genotyping tool was launched recently. Several national collaborations use the results of PeaMUST in their research projects.
Most significant collaborations showing the added value of project results	- Collaborations PeaMUST-NORFAB - Interaction on aphids - Interaction on WP5: agronomic data - Interaction on tomography for sitones
Types of results transferred for use outside the project	Genetic resources and genotyping data acquired on a wide range of peas and fava beans in the PeaMUST project are used as resources in many other projects. Data on the phenotyping of NIL lines (quasi-isogenic lines) in the field, and fine mapping data of a major resistance QTL for *Aphanomyces euteiches* are also being used in other projects.

Economic benefits/impacts

Current and future impacts of the project for the sector concerned and for French agriculture	The PeaMUST project has developed markers, a collection of genetic resources and stock that can be used by breeders in the protein sector. PeaMUST also provides methodological tools, which can be used in the implementation of genomic selection programs.
Impact of the project on the positioning of the scientific community at the international level	The PeaMUST project is positioned as a leader in pea genomics and claims co-leadership in fava bean genomics, through its interactions with the University of Aarhus (the NORFAB-PeaMUST collaboration). At the international level, PeaMUST is making a

	major contribution to pea and fava genetics.
Economic benefits for the project partners (at term)	The PeaMUST project will offer the possibility of new pea varieties within approximately 4 years, with improvements in yield stability, resistance to Aphanomyces and frost tolerance, and in fava beans with improvements in bruchus weevil resistance.

Publications

Number of publications in peer-reviewed journals	- 18 - 4 expected end 2019 - Others to come in 2020
	- 1 publication submitted on cold tolerance 1 publication submitted on resistance to *Aphanomyces euteiches* (strain diversity of *Aphanomyces euteiches* for the level of aggressiveness on pea lines differing in resistance QTLs
Themes of publications expected 2 years after the end of the project	- Pea diversity - GWAS/QTL bruchus weevil - QTL Aphanomyces - QTL frost - Characterisation of "best of" mutants

Communications

Training organised during the project	**Training courses for students:** - A training day was held in 2013 with presentations by project partners and a field trial visit for students from the schools AgroSupDijon and Agrocampus-Ouest (45 students) - A morning of presentations was held in 2016 and again in 2017 on the PeaMUST project for students at AgroSupDijon (between 5 and 10 students) **Training courses for PeaMUST partners:** - In 2014, 3 days of training on genomic selection were organised in collaboration with Breedwheat (32 people from the two PIA Investment for the Future projects) - Two training sessions were held in 2017 with the DiagVar modelling tool (14 people) Each year, training sessions for the GnpIS data storage and management tool are organised for partners wishing to participate and, in 2018, a complementary webinar on the GnpIS tool took place to specifically address the issue of phenotyping data.
Number of scientific posters	35
Number of oral communications at scientific conferences	40
Number of symposia (French and international) organised	Two international symposia: - In 2016, the first Francophone meeting on leguminous plants (*Rencontres Francophones sur les Légumineuses* - RFL1) took place in Dijon

	- In 2019, PeaMUST organised the ninth International Conference on Legume Genetics and Genomics (ICLGG) in Dijon
Newsletters and public communications	- 2 newsletters presenting the progress of the project, the technologies developed and projects connected to PeaMUST, along with researcher profiles and upcoming events - 1 special newsletter "*année des légumineuses*" (the year in legumes)
Other communication tools	- PeaMUST project presentation leaflet - A series of thematic booklets to reinforce communications in the various research themes - Three booklets, on Resistance to *Aphanomyces*, Functional validation of candidate genes and Sequencing and development of markers for high-throughput genotyping, have already been published within the framework of the project - Other documents to come at the end of the project (frost, bruchus weevil, genomic selection) - Twitter account (105 followers)
Notable communication actions	1. Production of a short booklet on resistance to *Aphanomyces*, which has been widely shared and appreciated by the scientific and technical community 2. Creation of the Francophone meetings of leguminous plants (*Rencontres Francophones des Légumineuses*, the first of which, RFL1, in 2016 in Dijon, generated a second meeting RFL2, in 2018 in Toulouse 3. Organisation of the ninth International Conference on Legume Genetics and Genomics (ICLGG) in 2019 in Dijon, which brought international exposure to the PeaMUST project

Description

Project title	French Plant Phenomic Infrastructure
ACRONYM (+ logo)	PHENOME-EMPHASIS
Website	https://www.phenome-emphasis.fr/
Coordinator	François TARDIEU (INRA LEPSE), Jacques Le Gouis (INRA GDEC)
Project manager	Pamela Lucas (Inra Transfert)
Number of researchers involved	53
Public/private ratio (%)	100/0
Number of trainees	60
Number of post-doc fellows	16
Project summary	PHENOME develops an infrastructure and methods to characterise hundreds of genotypes under environmental scenarios related to climate change. PHENOME-EMPHASIS: - Builds or improves facilities at nine sites for multi-scale analyses (-omics, controlled conditions, equipped fields, an experimental field network) - Develops hardware and software applications with technological advances, especially new sensors, vectors, processing chains and information systems capable of handling millions of data points - Disseminates techniques and methods to the French phenotyping community - Promotes the emergence of SMEs providing technologies for phenotyping and precision agriculture
Project aims	PHENOME faces an array of new challenges: - Allow the plant science community to re-analyse information collected in its infrastructure or in other projects, along with all necessary environmental data and metadata - Facilitate the agroecological transition, particularly with regard to analyses of biotic interactions - Fully integrate its activities into a European context (EPPN[2020] and EMPHASIS) - Strengthen the ecosystem of SMEs, in particular by accompanying the deployment of tools
In figures	- 116 "accesses" to PHENOME facilities in 2018: 22% of accesses linked to international projects, 58% to national projects and 20% to private companies - 64,000 plants or samples analysed, 20,200 micro-plots used, 605 Tb and 405 million experimental data points - Intense European and international collaboration, with 17

