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The meeting substituted for an in-person project meeting of the European Evaluation Network (EVA) on Wheat and Barley on 05-06 May 2020 in Quedlinburg/Gatersleben, Germany, and took place on 05 May 2020, 9:30 to 16:30, on MS Teams. The agenda of the meeting is attached as Appendix 1 and the list of participants as Appendix 2.

A number of preparatory documents had been made available to the project partners in advance of the meeting on MS Teams. These included presentations on ECPGR and the EVA networks, on EURISCO and its role within EVA and a presentation on EVA II, the German project which the European EVA networks are building on.

## **1. Welcome and introduction**

The EVA coordinator Sandra Goritschnig opened the meeting, reminding participants of the expected outcomes of the meeting and highlighting the available documents. She explained the functions of the virtual meeting platform used and the format of parallel discussions in breakout rooms for focused discussions among partners in the different geographic zones (Nordic, Central and Southern). Although several participants had problems accessing some of the functions, there were no major problems during the duration of the meeting.

## **2. Development of detailed project workplan**

### **2.1 Review of project proposal and new developments**

The EVA coordinator presented an update on the EVA project, reviewing the project plan and informing of an extension of the project until November 2022, granted by the German donors in December 2019. Within the framework of this extension, existing characterization and evaluation data will be collected from partners and integrated into the EURISCO database. Partners were invited to propose available datasets that might be suitable. Partners were also informed about the recently granted Horizon2020 project AGENT (Activated GENebank NeTwork), which contains a work package that allows for extending the current EVA Wheat and Barley network by providing funds for a third round of multiplications of up to 1000 accessions in 2021.

A draft workplan and timeline for the project was presented, and it was noted that multipliers had agreed to generate single seed descent (SSD) lines of the selected accessions in order to avoid population effects. The main tasks and activities involved in evaluating the wheat and barley accessions were listed and partners were invited to confirm their roles and responsibilities as well as evaluation sites for the different crops in a draft table. In order to facilitate coordination of these activities, the establishment of Task Forces for Genotyping and Phenotyping/Data collection was proposed for discussion.

ECPGR Secretary Lorenzo Maggioni provided additional background on the EVA project. He noted that the focus of the project is to generate evaluation data for accessions present in European genebanks, in public-private partnerships. In a meeting in Berlin in 2018, partners from public institutions and private companies agreed on the project plan.<sup>1</sup> After the project was granted, some partners decided that using SSD material would be preferable for successful genotyping. Already existing SSD lines were sought which could be multiplied quickly to generate

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<sup>1</sup> Maggioni L. 2019. Report of the ECPGR Workshop for the establishment of a European Evaluation Network (EVA) on wheat and barley, 27-28 November 2018, Berlin, Germany. European Cooperative Programme for Plant Genetic Resources, Rome, Italy.

material for the first round of evaluations starting in 2020. At the same time, landraces obtained from genebanks should undergo the additional step of SSD and these lines will then be multiplied in time for a second round of evaluations starting in 2021. Every batch of accessions in multiplication should consist of 200 lines per crop, of which 150 lines will be selected for evaluation.

## **2.2 Current activities in the EVA Wheat and Barley Network**

Partners who had provided existing SSD lines intended for multiplication for the first batch of evaluations as well as those involved in multiplication activities presented an update on their work.

Noam Chayut (John Innes Centre (JIC), Norwich, UK) introduced the A.E. Watkins collection available at JIC, which forms the basis of the SSD lines provided by their genebank. The A.E. Watkins collections of local wheat landraces from markets all over the world in the 1920s is an attempt at a global wheat survey and captures an overview of true landraces before they were displaced by modern varieties. JIC maintains a collection of the historic landraces as well as a collection of SSD of these landraces. The material provided within the EVA project are more advanced lines, originating from a subset of the Watkins collection which represent the existing diversity, both geographical and phenotypic. This subset was crossed to a UK elite line “Paragon” and mapping populations at F4, which are being genotyped, have been made selected for the EVA project. The selection for the three EVA geographic zones was based on geographic origin as well as phenotypic data indicating suitability for the geographic conditions (days to ear emergence, specifically). He noted that the Nordic zone especially had requested that lines of Nordic origin be preferred.

Andreas Börner (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany) summarized the selection of winter barley accessions provided by his lab. The IPK has previously sequenced their entire barley collection of ca. 22 000 lines<sup>2</sup>, from which a core collection was generated via an SSD step. This collection consists of ca.1000 barley lines (712 spring barley and 281 winter barley accessions). A subset of 204 winter barley lines covering a wide geographic origin was selected from this core collection for the EVA project and provided to JKI for multiplication. A. Börner noted that there seemed to have been a misunderstanding during the selection of spring barley, which was intended for the Nordic zone, but confirmed that the material was still available.

