



# **REPORT OF THE ECPGR WORKSHOP FOR THE ESTABLISHMENT OF A EUROPEAN EVALUATION NETWORK (EVA) ON WHEAT AND BARLEY**

**27-28 November 2018, Berlin, Germany**

L. Maggioni



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### Cover picture

Experimental fields at IPK, Gatersleben, Germany. © L. Maggioni

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## Welcome and introductory session

Chair: F. Ordon

After a short introduction by Frank Ordon, Vice-President of the Julius Kühn-Institut (JKI) ([PPT here](#)), Eva Thörn, Chair of the ECPGR Executive Committee thanked the German Federal Ministry of Food and Agriculture (BMEL) for its contribution to the project "Organization of an ECPGR Workshop for the preparation of a European Evaluation Network (EVA) on wheat/barley and a vegetable crop". This new initiative of ECPGR is intended to increase the use of genetic resources from the European genebanks and involve the private sector.

On behalf of the Federal Office for Agriculture and Food (BLE), Imke Thormann expressed support for this initiative.

After all participants introduced themselves, the ECPGR Secretary, Lorenzo Maggioni, presented the agenda and objectives of the meeting, offering an overview of the ECPGR initiative to establish the European Evaluation Network EVA ([PPT here](#)). Participants highlighted the importance of using accessions that are part of the European Genebank Integrated System (AEGIS) and defining genotypic standards, the opportunity to coordinate with other initiatives at EU level, the presence of a large amount of already existing evaluation data and their usefulness, even though standardization of past data would not be possible.

Albrecht Serfling (JKI) presented the German programme for the evaluation of cereal genetic resources (EVA II) ([PPT here](#)). He clarified that EVA II is using JKI material, some from the International Maize and Wheat Improvement Center (CIMMYT), the Spanish core collection, material from the Leibniz Institute of Plant Genetics and Crop Plant Research, (IPK, Germany) and 50 genotypes provided by partners each year. For the selection of material, the coordinator searches literature and tries to obtain access to new interesting material. Every year in November a meeting is scheduled to decide which diseases are important, look into literature and try to find the interesting material. Accessions are multiplied at JKI. Each year, in the framework of EVA II, 200 accessions are tested in 21 different locations, representing a combination of landraces and modern material, the latter being the main focus. Randomized replications are set up with standard genotypes in all locations. The main benefit for breeders was, for example, the evaluation for stripe rust resistance before the disease struck the fields.

Michael Schmolke (BASF, Germany) commented that the main attractiveness of a similar approach is the comparability of the tests with standards, the simple, not too complex approach, with not too many entries, and the main goal being only phenotypic characterization, which is of high interest (and not so much doing genomic selection).

## Information on other initiatives

Chair: L. Maggioni

Niels Stein (IPK) presented the BRIDGE project ([PPT here](#)), focusing on genotyping by sequencing (GBS) of more than 20 000 accessions of the IPK barley collection, which is offering a better informed selection of genetic resources in pre-breeding.

Jochen Reif (IPK) presented the project "Genebank 2.0" on genomics-based exploitation of wheat genetic resources for plant breeding ([PPT here](#)). The project is aiming to leverage the IPK collection to an actively deployed one in breeding and research. It is attempted to provide useful information on genebank IPK accessions by converting past evaluation data into a

bio-digital databank. The entire collection is made accessible with an effort to multiply it and each accession is fingerprinted. The collection is characterized for disease resistance and mined for valuable genes, such as for excellent pollinators and for nitrogen use efficiency.

Luigi Cattivelli (Council for Agricultural Research and Analysis of Agricultural Economics (CREA), Italy) and Roberto Tuberosa (University of Bologna), presented the tetraploid wheat collection system, as part of the “Wheat initiative” ([PPT here](#)).

The Global Tetraploid Wheat Collection (GTC) is a germplasm collection developed in the framework of the durum wheat genome sequencing, mainly focused on wild relatives (emmer), landraces and tetraploid subspecies (size: 1856 accessions).

The Global Durum Panel (GDP) is a breeding dedicated tool, mainly focused on modern varieties (size: 1056) and landraces. About 300 accessions are in common between the GDP and the GTC. Multiplication is carried out by the International Center for Agricultural Research in the Dry Areas (ICARDA) and material is now available upon request. Twenty sets were distributed this year around the world. Genotyping has been completed and population analyses are in progress. The joint analysis of the GDP and GTC based on detailed phenotyping has the potential to further speed and focus breeding activities.