	major partners in the fields of plant and data sciences

Results

TRL (Technology Readiness Level) Reference - 1 to 9

Most significant results achieved	1. **Combination of high throughput phenotyping in controlled conditions and a field trial network for genomic prediction of maize yields in the diversity of European environmental scenarios** The yields of 250 maize hybrids were dissected with environmental indices calculated from sensors in concert with phenological progression at the PhenoArch installation in Montpellier. A regression of sensitivities with genome markers allowed prediction of yield in a wide range of environmental scenarios, including 10 new trials and 40 new hybrids. TRL: 2 2. **Combination of high throughput phenotyping and metabolomics under controlled conditions: prediction of maize yields in Europe** 250 hybrids of maize were sampled at the PhenoArch facility in Montpellier for the measurement of 1,400 metabolites at the Bordeaux facility. A model, based on these variables, predicts the yield in the network of fields presented above. This is the first time that independent metabolite datasets have been used to predict field yields. TRL: 2
Prominent tools developed	1. **Innovative root phenotyping** With an industrial partner (Inoviaflow), PHENOME EMHASIS has produced innovative rhizotrons (RhizoTube) and a cabin adapted for dynamic and non-destructive monitoring of root systems *in situ*. These have been developed industrially, are patented and are distributed internationally. Such tools allow a genetic analysis of growth as affected by beneficial or adverse interactions with soil microorganisms. TRL: 7 2. **FACE installation + rain shelters** As the concentration of CO_2 increases, PHENOME analyses its effect on the growth and yield of plants interacting with biotic and abiotic constraints, for hundreds of genotypes. To achieve this, PHENOME has developed a large FACE system (Clermont-Ferrand) and large rain shelters at two sites in Clermont-Ferrand and Ouzouer-le-Marché, Arvalis TRL: 5 3. **Use of chlorophyll fluorescence for the objective phenotyping of pathogen impacts** The Angers facility has been investigating the acquisition of virulence genes by non-pathogenic strains of *Xanthomonas*

	bacteria and the potential for damage to leaves. Photosynthesis is spatially estimated on the basis of two fluorescence parameters. TRL: 3
Scientific and technical success stories	**1. A fully automatic "Phenomobile" for the field** The Phenomobile has been developed to give an accurate and rapid estimate (100–200 plots/hour) of leaf area or number of inflorescence spikes, alongside functional imaging. The system is guided by a high-precision GPS and can analyse a wide range of species. It is equipped with LiDAR, multispectral cameras and high spatial resolution cameras with active illumination, making imaging independent of natural lighting. This innovative robot was built by two French SMEs in collaboration with PHENOME. TRL 7 **2. A multi-source and multi-scale information system based on ontologies** This system allows the scientific community to reanalyse data collected or to conduct meta-analyses of data in the field and under controlled conditions (for example, re-analysis of data after 10 years to assess the effect of climate change), including all environmental data and metadata necessary. It unambiguously identifies all objects, events, and phenotypic traits in an experiment, and establishes relationships for the integration and management of data from diverse experiments and platforms. It is linked to information systems for modelling and for genetic analysis. It is in deployment in French, European and international infrastructures. TRL 5
Non-scientific success stories	**An ecosystem of SMEs based around and on PHENOME** Three spin-offs and 19 SMEs have participated in the developments of PHENOME, which has encouraged commercial developments, in particular through patents and licenses. Some examples: - HiPhen was created in 2014 for the commercialisation of drones and the Phenomobile solutions - Inoviaflow has been developing innovative and patented solutions for root imaging, now distributed internationally in collaboration with other French SMEs. - Meca3D and Robopec have developed the Phenomobile and market it through HiPhen - Viewpoint has developed innovative solutions under controlled conditions, and markets them internationally

Partnerships and transfers

Role and importance of the public-private partnership in the project	The achievements of PHENOME EMPHASIS would not be possible by any of the partners in isolation.
External collaborations on results at the national and international levels	- PHENOME EMPHASIS participates (WP leader) to the construction of a European infrastructure for Phenomics (EMPHASIS). It coordinates a UE infrastructure project,

	EPPN[2020] - PHENOME EMPHASIS platforms used by 7 PIA Investment for the Future projects and 15 European projects - Collaborations with European phenotyping platforms at Emphasis in Australia (APPF), China (MoU Nanjing), USA (Data Science), Latin America (LAPPN)

Economic benefits/impacts

Current and future impacts of the project for the sector concerned and for French agriculture	The plant phenotyping market is estimated to be 140 million € in 2018 and is projected to reach 236 million € by 2023 (Plant Phenotyping - Global Forecast to 2023). Along the different types of phenotyping equipment, the software segment is projected to grow very fast. The demand is particularly driven by the need to better characterize plants adaptation to biotic and abiotic constraints in a fluctuating environment. PHENOME has favoured the creation and maintenance of service and technology providers (Hiphen, Innoviaflow, Qubit phenomics, Capt-Connect…). Maintaining, updating and developing new installations, sensors and methods will ensure that this ecosystem is active and innovative and takes is share in the expected growing market.
Economic benefits for the project partners (at term)	SMEs are highly involved in the design of methods and tools in PHENOME. All companies concerned participate to 'stakeholder meetings' every year, together with breeding companies, technical institutes, PIA projects and provider companies.

