

Preparatory action on EU plant and animal genetic resources

BREEDWHEAT

Overview

Breedwheat is a nine-year French research project that combines genetics, genomics, and ecophysiology with high-throughput phenotyping and genotyping to perform association studies and identify markers and candidate genes for yield and quality traits under abiotic and biotic stress to support breeding for economically and environmentally sustainable wheat varieties.

1. Objectives

Breedwheat aims at increasing the value of the INRA wheat genetic resource collection by state of the art characterisation, both genotypically and phenotypically, and developing pre-breeding material that private companies can subsequently breed into elite varieties, thus improving the sustainability and competitiveness of French agriculture. To obtain insight into this project, we had interviews at INRA Clermont-Ferrand-Theix with the following members of Breedwheat: Jacques Le Gouis (Coordinator) & Emmanuelle Lagendijk (project manager) (Fig. 1); Etienne Paux (WP1 genotyping leader); Vincent Allard (involved in phenotyping (platform) in WP2); Francois Balfourier (involved in genetic resources and core collection work in WP3); and Gilles Charmet (WP4 pre-breeding leader). In addition, we had brief discussions with: Grégoire Berthe (Céréales Vallée, communication manager, WP6 dissemination leader) and Alain Murigneux (Limagrain, private breeding company, WP3 leader).

2. Description of the case

Breedwheat will run from 2011 to 2019, with a total budget of 34 million EUR, from the Investments for the Future programme of the Research National Agency (ANR), FranceAgrimer and the French Fund to support Plant Breeding (FSOV). It has a total of 26 participants, namely 14 public research institutes (INRA and GEVES), 1 technical institute (Arvalis), 1 competitiveness cluster (Céréales Vallée) and 10 companies.

Genetic resources

First, a core collection was selected from the accessions in the INRA genebank, consisting of 4,600 lines from all over the world in the INRA genebank. These were phenotyped,

particularly for adaptation traits, in a joined effort of INRA and five breeding companies. Subsequently, a subsample of 500 lines was selected, based on diversity (geographical and temporal, i.e. by variety registration year) and adaptability, and traits such as heading dates and plant height. These 500 lines were genotyped using 423,385 SNPs (the 420k Axiom array developed in WP1) in order to be able to perform association studies (WP2).

Phenotyping

The aim is to characterize 48,000 plots at 15 different locations for traits, such as yield and grain protein quality, as well as abiotic (heat and drought) and biotic (fungal diseases) stress tolerance. More sophisticated high-throughput phenotyping is performed using phenotyping platforms that have been developed in the separately funded Phenome project by a French network: LemnaTec controlled systems at two sites, and field platforms with limited environmental controls at three sites and with environmental control using rainout shelters at two sites. One of the latter sites is at INRA Clermont-Ferrand with movable rainout shelters (30 x 30 m) that can impose drought stress and controlled irrigation on the field trial (Fig. 2). Sensors measure all sorts of environmental parameters and phenotyping is done using a so-called phenomobile with cameras. All equipment is wirelessly connected to a data centre near the fields (Fig. 2).

Genotyping

For genotyping, SNPs (Single Nucleotide Polymorphisms) were developed based on 80 lines from the basic diversity genebank core collection. Using an array of 423,385 of these SNPs, the Breedwheat core collection of 4,600 lines was genotyped. In other WPs, the genotyping of lines for genomic selection, elite lines, etc. has been performed, adding up in total to 8,000 lines. Another part of the work is devoted to sequencing individual chromosomes and analysing them for structural variations, such as (gene) copy number variations (CNV), by re-sequencing other lines.

Pre-breeding

As pre-breeding activities a NAM (nested association mapping) population from a set of common parents is used in Breedwheat. Furthermore, private partners each make two advanced backcross populations for adaptability traits, such as abiotic stress, drought and heat, to a total of 9-10 populations. To genotype these populations, 35,189 SNPs have been used out of the set of 423,385. In addition, innovative breeding strategies are being developed, such as genomic selection.

Analysis

3. Funding and support

There is no funding specifically targeted at the genebank collection. Conservation management is paid from research projects, for which Breedwheat is presently an important

source. Though permanent funding for collection management could be more stable, the advantage of research funding is that it enhances the quality of the conservation work and improves data on the accessions using modern sophisticated methods such as genomics, which leads to more insight in the genetic structure of the collection.

4. Positioning at local or regional level

The project entails pre-competitive research at a national level very early in the supply chain, i.e. before the breeding of varieties which will be cultivated by commercial farmers at the start of the chain and distributed to consumers. In the second phase, socio-economic value of the innovative breeding methods will be assessed. Partners are from various regions in France, and trial fields are also located across the country.