## **Elements for an Evaluation Network on wheat and barley**

### **Expectations from breeders (traits, material, conditions of operation)**

A round of opinions were collected from breeders and the main points expressed are summarized below:

Albrecht Serfling (JKI, Germany)

There is interest in data about disease resistance of genotypes available from genebanks. One problem might be how to get access to enough seed of genebank materials.

Tanja Gerjets (German Federation for Plant Innovation, GFPI)

Breeders expect different things: material with description of agronomic traits and information on diseases. They would like to test material in their own conditions. It should not be a large number of accessions, but easily fit within their working framework and be suitable to the respective environmental conditions.

Klaus Oldach (KWS, Germany)

It would be useful to standardize evaluation protocols so that everyone can trust the procedures. It is also important that accessions received correspond to their description. It should be useful to know whether certain traits are novel or already exist in breeding material. Other background information about the accessions would also be helpful. In case of disease resistance, it would be important to know if this refers to single or multiple isolates.

Philipp Boeven (Limagrain, France)

The material should be adapted to specific areas. It would be useful to collect general phenotypic information, but mainly special traits, such as disease resistance or tolerance, also against insects, or evaluate traits that are not considered on a regular basis in breeding programmes. For genotyping, it is necessary to have standard protocols, otherwise it would not be possible to combine phenotypic data.

Monika Spiller (Syngenta, Germany)

It would be appreciated to test a diversity of phenotypes, but the material needs to be reliable and adaptable (for example without vernalization requirements). It would be useful to have genotypic information in addition, and to know if known genes are already present in such material. It should also be small volumes of accessions that can be manageable. Additionally, the more locations can be tested, i.e. involving as many breeders as possible, the better it would be.

Michael Schmolke (BASF)

We have been involved in similar projects in the past, investing many resources, but the results have not been what was expected. We do not necessarily need adapted material, but ideally pre-screened collections that we can then pheno-genotype and not having to deal with too many traits at the same time. It is important to pre-define the target right from the start. Regarding standardization of phenotyping protocols, we experienced that in the end they tend not to be respected and this is a problem.

Ahmed Jahoor (Nordic Seed, Denmark)

It is surprising not to see small seed companies in the meeting, but we should try to involve them. Serious problems in the Nordic countries are fusarium and septoria; drought tolerance and winter hardiness will also be upcoming issues. Collaborative pre-breeding projects using the best genotyped lines would be useful and would suggest going beyond simple screening and genome-wide association study (GWAS), thus engaging in improvement breeding. It is not possible to test fusarium in Denmark, but it is possible in Norway. We need to test where the disease pressure is present.

Roberto Tuberosa (University of Bologna, Italy)

It is important to enlarge the scope of breeding material in order to look for genes and quantitative trait loci (QTLs). Genomics is mature to help, and networking offers a very good opportunity.

Luigi Cattivelli (CREA, Italy)

We are open to collaborations with breeding companies. It will be interesting to test traits, such as simple disease resistance. The difficulty on setting up a common set to be tested all over Europe poses a practical issue. We need to pay attention to the way we organize and distribute material and data. There is an Italian interest for barley, durum and bread wheat. We need to be very careful, since material is not behaving the same way in different environments.

Points of agreement emerging from the discussion:

- Set up small scale experiments
- Focus on targeted traits (disease)
- Use adapted material
- Involve more small companies
- Need for very good organization and reliability of the network

### **Expectations from genebanks (availability of material, conditions of operation)**

A round of opinions were collected from genebank representatives and the main points expressed are summarized below:

Benedetta Margiotta (National Research Council (CNR), Italy)

The genebank conserves old materials; phenotypic data on accessions are often not available. The genebank would appreciate to receive feedback on phenotypic traits of the material. We agree on the standardization of protocols and the opportunity offered by the network. The adoption of digital object identifiers (DOIs) on accessions is also an interesting step. The genebank is interested to offer Italian accessions. By experience, landraces collected in one site and evaluated in a different location gave very different results.

Katya Uzundzhaliyeva (Institute for Plant Genetic Resources (IPGR), Bulgaria)

There is currently no link in Bulgaria between breeders and genebank material, therefore the EVA network would be useful to raise awareness. Farmers coming to ask for material usually ask for resistance to one trait. There is a need to have seeds multiplied by breeders.

Jochen Reif (IPK, Germany)

The genebank is a resource not sufficiently used in breeding and we need to activate the collection. We also wish to bring life to a federal European genebank and this network could provide valuable phenotypic data to the collection. It will be very important to think how to cluster the testing environments. If breeders invest in pre-breeding, the result can be shared. Starting with a small-scale initiative would be ok. The full collection can be phenotyped in 15-20 years.