Publications

Number of publications in peer-reviewed journals	- 104 expected end 2018 - 130 expected end 2019
Themes of publications expected end 2019	- Phenotyping by imaging, focus on biotic interactions - Massive data management and analysis
Notable publications	1. Millet EJ, Kruijer W, Coupel-Ledru A, Alvarez Prado S, Cabrera-Bosquet L, Lacube S, Charcosset A, Welcker C, van Eeuwijk F, Tardieu F (2019) Genomic prediction of maize yield across European environmental conditions. ***Nature Genetics,*** accepted. 2. Coupel-Ledru A., Lebon E., Christophe A., Gallo A., Gago P., Pantin F., Doligez A., Simonneau T. (2016) Reduced night time transpiration is a relevant breeding target for high water-use efficiency in grapevine. ***Proc Natl Acad Sci USA*** 113: 8963-8968 3. Tardieu F, Cabrera Bosquet L, Pridmore T, Bennett M (2017) Plant Phenomics, From Sensors to Knowledge. ***Current biology*** 27: R770-R783

Communications

Training organised during the project	81 sessions organised up to 2018

Description

Project title	Optimization of the RAPeSeed Oil content anD Yield under low Nitrogen input : improving breeding of adapted varieties using genetics and genomics
ACRONYM (+ logo)	RAPSODYN
Website	https://www.rapsodyn.fr/
Coordinator	Nathalie NESI (INRA IGEPP)
Number of researchers involved	180 *(researchers & technical institute staff)*
Public/private ratio	77/23
Number of trainees	24
Number of PhDs	10
Number of post-doc fellows	2
Project summary	Oilseed production has to face an increasing worldwide demand in oil and proteins. In a context of stable cultivated land surfaces, a significant increase in seed yield is needed, while a reduction of synthetic nitrogen inputs is imposed. Oilseed rape (OSR) is the third main oil crop worldwide and can partly fulfill this challenge. However, despite its outstanding economical importance, OSR has a negative image in terms of sustainability due to its high dependence on inorganic nitrogen (N) combined with low nitrogen use efficiency (NUE). Improving oil production per hectare and/or maintaining yield stability across contrasted environments while limiting the input of N during the crop cycle will therefore insure OSR long-term competitiveness in the future. These are the major goals of RAPSODYN, along with a better understanding of both hybrid value and G×N interaction.
Project aims	**The main ambition of the project is to deliver the right nutrient rate at the right time on the right variety grown under the right environment.** The project is mainly centered on the development and application of smart methods to decipher the relationships between molecular polymorphisms and fine N-phenotypic traits related to agronomical targets. Therefore RAPSODYN aims at 1) identifying favorable alleles at loci contributing to phenotypic variation, 2) characterizing N-traits at the functional level (from molecular determinants to crop integrative processes) and 3) providing robust multilocus SNP-based predictors of the breeding value of agronomical traits under polygenic control. Moreover,

	RAPSODYN will allow the identification of new genetic variability for trait improvement.
Achievement of objectives	- 270K SNP array using resequencing data (whole genome reseq. and exome capture sequencing) - Establishment of a reference winter OSR panel used for genotyping and sequencing. This panel was used for side projects - >90 QTL for seed yield and yield components - Transfer of favourable alleles in breeding lines - Improvement of a crop model (AZODYN) - Genomic calibrations for traits related to seed yield and NUE - Tools for middle-throughput phenotyping of NUE traits - NIRS calibrations for evaluation of N and C contents in a wide panel of OSR tissues/organs - A bunch of OSR side projects using RAPSODYN data, tools and methods in connection with different issues (genome organization, disease resistance, seed quality)
In figures	- More than 40,000 experimental plots (2013-2019) - Resequencing of 30 OSR accessions (2014) - Assembly of a genome (2020) - Using a panel of 206 accessions and a NAM population of 14 x 250 RILs

Results

TRL (Technology Readiness Level) Reference - 1 to 9

Most significant results achieved	**1. Architecture of seed yield elaboration under low N** The phenotyping data of the RAPSODYN panel over 3 years (2013-14, 2014-15, 2015-16), several locations and 2 N nutrition levels were analyzed. The GWAS analyses revealed a high number of QTL for NUE and yield, and a set of QTL was prioritized. The statistical analyses of the dataset highlighted the low GxN and the high GxE interactions over the field network. As a consequence, a high number of QTL were specific to environmental conditions (year x location). TRL: 1-2 **2. Characterization of the proteolytic mechanisms associated with leaf senescence** RAPSODYN data showed the relevance of cysteine proteases (SAG12, RD21) as molecular markers of high NRE in OSR and the existence of complementation mechanisms between cysteine/aspartate proteases. The study of protease activities during senescence of cotyledons seemed to be a promising experimental model to investigate the regulation and the genotypic variability of proteolysis associated with NRE. The spatio-temporal pattern of proline fate during foliar senescence demonstrated its contribution to respiratory and energy metabolism.