5. Partnerships and networking

Breedwheat takes advantage of the separately ANR-funded Phenome project (cf. section 2, Phenotyping). There are also interactions with several other French projects on wheat, such as ANR-NewNAM on NAM populations (cf. section 2, Pre-breeding). Internationally, there are many interactions within the EU, for instance with a comparable programme in the UK, WISP (2 x 5 years funding). Most interactions are through EU-funded research projects, e.g. previously FP6 Healthgrain and FP7 Triticeae. Presently, INRA is involved in FP7 Adaptawheat, co-ordinated by the John Innes Centre, which will end this year, and coordinates FP7 Whealbi which started in 2014, and is also making a large effort in developing genomics (expressed sequences), in this case for both wheat and barley (500 lines each), and in developing low input/resilient varieties and innovative cropping systems. The core collection of wheat in Whealbi is not identical to the Breedwheat core collection, but important ones for NAM populations and those used for SNP discovery are included in both collections.

Worldwide, INRA carries out a significant part of the sequencing effort in the International Wheat genome sequencing consortium (IWGSC, two chromosomes, and more are being planned). There are discussions about a phenotyping platform network with Germany and also possibly Australia. Other collaborations are with CIMMYT, ICARDA and the recent Wheat Initiative supported by the G20.

6. Communication

The project will have the normal output of research projects: scientific publications, presentations at conferences, workshops and project meetings. In addition, special attention is paid to dissemination to a wider audience, including farmers and consumers. There is a dedicated WP6 for this, led by Céréales Vallée. A Breedwheat website¹, a brochure, a poster and a Powerpoint presentation were created. Furthermore, regular newsletters and booklets for professionals and stakeholders address specific topics, such as high-throughput genotyping and breeding for adaptation to abiotic and biotic stresses. At the opening of the phenotyping platform, journalists will be invited and media interest will also come from the

¹ <http://www.breedwheat.fr>

work on abiotic stress with relevance to the effects of climate change on crops. In addition, training courses and technology transfer are part of the dissemination programme.

7. Outputs and added value

The extended characterisation of genebank accessions and detailed structural knowledge of variation in the wheat genome help breeders in making choices regarding which material to include, and how to use it in their breeding programmes. By filling this gap consisting of knowledge and tools between collections and breeders, both the value of the genebank collection and the innovation strength of breeding companies are increased, in turn improving the competitiveness of French agriculture. In the second phase of the project, pre-breeding should lead to promising material to develop varieties adapted to low input cultivation or showing resilience to harsher growth conditions as a consequence of climate change. Additional added value can come from results which are of interest to a wider scientific public: for instance, a population-genetic analysis of worldwide diversity in wheat showing regional differences and the routes of dispersal across the world from the Fertile Crescent in historical times, or structural variation in wheat chromosomes being useful for research on evolution, domestication and selection effects.

There are bottlenecks in genotyping data management. The enormous amount of marker data generated are too great for the bio-computing scientists and pre-breeders in Breedwheat to fully analyse. Furthermore, the data used by companies will depend on their capacity to integrate such large amounts of data, which is more practicable for bigger companies. A bigger problem is how phenotyping can keep up with the large-scale genotyping, as even the 9-10 advanced mapping populations (comprising about 7,000 progeny plants) being produced will already be difficult to assess on the phenotyping platforms in the coming five years. The main challenge in developing the phenotyping platform was its large size. Dedicated sensor systems were developed by INRA technicians, also because this proved more cost-efficient than buying from specialised companies.

8. Sustainability

In order to ascertain the proper development of this long-running project, a management structure was set up according to a consortium agreement. Project manager Emmanuelle Lagendijk is with the INRA subsidiary INRA Transfert, where she is mainly managing EU projects but also large French projects. She is devoting 40-50% of her time to Breedwheat. For coordinator Jacques Le Gouis, it is 20-25% of his time. There is an executive committee meeting twice a year and there are larger assemblies, i.e. annual 2-3 day meetings with 90-100 people discussing scientific results and a general assembly discussing strategy. There are WP meetings once or twice a year. Regarding administrative burdens, reporting is simpler than with EU projects, with different formats: a certified financial report and a 10-page annual report on the activities and milestones.

Projects such as Breedwheat were set up in France for maize, and later on also for pea, oilseed rape and sugar beet. The coordinators meet once a year to exchange data and experiences, e.g. on genomic selection. Pre-existing (informal) networks comprising companies and research institutes discussing priorities for joint research have been very

important in laying the foundations for applying for such long-term projects with a strong funding basis encompassing a whole chain, from resources to breeding. So as to draw up a consortium agreement, thorough discussions were held on the pre-competitive structure of the pre-breeding activities and on arrangements for intellectual property and communication. Before Breedwheat, there already was an informal research network comprising INRA and breeding companies (associated in UFS, Union Française des Semenciers) around the genebank, and there was smaller public-private cooperation, supported by the investment for the future network Génoplante-Valor SAS / GIS Biotechnologies Vertes. Breedwheat was more complex with 26 participants, and the experience gained in organising such a project could be used in applying for similar projects in the future. Such networking between companies and research organisations could also be promoted at EU level.