Jochen Reif (IPK, Gatersleben, Germany) provided background on the selection of 100 winter wheat accessions. IPK has generated SSD lines for all of their ca. 10 000 wheat accessions and has genotyped them using genotyping by sequencing (GBS), which gives good unbiased data but may not provide high enough marker density for genome-wide association mapping (GWAM) using this material. Targeted selection taking into account yellow rust resistance and genetic diversity allowed development of a core collection of 800 wheat accessions, which covers the entire diversity space and should be amenable to GWAM analysis. One hundred lines were provided to EVA partners in all zones for multiplication already, and the remaining 700 could be made available as needed.

Delfina Barabaschi (Council for Agricultural Research and Analysis of Agricultural Economics (CREA), Italy) updated on the current activities in the Southern zone, for which CREA has been

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<sup>2</sup> Milner SG, Jost M, Taketa S et al. 2019. Genebank genomics highlights the diversity of a global barley collection. *Nature Genetics* 51:319–326 (2019). <https://doi.org/10.1038/s41588-018-0266-x>

providing SSD lines and is also involved in multiplication activities for both rounds of evaluations. CREA are currently multiplying 200 accessions each of *Triticum aestivum* (provided by JIC and IPK), *T. turgidum* (provided by CREA) and *Hordeum vulgare* (provided by CREA and the Italian genebank Institute of Biosciences and Bioresources-National Research Council (IBBR-CNR)). The SSD lines for durum wheat have been generated within a larger wheat initiative and were developed by the International Center for Agricultural Research in the Dry Areas (ICARDA) in Lebanon in 2015. All barley lines are from Italy and were not generated using a classical SSD protocol, however, CREA are confident that they are sufficiently pure. For the second round of SSD and multiplication, 200 accessions each of *T. aestivum*, *T. turgidum* and *H. vulgare* have been received from genebanks in Bulgaria, Italy, Portugal, Spain and Switzerland and represent a wide range of geographical origins. These were planted in December 2019 and a single plant of each accession will be harvested in July 2020 and used for multiplication in winter 2020.

Albrecht Serfling (Julius Kühn-Institute (JKI), Quedlinburg, Germany) presented a review of the EVA II project, which has been successfully operating on a national level in Germany with partners from the private and public sector. He outlined the management of the national programme and noted the parallels to the European EVA Networks for which it serves as a blueprint. He highlighted the importance of using standard protocols, some of which he has already shared with the project partners and should be used as templates for the protocols that still need to be developed for EVA.

He then reported on JKI activities in the multiplication of material. JKI are currently multiplying SSD lines received from JIC (148 lines of spring wheat) and IPK (102 lines of winter wheat, 204 lines of winter barley), which are currently in the field. Material received from genebanks in Austria, Bulgaria, Czechia, Romania, Slovakia and Switzerland has been used to generate SSD lines in the greenhouse and will be multiplied in the field in 2020. Although the numbers of accessions do not reach 200 for all crop types at the moment, it was confirmed that for the trials starting in the fall of 2020 enough material would be available. He noted that there were few accessions of spring barley, but indicated that the focus could initially be on evaluating winter barley, for which there are sufficient lines in multiplication. He invited genebanks to provide additional relevant information on the provided material. Spring barley should be sourced from IPK.

Jihad Orabi (Nordic Seed, Denmark) reported on their multiplication activities for the Nordic zone. He highlighted the challenges for cultivation of wheat and barley in the Nordic zone and noted that breeders therefore wanted to focus on accessions suitable for this climate. They received ca. 200 accessions each of spring and winter wheat and spring barley from NordGen and genebanks in Estonia, Latvia and Lithuania, which had been developed into SSD lines in the greenhouse. Spring wheat and spring barley are currently being multiplied in the field in two locations in Denmark and will be available for evaluations starting in spring 2021. Winter wheat will be sown for multiplication in the fall of 2020. Nordic seed had also received ca. 130 spring wheat lines from JIC and 104 winter wheat lines from IPK, but noted that the quantity was too little to grow them directly in the fields. It was not clear to Nordic Seed that these lines had already undergone SSD, highlighting the need to ensure more effective communication between providers and users of the material, and to share as much information about the provided material as possible. No spring barley has so far been provided to Nordic Seed for multiplication for a second batch of evaluations.

### **3. Discussions on workplan**

Ahmed Jahoor (Nordic Seed, Denmark) opened the Q&A with a comment on the origins of the material for evaluation, noting that in previous discussions it had been agreed to focus on accessions obtained within the geographic regions and that it seemed that the project plan has significantly changed since the meeting in Berlin 2018. He also inquired about the exact type of material provided by JIC, and whether evaluation of mapping populations would yield useful data as the parents of these F4 mapping lines would need to be included. Noam Chayut (JIC) clarified that the provided lines are not actual mapping populations, but lines selected from within the mapping populations predicted to be compatible with the growing conditions in each geographic zone based on flowering times and other agronomic traits which have been previously assessed and are not the focus of the EVA project. The parental lines of said populations are being sequenced at high resolution. This information would allow to identify single-nucleotide polymorphisms (SNPs) for markers based on the phenotypic information generated in EVA and the genotyping planned for these lines.