	TRL : 1-2
	3. Plant functioning under low nitrogen nutrition and analysis of the relevant traits underlying the genetic variability of NUE Our results show that the NUpE is a major component (both in the field and in semi-controlled conditions), and that the NUE at harvest is strongly determined from the vegetative phase onwards. Using a conceptual framework for modelling, it has also been possible to show that the genetic variability was based on a few key traits, including the number of seeds, the LAI dynamics and the root exploration ability. TRL: 1-2
Prominent tools developed	**1. Genotyping and sequencing resources** Development of a high-throughput genotyping resource (270K SNP) with resequencing of the 30 OSR accessions and exome sequencing of 200 accessions. Use of bioinformatics workflows for the detection of molecular variants (SNPs). Sequencing and assembly of a winter OSR genome available for the Brassica community (2020). TRL: 4 **2. AZODYN rapeseed** Significant improvements and attempt to genotypically parametrise a crop model for winter OSR (Azodyn) for a different uses: monitoring of stress and growth kinetics, a posteriori identification of yield-limiting abiotic factors, a priori testing of fertilisation strategies or the different crop pratices. TRL: 3 **3. Genomic calibrations** Pooling of plant material by rapeseed breeders and development of genomic prediction equations based on data from the project to predict the traits related to seed yield. Use of these calibrations on elite material by private partners. TRL: 7
Scientific and technical success stories	**1. Characterization and use of semi-synthetic lines** Starting with plant material created within the framework of the ProBioDiv project (funded by Promosol), RAPSODYN has made doubled haploids from semi-synthetic lines available to its partners, allowing the genetic diversity of OSR to be increased. This material is characterised phenotypically (field trial in limited nitrogen nutrition conditions) and genotypically (15K SNP chip to characterise the chromosomal rearrangements). TRL: 3 **2. Mounting of a phenotyping device on board a 4X4 vehicle** In the development of methodological tools for characterisations in the field, Irstea will operationalise its mobile phenotyping platform (4x4 vehicule) in 2019, to include an NMR device as well as other physiological measurement devices. This vehicle will focus on characterisation at the scale of the individual plant, but may

	also support collaborations involving larger-scale measurement tools. TRL: 3-4
Non-scientific success stories	**Strengthening the French public-private community on rapeseed** The RAPSODYN project has strengthened the public-private partnership around rapeseed, already very solid in the past.

Partnerships and transfers

Role and importance of the public-private partnership in the project	- Exchange of plant material for construction of a common panel (206 accessions) - Establishment of a public-private network for the characterisation of GxN and GxE interactions - Validation of phenotyping tools developed by public partners using trials and materials of private partners - Coordination of genotyping and sequencing actions - Development of specific actions by the public partners (knowledge of the plant functioning) contributing to the identification of candidate genes and traits for the control of the NUE - Development of specific actions of private partners (genomic calibrations) on the basis of results acquired by the whole consortium - Development of an original resource (semi-synthetic rapeseed) for all partners - Flow of ideas, data and information - Mutualisation of tools and methods in bioinformatics, modelling
External collaborations on results at the national and international levels	6 collaborations based on the RAPSODYN data.
Most significant collaborations showing the added value of project results	1. Collaboration with C. Hermans on root architecture: phenotyping of genetic resources characterised by RAPSODYN. Oral communication at PAGXXVI. 2. Collaboration with Sophie Brunel-Muguet (INRA Caen) and Julianne Lilley (CSIRO Australia): use of the results of the RAPSODYN field trials for the parametrisation of the APSIM model on winter rapeseed.
Types of results transferred for use outside the project	- Genotyping data - Phenotyping data on seed quality (oil, protein, glucosinolate content), early flowering, seed yield and components - Seeds produced over the Rapsodyn field network - Bioinformatics workflows
External partners having benefited from the results of the project	- Christian Hermans, Univ. Libre de Bruxelles,, Belgium - Rod Snowdon, Giessen Univ., Germany - Julianne Lilley, CSIRO, Canberra, Australia - Véronique Solé-Jamault, INRA Nantes - Sophie Jasinski, INRA Versailles - Alexandre Termier, IRISA Rennes - Loïc Pagès, INRA Avignon

Economic benefits/impacts

Current and future impacts of the project for the sector concerned and for French agriculture	- Knowledge on nitrogen nutrition and determinisms of the mechanisms involved. This may make it possible to revisit the consistency of current fertilisation practices and to encourage, for example, delays or further fractioning of nitrogen input. - Methods to track the plant nutritional status or identify yield limiting factors In the long term, we might imagine reductions in fertilisation levels and improvements in energy and environmental balances. Nevertheless, this will depend mainly on long-term investments in breeding, which can be slow and difficult to predict.
Impact of the project on the positioning of the scientific community at the international level	RAPSODYN produces a large number of scientific papers and conference papers on NUE-related topics. In addition, the project has contributed to the organisation of several scientific symposia. On Brassica, it has given visibility and originality to the French community. RAPSODYN will also support the rapeseed community to promote enhanced valorisation of seed stock in terms of quality and as a major source of protein production.
Economic benefits for the project partners (at term)	The interest of private breeders for this project is in the development of knowledge and selection tools to enable a better orientation for their varietal creation programs in rapeseed. On this point, RAPSODYN provides elements which are already, or about to be, integrated into breeding programs: - Development of knowledge in the field of NUE phenotyping and understanding of the plant functioning in a context of low nitrogen input: these elements, when known, can influence the choices made by breeders, - Identification of genetic resources relevant for the NUE, and development of new genetic resources through original crosses that will enter into pre-breeding programs, - Development of tools (markers, phenotyping methods, etc.) that are quickly internalised into the selection processes. However, the creation of varieties is a long-term activity, which requires several iterations and stages of individual selection, involving many factors.

