



## **BreedWheat:**

### **Mid-term achievements of a French project open to the international wheat community**

**After four years, the French Investment for the future BreedWheat (BW) project is well on track. The 27-partners collaborative project has produced more than two billion genotyping data points, phenotyped around 70 000 experimental plots for agronomic traits and established unique resources such as a panel of 4 600 accessions representing the worldwide genetic diversity. At mid-term, the BW consortium wants to present some of its achievements and how they can be accessed by the wheat community.**

#### **Unique data and resources to improve wheat varieties have been generated**

##### **BW genotyping array, SNP and sequence data**

Among the main scientific results, BW has designed an Affymetrix Axiom genotyping array containing more than 420 000 SNP markers (single nucleotide polymorphisms) and genotyped about 7 800 wheat accessions at INRA-GDEC Gentyane platform (<http://gentyane.clermont.inra.fr/>). For the whole community to benefit from BreedWheat results, a large part of this array representing 280 000 SNPs is made available to third parties for both research and breeding purposes. A genetic map comprising more than 307 000 SNPs has been constructed, one of the highest density genetic map for wheat so far. A chromosome 1B sequence has been produced and is currently being used to improve the whole-genome reference sequence developed by the International Wheat Genome Sequencing Consortium (IWGSC).

##### **Modelling, transcriptomic analysis and phenotyping**

A Carbon-Nitrogen Wheat ecophysiological model able to simulate the post-flowering period was completed and evaluated against experimental data (Barillot *et al.*, 2016a ; Barillot *et al.*, 2016b). The software is available on the platform SourceSup upon request to the authors. A platform for regulatory gene network inference, RulNet (<http://rulnet.isima.fr/>), has been developed (Vincent *et al.*, 2015). A number of proteins involved in the regulation/ control of protein synthesis in the grain and some regulatory mechanisms have been revealed (Bancel *et al.*, 2015 ; Bonnot *et al.*, 2015). Data from 27 experiments conducted on more than 200 varieties related to tolerance to nitrogen deficiency, drought and diseases, mainly in field conditions, have been analyzed and adjusted for Genome Wide Association Studies (GWAS).

##### **Exploitation of natural genetic variability**

A "diversity panel" of 4 600 accessions representing the worldwide diversity has been selected among the 11 000 wheat accessions available at the INRA-GDEC small grain cereals Biological Resources Centre (<http://www.clermont.inra.fr/umr1095/>). This panel has been genotyped and phenotyped. The list of these 4 600 accessions and the phenotyping data generated are today available to the scientific community. A new "association panel" of 500 lines has been selected from the "diversity panel" and seeds are currently being multiplied. Nine recombinant populations are being generated with the aim of introducing genetic diversity into French elite material. These populations will be shared between all partners.

##### **Genomic selection**

An R-based pipeline, called BWGS (BW Genomic Selection), has been designed, offering various combinations of methods for dimension reduction, missing data imputation and genomic prediction (Charmet, IWIW November 2015, EUCARPIA general congress-Zurich August 2016). Its ability to accurately predict breeding values has been validated on a set of historical breeding data. Ideotypes have been defined by assembling adaptive traits for various French conditions and experiments have been defined to evaluate 25 varieties close to the desired ideotypes.

### A unique web portal to access the data

The BW Information System (BWIS) has been developed to store and share the huge amount of data generated within the BW project. Based on existing resources developed by INRA-URGI and Biogemma, the BWIS has been improved to meet user needs (such as breeders), especially in the genotyping and phenotyping database architecture. So far, both BW genotyping and phenotyping data were integrated. The BWIS is also included in the URGI wheat portal (<https://wheat-urg.versailles.inra.fr/>) which is the worldwide reference for wheat data storage and sharing.

### A capacity to bring together different countries working on the same target

The first BW international conference, the International Wheat Innovation Workshop (IWIW), was held in Clermont-Ferrand (France) on 16<sup>th</sup> and 17<sup>th</sup> of November 2015. More than 170 researchers from the public and private sectors attended this event. The UK WISP project, the German ProWeizen alliance, the international research programme WHEAT CRP as well as the IWGSC and the Wheat Initiative participated to the organization. This meeting enabled to inform the scientific and seed communities on the main progress in genetics, genomics, ecophysiology and on wheat adaptation to major environmental constraints, and to foster discussions between teams working on wheat in major national projects. The detailed programme, pictures and presentations made are available on the website specifically created for that event: <https://colloque.inra.fr/iwiw>

#### About BreedWheat:

BreedWheat aims at strengthening the competitiveness of the French wheat breeding sector as well as to address the societal demand for sustainability, quality, and safety in agricultural production.

This pre-competitive project developed over a period of nine years, for a total investment of 34 million Euros by 27 partners, receives a 9M€ grant from the French Investment for the future program (ANR-10-BTBR-03) managed by the Research National Agency (ANR). It brings together 15 public research laboratories, 10 private companies, 1 technical institute, 1 competitiveness cluster and 1 company specialized in project management and technology transfer.

In an unprecedented effort, BreedWheat combines genetics, genomics, and ecophysiology analyses 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. Moreover, the BreedWheat project characterizes and taps unexploited genetic resources to expand the diversity of the elite germplasm. Finally, new breeding methods are developed and evaluated for their socio-economic impact. A robust bioinformatics platform enabling efficient association analyses and breeder friendly access to the data is also established.



**For more information about the project and the accessibility to its results**, please contact the project coordinator:  
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