Noam Chayut (John Innes Centre (JIC), UK)

There is a governmental breeding programme on wheat. Breeders receive already material crossed with elite genotypes and the programme is well funded. A bottleneck is that we have a lot of information that is not ending up in the right databases. There is a need to harvest data and we can offer advice in this direction. For phenotyping it is important to define what and how we measure and what we want to do with it. Standardization is a key aspect.

Beate Schierscher (Agroscope, Switzerland)

We are describing phenotypes and genotypes, but there is no breeding programme using the genebank. We have a wheat breeding programme, but the genebank is just receiving material from breeders. It is important to do networking and collaborating, we are keen to offer material to projects that could evaluate and use it.

Nils Stein (IPK, Germany)

We need multiple expertise to capture the value of the genetic diversity. Genebanks are resources for working towards a bigger picture. We need to understand much better the biology and the available diversity. At the moment we do not know how many diverse genotypes we have. We need a more visionary approach.

Stephan Weise (IPK, Germany)

The European Internet Search Catalogue (EURISCO) is prepared to become a central repository of data and work towards harmonization of both traits and methods.

It was agreed that it is necessary to define realistic, achievable goals towards cataloguing the European collections in order to understand what diversity is present in Europe and what is missing. This is achievable and a basis for moving in the future towards genes, alleles and QTLs. The breeders' perspective is important, without leaving aside the possibility for scientific advances.

## **EURISCO as central information system for data sharing (current status and options for EVA)**

Stefan Weise introduced EURISCO as a central information system for data sharing ([PPT here](#)). The catalogue provides passport and phenotypic data about plant germplasm accessions maintained in Europe. As of 2016, it is possible to also include non-standardized phenotypic data. These are currently available and searchable for ca. 70 000 accessions. The challenge is that many different standards are used to express the same traits (different trait names and different scales), and also different amounts of meta-information are provided for each experiment. Through an EVA project, it could be possible to support a better data harmonization with the adoption of better experiment description and harmonized protocols, as well as a better structuring of traits/methods/scales, also with the use of agreed ontology terms.

## **Comments and discussion towards the establishment of EVA-Wheat/Barley**

Some debate developed, discussing whether the starting point should be a common crop ontology for the database or rather agreement on how to perform collaborative phenotyping.

It was also proposed to move from screening to application and starting a pre-breeding programme. However, it was pointed out that parental selection and the use of top performing lines would be needed for pre-breeding and this is not likely to happen within a pre-competitive effort.

It was reiterated that the EVA Network should be driven by the definition of traits of interest. Clear challenges in Europe at the moment are climate change and changed fungicide patterns.

## **Towards the establishment of EVA-Wheat/Barley**

Chair: F. Ordon

The expectation was of creating an “EVA II-like network”, following a similar blueprint as that of the German evaluation network, extended to Europe. A network slightly funded by Germany during a 3-year establishing phase should then try to establish links with Horizon2020 successful proposals.

The possibility to raise funds from the breeding companies for training of PhD students was proposed.

Regarding the need to enlarge the network also to small companies from other countries, participants offered to intermediate with Austria, Czech Republic and Nordic countries (A. Jahoor), France (P. Boeven), Italy (L. Cattivelli), Hungary, Poland and Spain (L. Maggioni), and Switzerland (B. Schierscher). A synopsis of the proposal would be needed to invite newcomers.

## **Discussion: Which material could be evaluated, where, by whom – what is missing**

It was agreed to focus on both wheat and barley and to consider only material that could be circulated under Standard Material Transfer Agreement (SMTA).

In EVA II, seeds are propagated in a row and 50 g are distributed to each partner by JKI. The logistic should be determined by a trait-driven strategy. At the same time, three mega-environments (North, Central and South Europe) should be defined and for each mega-environment there should be one institution carrying out the multiplication centrally. Ideally, genebanks of every mega-environment could pre-select 200-300 accessions to be sent to the central multiplication and then a part of these could be sent to breeders. Possibly a team of breeders should decide which accessions need to be eventually evaluated.

Eventually, 500 accessions would be sufficient for gene search (such as 100 accessions \* 5 years). It is necessary to carry out genotyping on all accessions and to assign the task to one company. The use of single nucleotide polymorphism (SNPs) is the cheapest option. It would be preferable to start with single seeds.

### **Discussion: Which standards should be agreed for the evaluation – Workplan for agreement on standards**

The adoption of JKI protocols, including disease assessment sheets, was proposed, although any adopted document should be translated into English.

Other points to consider are the definition of the ontology and considering the experimental design of various private breeding companies. Coordination with the documentation requirements will be necessary.