Publications

Number of publications in peer-reviewed journals	- 14 - 10 expected end 2020
Themes of publications expected end 2020	- Characterization of semi-synthetic rapeseed lines - Effects of the GxE interactions on yield in rapeseed - Identification of genetic and molecular determinants controlling yield stability and seed quality in rapeseed - Development of NIRS calibrations for the prediction of C and N contents - Use of NMR relaxometry to monitor the rapeseed responses to nitrogen constraints - Development and validation of a rapeseed crop model:

	AZODYN
	- Role of proteases and protease inhibitors in stress remobilization
	- Role of proline metabolism in the efficiency of nitrogen remobilisation
	- -Omics analyses of leaf senescence and nitrogen remobilisation efficiency
	- Genetic variability of root architecture and NUE in rapeseed
	- Identification of early determinants of NUE at the scale of the plant
	- Development of an innovative growing device PERISCOPE
Themes of publications expected 2 years after the end of the project	- Economic analyses of innovations: on improved NUE varieties (WP4)
	- Medium and high throughput tools for phenotyping the nitrogen status of the plant
Notable publications	1. Bouchet et al. 2016, Genetic basis of nitrogen use efficiency and yield stability across environments in winter rapeseed. BMC Genet. 17(1):131. doi: 10.1186/s12863-016-0432-z.
	2. Poret et al. 2016, Characterization of senescence-associated protease activities involved in the efficient protein remobilization during leaf senescence of winter oilseed rape. Plant Sci. 246:139-153. doi: 10.1016/j.plantsci.2016.02.011.
	3. Musse et al. 2017, A mobile NMR lab for leaf phenotyping in the field. Plant Methods, 13, 53. DOI : 10.1186/s13007-017-0203-5
Notable publication coming soon	Corlouer et al. In prep. Introducing key pedoclimatic factors to better handle environmental effects and genotype by environment interactions on seed yield of winter oilseed rape grown over a large French field trial network

Communications

Training organised during the project	- In-house project training for the use of GnpIS (2013)
	- In-house project training for the use of the MAPHiTS workflow (2013)
	- Training in phenotyping tools and genomic selection for Agrocampus-Ouest engineer students (7 days - 2014, 2015, 2016)
	- In-house training for the use of the AZODYN model (2018)
Number of scientific posters	21
Number of oral communications at scientific conferences	33
Number of symposia (French and international) organised	Three international workshops:
	- Joint workshop "Genomic Selection" of PreBreedYield (Germany) + Rapsodyn (France) (18–19 November 2014, Hohenlieth, Germany)
	- Workshop "Plant Abiotic Stresses" (2–3 November 2016, Rennes, France)

	- Workshop "Nitrogen Use Efficiency" in the context of the symposium Brassica2018 (1–4 July 2018, Saint Malo, France)
Newsletters and public communications	2 brochures, 3 newsletters, 1 booklet, 1 movie
Other communication tools	1 brochure produced as part of a project with middle school students
Notable communication actions	1. International workshops (x 3) 2. Movie made by the INRA Rennes communications department 3. Newsletters (x 3)

Description

Project title	**SUNflower Resources to Improve yield Stability in a changing Environment**
ACRONYM (+ logo)	SUNRISE
Website	http://www.sunrise-project.fr/
Coordinator	Nicolas LANGLADE (Inra LIPM)
Project manager	Pierre MARTIN (Inra LIPM)
Number of researchers involved **Public/private ratio**	86 publics including 32 researchers 100 private 46%
Number of trainees	18
Number of PhDs	3
Number of post-doc fellows	9
Project summary	**The SUNRISE project has 3 main objectives:** - Improving oil production under climate change with environmentally friendly practices - Understanding the genetic and molecular bases controlling the plant physiology and development to predict the characteristics of hybrids - Developing tools and methods for the whole sector for better cropping control **The SUNRISE project is based on 3 scientific axes:** - Characterising the sunflower genome to identify the genes of interest and understand the molecular mechanisms allowing the plant to resist to drought - Modelling the agronomic characteristics of future varieties to predict their behaviour in different climate scenarios - Evaluating socio-economic impacts associated with the dissemination of innovations from the project for sunflower hybrids breeding
Project aims	The public and industrial partners collaborating on SUNRISE aim to propel sunflowers into the post-genomic era. Through an innovative and multi-disciplinary approach, the project is preparing this crop, with a great potential, to meet the environmental and societal challenges of tomorrow.
Achievement of objectives	On multiple aspects, the SUNRISE project met or overcame the initial objectives.

	The efficient public-private partnership produced innovative genetic resources by characterizing and exploiting the natural biodiversity present in public and private genebanks.
	We pioneered the use of state of the art genomic technologies and obtained the world first sunflower genome sequence.
	We also innovated on other aspects of our scientific field with the creation of a high-throughput phenotyping platform and a multi-scale field-to-molecule analysis tools.
	We implemented both phenomic and genomic data in statistical genetics and eco-physiological models taking into account genetic diversity, field practices and climate data (present and future).
	We discovered physiological mechanisms and genes involved in abiotic stresses tolerance that control key processes that will enable the breeding of climate change –ready sunflower varieties. Our strongly involved private partners have already implemented some tools and genetic solution delivered by SUNRISE to make tomorrow's varieties.
In figures	- 45 field trials representing more than 40,000 plots in France and abroad (Romania and Chile) - 4,700 genotypes created and/or used by the project (600 GWA hybrids, 300 RIL-BCs, 500 NAM RILs and 1800 NAM RILs on testers, 600 ILs, 900 mutants) - 516,000 agronomic data points archived and accessible to all partners on a database - 7,020 phenotyped plants on the Heliaphen platform - 15Tb of compressed raw genomic and transcriptomic sequencing data - Measurement of 5,000,000 quantities of RNA, 1,200,000 DNA methylation levels, 850,000 metabolite quantities, 172,000 protein quantities