9. Upscaling and out-scaling

There are already discussions about new calls with this type of funding for the period starting in 2020, but these may be more applied and coordinated by private organisations, which could be a group of companies. There are existing structures for this in France.

The duplication of the project should be feasible. In the UK, a comparable BBSRC project is already running, named WISP. In WISP, only public partners receive funding. USA and Canada have similar arrangements. In Breedwheat, the companies also receive funding (25%). Breedwheat could not work with foreign companies (their headquarters need to be in France), but cooperation with foreign companies exist at INRA. In the UK, mostly the same companies are active in wheat as in France, in Germany this is slightly different. With the examples of the Breedwheat and maize projects, projects on other crops were easier to set up in France as there were already examples of consortium agreements. Important preconditions are good management structure and IP (intellectual property) agreements. INRA Transfert is helpful in the practical management of large projects. Problems could arise from different outlooks of small and large companies. This was addressed by having all companies carry out the same, similarly sized tasks with similar levels of funding, with a focus on pre-breeding. Collaboration is satisfactory as there was already a well-developed “wheat community”.

The long-term character of the work makes Breedwheat an attractive partner in international contacts. Thus, the long length of the project itself makes it more valuable. A drawback of long-term projects is that things may evolve in time, so one needs an adaptable structure. For instance, developments in sequencing and marker arrays are so fast that goals will need to be adapted along the way. Other aspects, such as the type and number of mapping populations, are carried out as foreseen.

Conclusions

STRENGTHS	WEAKNESSES
<p>Long-term research project increasing the value of genetic resources for breeding by generating genotypic and phenotypic characterisations and developing tools;</p> <p>Additional value of producing fundamental knowledge on genomics, evolution, domestication and selection.</p>	<p>Phenotyping efficiency currently lags behind that of genotyping as the latter has become high-throughput at an unprecedented rate in recent years;</p> <p>A long-term project implies a need for flexibility as developments in science and breeding may easily change over such period of time.</p>
OPPORTUNITIES	THREATS
<p>Strengthening strategic networks between research institutes and breeding companies for attaining long-term sustainability goals;</p> <p>A long-term project is an attractive partner for international collaboration, thus increasing its output.</p>	<p>To let such a complex combination of research institutes and private companies work together, good preparatory discussions are necessary taking into account research priorities and IP issues.</p>

Strong points are the large increase in knowledge at both the genotypic and phenotypic level enabled by the long-term funding, significantly improving the value of wheat genetic resources at the INRA genebank for breeding and science. Strong funding is also necessary because phenotyping lags behind in terms of efficiency compared to high-throughput genotyping to such an extent that the latter even generates far more data than can be analysed within the network of Breedwheat. Setting up such large-scale projects combining research institutes and the private industry calls for an extensive preparatory phase thoroughly discussing terms regarding the contents of the research and IP issues, for which existing networks and discussion platforms will be helpful. This offers advantages as well as disadvantages: the network created could generate added value in the future as well, but it could also be difficult to set it up from scratch when there are many different interests involved. With Breedwheat, there was already a strong “wheat research community” in France.

Figure 1. Breedwheat coordinator, Jacques le Gouis and project manager, Emmanuelle Lagendijk at INRA Clermont-Ferrand-Theix.



Figure 2. Phenotyping platform at INRA Clermont-Ferrand-Theix: movable rainout shelters and control centre.



Annex 1 – List of interviewees

- Jacques Le Gouis (Coordinator) & Emmanuelle Lagendijk (project manager)
- Etienne Paux (WP1 genotyping leader)
- Vincent Allard (involved in phenotyping (platform) in WP2)
- Francois Balfourier (involved in genetic resources and core collection work in WP3)
- Gilles Charmet (WP4 pre-breeding leader)

In addition, we had brief discussions with:

- Grégoire Berthe (Céréales Vallée, communication manager, WP6 dissemination leader)
- Alain Murigneux (Limagrain, private breeding company, WP3 leader)

Annex 2 – List of references

Selection of recent scientific publications by interviewees:

Bogard M, Allard V, Martre P, Heumez E, Snape JW, Orford S, Griffiths S, Gaju O, Foulkes J, Le Gouis J (2013) Identifying wheat genomic regions for improving grain protein concentration independently of grain yield using multiple inter-related populations. *Molecular Breeding* 31:587-599

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