### **Discussion: Conditions of operation – Suitability of format cooperation agreement**

Differently from other genebanks represented in the meeting, the Bulgarian genebank specified its interest to receive back multiplied material. As the breeding companies would not be available to do this, it will be a task of the multiplier institution to return multiplied seed to the Bulgarian genebank.

An embargo period for the open publication of data was considered necessary and agreed to be set at 3 years.

Concerning point 7 of the draft Cooperation Agreement (Annex C of the document "[Establishment of the European PGRFA Evaluation Network \(EVA\)](#)"), it was suggested to include the words "for breeding purposes".

### **Discussion: suitability and improvements required by the Central Information System (EURISCO)**

An Intranet platform for the EVA project will have to be prepared within the EURISCO framework, enforcing an embargo period. This would be password-protected with exclusive access for the project partners, who will be enabled to download all the data. EURISCO will perform a quality check (to be identified) and only reliable data will enter EURISCO.

A separate infrastructure for the genotypic data will have to be set up.

A website should be maintained, illustrating the work of the partners having provided evaluation data, offering visibility of the project consortium to those searching the data.

It will be critical to make sure that evaluated accessions enter EURISCO, if they are not yet included.

**Discussion: Funding requirements and opportunity to submit a request for funding for the implementation of EVA-Wheat/Barley (2019-2021) and wrap-up of decisions**

L. Maggioni

An outline of “Elements for submission of an EVA project to donors” was prepared and it is included as Annex 1.

A Workplan for next steps was agreed as follows:

1. ECPGR prepares the outline of a proposal for submission to Germany (by end of January 2019)
2. Circulation and replies before end of February 2019
3. The same outline can be sent out to other potential partners (end of February 2019)
4. Focal points contact potential partners (January-March 2019)
5. Vegetables component added by the end of March 2019
6. Submission of proposal (April 2019)
7. Reply from the donor (May 2019)
8. Letters of commitment signed (December 2018-April 2019)
9. Start of the project (September 2019)

## **Annexes**

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## **Annex 1. Elements for submission of an EVA Project to Donor**

### **Scope**

- Evaluation of disease resistance (few priority traits) on European genebank accessions (long-term systematic approach)
- Three components with specific partners: spring and winter barley, spring and winter wheat, durum wheat (only southern region)

### **Principles**

- Evaluate same relevant material in different environments (three macro-zones: north, central and south)
- Maximum 200 plots per year for every partner per crop
- Use same evaluation protocols (experiment set up; scoring methodology)
- Include phenotypic + genotypic data in public central place – EURISCO
- Use SMTA

### **Technical requirements**

- Each year, selection of traits based on agreed principles for specific crops (Task Force)
- Design of the experiment (Task Force: J. Reif, F. Ordon, S. Weise)
- In the three zones, trait- and environment-driven selection by genebanks of at least 200 accessions (30-50 seeds) per year per crop
- Acquisition, multiplication (pre-screening) by JKI, CREA and Nordic Seed and distribution of material to partners in possibly about 20 locations (or 10+10)
- Define genotyping methodology reproducible and long-term (DNA chips?) (Task Force)
- Carry out the genotyping (commercial provider)
- Agreement on evaluation protocols (ex. JKI disease assessment sheets) and data collection standards (ontologies) (Task Force)
- Special functionalities required from the documentation system (e.g. embargo of 3 years; analysis of requirements) (Task Force)
- Data analysis (S. Weise, J. Reif)

### **Administrative requirements (Project coordination)**

- Involvement of missing partners (L. Cattivelli, A. Jahoor, JKI / S. Weise)
- Conclusion of cooperation agreements
- Activating and monitoring of project operations

### **Financial requirements**

#### **To be funded**

- Task Force activity (meetings)
- Kick-off meeting + annual meetings
- Multiplication and distribution
- Genotyping
- Upgrade of EURISCO (2 years)
- Project coordination

#### **Self-funded**

- Inputs to project preparation
- Evaluation and data dispatching
- Dispatching of seed from genebanks

**Duration: 3 years**

- Year 1 (2019-20): setting up of standards, acquisition, multiplication and redistribution of material
- Year 2 (2020-21): first round of evaluation; second round of acquisition, multiplication and redistribution
- Year 3 (2021-22): second round of evaluation; third round of acquisition, multiplication and redistribution

**Table to be completed for management purposes**

	<b>Barley</b>	<b>Exaploid wheat</b>	<b>Tetraploid wheat</b>
<b>Traits</b>			
<b>Environments</b>			
<b>Interested partners</b>			
<b>Desirable partners</b>			