Results

TRL (Technology Readiness Level) Reference - 1 to 9

Most significant results achieved	**1. The sunflower genome reveals the orchestration of genes involved in oil production and flowering**
	A deep analysis of the sunflower genome has identified hundreds of genes that work together to regulate flowering and oil production. The researchers compared the DNA of 80 sunflower varieties selected for their oil production traits. The analysis of the differences, combined with published data, has allowed scientists to build the complete overview of the network of genes involved in oil production, but also to identify those with the greatest agronomic potential. Genes expressed specifically in floral organs or that control the time of flowering have also been identified. Knowledge of the organisation of these genes in the genome will serve to accelerate the process of varietal improvement for the sunflower.
	TRL: 4

	2. Identification of genetic markers for improving cold and drought tolerance and nitrogen absorption
	The development of robust breeding tools to improve tolerance to abiotic stresses is a key objective of the SUNRISE project. The combination of a crop modelling approach to quantitatively and dynamically describe abiotic stresses in a national multi-environment network and quantitative genetics having identified 35 regions controlling cold and drought tolerance and nitrogen absorption in sunflower species. Associated markers in these regions can be directly used to improve these traits in cultivated varieties and to develop an understanding of these processes.
	TRL: 4/5
	3. Seed resistance to drought
	Germination is a key step, controlling the impact of drought, predators, disease, and weed competition. The development of large-scale tests has shown great genetic diversity and the role of reactive oxygen species in drought tolerance. These new tools will be useful to seed providers and farmers to identify the best sunflower varieties for a given soil and region.
	TRL: 3
Prominent tools developed	**1. Drone, Phenomobile and Heliaphen platform: unique phenotyping robots**
	The Phenomobile and the drones make it possible to increase the flow and the frequency of acquisition of experimental data over large crop areas. The Heliaphen platform allows simultaneous and automatic experimentation on 1,300 sunflower plants. The robot is a unique prototype specifically designed to measure water supply levels and measure different morphologies and growth characteristics.
	TRL: 6/7
	2. Axiom® chips: innovative genotyping tools with high throughput
	Two Axiom chips, innovative high throughput genotyping tools, with a capacity of 50,000 and 600,000 SNPs (polymorphic sites on the genome), were designed for the project. These chips are already used internally by the partners of SUNRISE.
	TRL: 7/8
	3. Genomic selection
	The first genomic selection models on sunflower plants were developed for the project. They use genomic information from parents to predict offspring and are thus particularly suitable for hybrid varieties used in sunflower production.
	TRL: 7/8
Scientific and technical success stories	**1. The sunflower genome reveals the orchestration of genes involved in oil production and flowering**
	The decryption of the sunflower genome and an in-depth analysis

	have identified hundreds of genes that work together to regulate flowering and oil production. This work, conducted by INRA scientists working in the SUNRISE project and in collaboration with the International Consortium of Sunflower Genomic Resources, was published online in Nature in May 2017. The first results will make it possible to design the cultivated varieties of the future, more efficient and better adapted to the necessary changes of agriculture facing new environmental requirements, in particular in a context of climate change. TRL: 5 **2. The SUNFLO crop model** The SUNFLO model, developed by the AGROECOLOGY - Innovations - Territories (AGIR) Laboratory with the support of Terres Inovia and the Laboratory for Plant Ecophysiology under Environmental Stress (Laboratoire d'Ecophysiologie des Plantes sous Stress Environnementaux - LEPSE), makes it possible to characterise the limiting factors of an experimental environment. and to model the behaviour of a plant or area under cultivation in a wide range of agronomic conditions. TRL: 6/7
Non-scientific success stories	**A world-wide unique research community** More than 80 scientists from public and private research are involved in the SUNRISE project. The project also benefits from modern equipment and scientific expertise at the Toulouse research cluster. We have the latest generation sequencers (PacBio RS II and Illumina NovaSeq) at the Génome & Transcriptome platform of the Génopole de Toulouse, the National Plant Genomic Resource Centre, which centralises and promotes plant genomic resources of interest to the international scientific community. We also benefit from the bioinformatics platforms of the Plants-Microorganisms Interactions Laboratory (Laboratoire des Interactions Plantes-Microorganismes - LIPM) and the Toulouse Genopole, which provides state-of-the-art computing and bioinformatics resources for processing genome data. The phenotyping platforms nearby use drones and the "Phenomobile" that allow more precise, more frequent and quicker analyses of the characteristics of sunflowers under controlled conditions and in the field.

Partnerships and transfers

Role and importance of the public-private partnership in the project	The Occitanie region, the leading sunflower producing region in France, brings together the world's leading seed companies. The majority of global seed companies working in the sunflower sector have their R&D centres in the Toulouse area. Toulouse brings together a public-private research initiative working on the sunflower, with a European and global influence.
External collaborations on results at the national and international levels	10 projects: - The projects of Promosol - MilVarSunRes, HeliaDiv 1 and 2, ResOrobanche, HeliaSen - all exploit and deepen the results

	obtained by SUNRISE
	- Projects of the International Consortium for Sunflower Genomic Resources (ICSG) and Helior, in collaboration with the University of British Columbia (Canada) and the University of Georgia, Athens (USA), the MIGAL Institute (Israel), KWS, BASF, Pioneer, Advanta, and Nuseeds
	- The Helia3D project with the LAAS (CNRS Toulouse) studying methods of phenotyping from images of individual plants, and the Phenome project for phenotyping methods based on images of field plots acquired with drones or the "Phenomobile" with the UE at Auzeville and UMR, EMMA and INRA Avignon
	- Collaboration with INTA (Argentina) on leaf senescence
Most significant collaborations showing the added value of project results	1. Collaboration with the International Consortium for Sunflower Genomic Resources (ICSG) with the Universities of British Columbia Vancouver (Prof. Loren Rieseberg), the University of Georgia, Athens (Prof. John Burke) and the MIGAL Institute, Israel (Dr. Sariel Hubner). This collaboration made it possible to gather the necessary data for the assembly of the sunflower reference genome. It is continuing for additional sequencing of other cultivated sunflower genotypes and wild species.
	2. The project to develop a method for the 3D reconstruction of sunflower plants from 2D images in association with the LAAS has made progress in the use of data from the Heliaphen phenotyping platform.
	3. The collaboration with the Phenome project has allowed development of the phenotyping methods using drone and Phenomobile v2 images, to characterise the population and the development of the leaf surface and thereby senescence.
Types of results transferred for use outside the project	Results on the reference genome
External partners having benefited from the results of the project	Pioneer (USA), KWS (DEU), Advanta (USA), Nuseeds (USA), UBC Vancouver (CAN), UGA Athens (USA), MIGAL (ISR), LAAS (FRA), INTA (ARG), UE Auzeville (FRA), UMR INRA EMMAH (FRA)

Economic benefits/impacts

Current and future impacts of the project for the sector concerned and for French agriculture	- Accelerated selection of sunflower varieties: aid in the development of markers for regions of interest (genome sequence)
	- Development of genomic selection methods for sunflower and hybrids
	- Provision of high-throughput genotyping tools
	- Development of varietal characterisation methods for tolerance to abiotic stress: drought, cold and nutrient stress
	- Identification of genes of interest for the development of varieties with new fatty acid profiles
	- Evaluation of the variety registration system
Impact of the project on the positioning of the scientific	The SUNRISE project has enabled the French community to take a central place at the international level by enabling collaborations

community at the international level	with the various stakeholders in sunflower research - the Canadian, American and Argentinian labs. In addition, the organisation of the International Symposium "Sunflower and Climate Change," which took place in Toulouse in February 2018 within the framework of the SUNRISE project, brought together the entire international scientific community working on sunflower genetics.
Economic benefits for the project partners (at term)	It is too early to put numbers on the economic benefits for the private partners. It should become easier in the near future

Publications

Number of publications in peer-reviewed journals	- 20 - 10/20 expected end 2019

Themes of publications expected end 2019	- Method for phenotyping
	  o by 3D reconstruction of individual plants from images
	  o captured by an image analysis drone and the "Phenomobile" for the study of senescence and population distribution
	- Identification of molecular processes involved in
	  o the tolerance of yield to water stress
	  o the tolerance of yield to cold
	  o nitrogen absorption and yield
	  o heterosis
	- Identification of a metabolic biomarker for predicting drought tolerance
	- Epigenomic regulation in the response to water stress
	- Molecular processes involved in the tolerance of germination to water stress
	- Competitiveness factors of the registration system
	- Genomic prediction of tolerance to drought and different abiotic stresses
	Innovative selection method: "Breeding by design" combining genomic prediction and crop models

Themes of publications expected 2 years after the end of the project	Compared genomic analyses Properties of QTL introgression inside each partner's elite lines Methods to phenotype and genetic control of cold resistance
Notable publications	1. 2017 The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. Badouin, H., Gouzy, J., Grassa, C.J., Murat, F., Staton, S.E., Cottret, L., Lelandais-Brière, C., Owens, G., Carrère, S., Mayjonade, B., Legrand, L., Gill, N., Kane, N.C., Bowers, J.E., Hubner, S., Bellec, A., Bérard, A., Bergès, H., Blanchet, N., Boniface, M.-C., Brunel, D., Catrice, O., Chaidir, N., Claudel, C., Donnadieu, C., Faraut, T., Fievet, G., Helmstetter, N., King, M., Knapp, S.J., Lai, Z., Le Paslier, M.-C., Lippi, Y., Lorenzon, L., Jennifer Mandel, Marage, G., Marchand, G., Marquand, E., Bret-Mestries, E., Morien, E., Nambeesan, S., Nguyen, T., Pégot-Espagnet, P., Pouilly, N., Raftis, F., Sallet, E., Schiex, T., Thomas, J., Vandecasteele, C., Varès, D., Vear, F., Vautrin, S., Crespi, M., Mangin, B., Burke,