**Project drafting team: ECPGR (L. Maggioni); J. Reif, L. Cattivelli, A. Jahoor, F. Ordon, T. Gerjets**

**Annex 2. Acronyms and abbreviations**

AEGIS	A European Genebank Integrated System
BLE	Federal Office for Agriculture and Food, Germany
BMEL	German Federal Ministry of Food and Agriculture
CNR	National Research Council, Italy
CREA	Council for Agricultural Research and Analysis of Agricultural Economics, Italy
CIMMYT	International Maize and Wheat Improvement Center
ECPGR	European Cooperative Programme for Plant Genetic Resources
EU	European Union
EURISCO	European Internet Search Catalogue
EVA	European Evaluation Network
EVA II	National Evaluation Programme for Plant Genetic Resources (Germany)
ExCo	Executive Committee
GDP	Global Durum Panel
GFPI	German Federation for Plant Innovation, Bonn, Germany
GTC	Global Tetraploid Wheat Collection
ICARDA	International Center for Agricultural Research in the Dry Areas
IPGR	Institute for Plant Genetic Resources, Bulgaria
IPK	Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany
JIC	John Innes Centre, UK
JKI	Julius Kühn-Institute, Germany
SMTA	Standard Material Transfer Agreement

**Annex 3. Agenda****ECPGR Workshop for the establishment of a European Evaluation Network (EVA)  
on wheat and barley**

27-28 November 2018, Berlin, Germany

Venue: Julius Kühn-Institut (JKI), Königin-Luise-Straße 19, Berlin, Germany

<b>TUESDAY 27 NOVEMBER</b>		
	<b>Welcome and introductory session</b>	<b>CHAIR: F. ORDON</b>
09.00 – 09.10	Welcome by local host, ECPGR and BLE	<i>F. Ordon, E. Thörn, I. Thormann</i>
09.10 – 09.20	Introduction of participants	<i>All</i>
09.20 – 09.50	Introduction of agenda and objectives - Overview of the ECPGR initiative to establish the Evaluation Network EVA	<i>L. Maggioni</i>
09.50 – 10.00	Q&A	
10.00 – 10.20	The German programme for the evaluation of cereal genetic resources (EVAII)	<i>A. Serfling</i>
10.20 – 10.30	Q&A	
<b>10.30 – 11.00</b>	<b>TEA/COFFEE BREAK</b>	
	<b>Information on other initiatives</b>	<b>CHAIR: L. MAGGIONI</b>
11.00 – 11.20	The BRIDGE project	<i>N. Stein</i>
11.20 – 11.30	Q&A	
11.30 – 11.50	Genebank 2.0	<i>J. Reif</i>
11.50 – 12.00	Q&A	
12.00 – 12.20	The durum wheat diversity collection	<i>R. Tuberosa</i>
12.20 – 12.30	Q&A	
12.30 – 14.00	<b>LUNCH</b>	
	<b>Elements for a Wheat/Barley EVA</b>	<b>CHAIR: E. THÖRN</b>
14.00 – 14.30	Expectations from breeders (traits, material, conditions of operation)	<i>All breeders</i>
14.30 – 15.00	Expectations from genebanks (availability of material, conditions of operation)	<i>All genebanks</i>
15.00 – 15.30	EURISCO as central information system for data sharing (current status and options for EVA)	<i>S. Weise</i>
15.30 – 16.00	<b>TEA/COFFEE BREAK</b>	
16.00 – 17.00	Comments and discussion towards the establishment of EVA-Wheat/Barley	
<b>20.00</b>	<b>SOCIAL DINNER</b>	

<b>WEDNESDAY 28 NOVEMBER</b>		
	<b>Towards the establishment of EVA-Wheat/Barley</b>	<b>CHAIR: F. ORDON</b>
09.00 – 10.00	Discussion: Which material could be evaluated, where, by whom – what is missing	
10.00 – 10.30	Discussion: Which standards should be agreed for the evaluation – workplan for agreement on standards	
10.30 – 11.00	<b>TEA/COFFEE BREAK</b>	
11.00 – 11.45	Discussion: Conditions of operation – Suitability of format cooperation agreement	
11.45 – 12.30	Discussion: suitability and improvements required by the Central Information System (EURISCO)	
<b>12.30 – 14.00</b>	<b>LUNCH</b>	
14.00 – 15.00	Discussion: Funding requirements and opportunity to submit a request for funding for the implementation of EVA-Wheat/Barley (2019-2021)	
15.00 – 15.30	Discussion: Workplan for next steps	
15.30 – 16.00	Wrap-up of decisions	<i>L. Maggioni</i>
16.00	<b>END OF WORKSHOP</b>	

## Annex 4. Participants

### ECPGR Workshop for the establishment of a European Evaluation Network (EVA) on wheat and barley

27-28 November 2018, Berlin, Germany

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