	J.M., Salse, J., Muños, S., Vincourt, P., Rieseberg, L.H., Langlade, NB. Nature in press. doi:10.1038/nature22380 (link)
	2. 2017 Genomic Prediction of Sunflower Hybrids Oil Content. B. Mangin, F. Bonnafous, N. Blanchet, M.-C. Boniface, E. Bret-Mestries, S. Carrère, L. Cottret, L. Legrand, G. Marage, P. Pegot-Espagnet, S. Muños, N. Pouilly, F. Vear, P. Vincourt, N. Langlade Front. Plant Sci. | doi: 10.3389 (link) https://doi.org/10.1016/j.jclepro.2017.11.189 2017 Eco-innovation in Plant Breeding: Insights from the Sunflower Industry. D. Galiano, M.-B. Magrini, C. Tardy, P. Triboulet. Journal of Cleaner Production
Notable publication coming soon	Heliaphen, an outdoor high-throughput phenotyping platform designed to integrate genetics and crop modeling. F. Gosseau, N. Blanchet, D. Varès, P. Burger, D. Campergue, C. Colombet, L. Gody, J.-F. Liévin, B. Mangin, G. Tison, P. Vincourt, P. Casadebaig, N. Langlade. Submitted to Frontiers in Plant Science

Communications

Training organised during the project	- Training day about AXIOM genotyping chips April 10 2015 - Workshop on the R package mixOmics from September 12 to 14 2016 - Training day on the genome Browser on July 13th 2017 - Training on SUNFLO and Genomic Selection - Every year : a visit from the ADAM master (Toulouse) on the Heliaphen platform - The ENSAT students took part in the Symposium Sunflower and Climate Change (February 5th and 6th 2018) with talks and posters
Number of scientific posters	15
Number of oral communications at scientific conferences	30
Number of symposia (French and international) organised	- 1 opening meeting in 2013 - 6 annual meetings from 2012 to 2017 - French Sunflower Exchange Day "*Journée d'échanges Tournesol*" 28 and 29 June 2016 - 1 international symposium organised by SUNRISE "International Symposium on Sunflower and Climate Change" on 5 and 6 February 2018
Newsletters and public communications	- An internal newsletter "SunNews" 11 editions - One external newsletter (French and English): 4 editions
Other communication tools	- Video of the Heliaphen platform: http://www.sunrise-project.fr/resultats/heliaphen-plateforme-de-phenotypage - Video of the Phenomobile - Leaflet presenting the project (link) - Brochure and computer graphics on germination work (link) - Infographic on decryption of the sunflower genome (link) - Twitter account
Notable communication actions	1. Press conference and press release on the sunflower reference genome (link to press release) and an associated information

	graphic ([link to graphic](link)) 2. Video of the Heliaphen platform: http://www.sunrise-project.fr/resultats/heliaphen-plateforme-de-phenotypage 3. [Production of sunflower oil bottles as premium goodies](link)

List of project's public and private partners

A3i • Addiplast •
Agri-Obtentions • Agrocampus Ouest • Armines
• Arvalis Institut du Végétal • Axereal • BASF France SAS •
Biogemma • Caussade Semences • Ciments Calcia • Communauté
d'Agglomération Marne et Gondoire • Cosucra Groupe Warcoing • EURALIS
Semences • Eurosorgho • Faurecia • Florimond Desprez • Germicopa • GEVES
• Grand Paris Seine Ouest • Innolea • INRA Transfert • IRSTEA • ITB • KWS France
• Limagrain Europe • LIMOS (UCA) • MAS Seeds • Naskeo • Novozymes Biologicals FR
• Pépinières et roseraies Georges Delbard • Phytorestore • PSA Peugeot Citroën • RAGT 2n •
Roquette Frères • SATT Grand Est • SECOBRA Recherches • SOLTIS • Syngenta Seeds • Terres Inovia •
Terres Univia • UE DIASCOPE (INRA) • UE GAFL (INRA) • UMR AGAP (Cirad, INRA, Montpellier SupAgro,
MUSE) • UMR AGIR (INRA, ENSAT) • UMR Agroécologie (AgroSup Dijon, CNRS, INRA, Université
de Bourgogne) • UMR Agronomie (INRA, AgroParisTech) • UMR BFP (INRA, Université de Bordeaux) •
UMR BIOGER (INRA, AgroParisTech) • UMR ECOSYS (INRA, AgroParisTech) • UMR EMMAH (INRA, Université
d'Avignon) • UMR EVA (INRA, Université Basse Normandie) • UMR GAEL (INRA, UPMF) • UMR GDEC
(INRA, UCA) • UMR GQE (INRA, UPS, CNRS, AgroParisTech) • UMR GV (CNRS, INRA, Université Sud) •
UMR IEES (UPMC, CNRS, INRA, IRD, Université Paris-Diderot, UPEC) • UMR IGEPP (INRA, Agrocampus-Ouest,
Université Rennes 1) • UMR IJPB (INRA, AgroParisTech) • UMR IPS2 (CNRS, INRA, Université Paris Sud) •
UMR IRHS (INRA, AgroCampus Ouest, Université d'Angers) • UMR IRISA (CNRAS, Université Rennes 1)
• UMR LEPSE (INRA, Montpellier) • UMR LIPM (CNRS, INRA) • UMR LSTM (Cirad, INRA, IRD, Montpellier
SupAgro, UM2) • UMR MIA-J (INRA) • UMR MIA-P (INRA, AgroParisTech) • UMR MISTEA (INRA,
Montpellier SupAgro, MUSE) • UMR RDP (INRA, ENS Lyon, CNRS, Université Lyon 1) • UMR SADAPT
(INRA, AgroParisTech) • UMR SADV (INRA, Université Lille 1) • Unisigma, Université d'Angers •
Université de Lille • Université de Picardie Jules Vernes • Université Toulouse 1 (LEREPS)
• UPR BIA (INRA) • UPR CNRGV (INRA) • UR AgroImpact (INRA) • UR LBE (INRA)
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