A. Jahoor further asked about genotyping analysis, and compatibility between GBS data and SNP arrays. Jochen Reif clarified that IPK has an open publication policy which means that the data generated by GBS, including the sequences surrounding identified SNPs would be available for marker development by all partners.

One partner inquired about the standard protocols for trait evaluation provided by JKI. Albrecht Serfling clarified that those he shared were focusing on winter wheat and noted that protocols were available also for spring barley and spring wheat and for all diseases evaluated within the EVA II project. Standard cultivars included within the protocols could be modified to suit the geographic region. Additional protocols will be provided in the project space.

#### **3.1 Agreement on genotyping protocol and data analysis pipeline**

Delfina Barabaschi (CREA) presented the proposed genotyping strategy for the project. The suggestion is to genotype all accessions from the two batches of evaluation at the same time in autumn 2021, to reduce costs and improve comparability. For that, the multipliers should select during harvest 150 accessions of each of the crop types they are multiplying and that would be distributed to evaluators and be evaluated in the coming season. Thus, multipliers from each zone should sample 10 seeds from 450 accessions for genotyping in two years (in summer 2020 from the first batch and in summer 2021 from the second batch). The resulting 900 lines would then be grown in a growth chamber in autumn 2021 and young leaves sampled for DNA extraction (either from a single plant or from a pool of five plants per accession).

Use of a common code for all accessions within the EVA project was proposed, to facilitate processing and data management. The proposed code would consist of letters for the geographical zone, taxon and consecutive numbering of the ca. 2700 accessions expected to be processed within the project.

It was noted that for a number of accessions within the project (especially existing SSD lines) genotyping data were already available and a survey should be conducted to identify and link these existing data, which would also guide the genotyping strategy for the project. In relation to choosing the right genotyping method for the project, it was noted that this should be simple, accurate, robust, high-throughput and cost-effective and allow genome-wide genotyping (SNP discovery, genetic diversity, gene mapping and genomic selection). Two common technologies

for genotyping of cereals are genotyping by sequencing (GBS) and SNP arrays. GBS is based on next-generation sequencing, with its main advantage being that SNP identification is independent of existing genome information, and there are a number of examples for its use in wheat and barley in the literature. Major drawbacks are the complexity of SNP calling in the absence of a pan genome and that there can be a large amount of missing data. SNP genotyping arrays on the other hand have been used extensively and are a cost-effective solution, especially when analysing a large number of samples. One major drawback is that SNP arrays are derived only from genes, which typically make up only 1-2% of the genome.

A number of arrays suitable for wheat and barley are commercially available and the genotyping Task Force (TF) should evaluate them in order to select the best and most cost-effective methodology. The next steps for the genotyping would be to agree on the methodology, collect quotes from commercial providers and to distribute the tasks of sampling, extraction and analysis of generated data among the partners.

It was noted that if the genotyping will only be done in 2021 there was sufficient time for the genotyping TF to discuss specifics, and that this meeting should generally agree on creating this TF and select members for it. The floor was opened for a general discussion.

Luigi Cattivelli (CREA) highlighted the urgent need to agree on a unique EVA code for all accessions within the EVA programme, and invited comments on the proposal. He also noted that there should be agreement on conducting the survey of existing genotyping data which should identify which method was used on what material. The cost for genotyping was noted to be comparable for the suggested methods, which should be chosen based on the need to be robust, easy and reliable and also to be able to connect with the existing data.

Jochen Reif noted that there was a need to guarantee connectivity of data generated in the EVA with those generated in AGENT. He also suggested to use digital object identifiers (DOIs) as a common code, but Stephan Weise (EURISCO) noted that it would be more suitable for daily practice to use simple code as suggested. DOIs would need to be published along with metadata and this could be problematic for the confidentiality within the project. EURISCO would be assisting with generation of accession codes that could be used for genotyping, phenotyping and data management.

Some breeding companies noted that for them the used platform was of less importance as long as it could be guaranteed that it is an established technology and provides robust SNP information that can be used for marker development.

Partners agreed to establish a genotyping Task Force which should further discuss the strategy and be made up of members from public and private entity partners. Volunteers for the TF were Nils Stein (IPK), Luigi Cattivelli (CREA), Noam Chayut (JIC), Külli Annamaa (Estonian Crop Research Institute), Ahmed Jahoor (Nordic Seed), Monika Spiller (Syngenta), Rasmus Hjortshoj (Sejet plantbreeding) and Outi Manninen (Boreal Plant Breeding Ltd.), with support from the ECPGR Secretariat. Noam Chayut (JIC) would join the first meetings to provide their existing genotyping information.

Tasks for the TF would be defined but in the beginning should include to 1) define rules and codes for identification of accessions, 2) discuss the appropriate technology for each crop, 3) survey existing genotyping data and 4) define the sampling protocol.

## **3.2 Breakout sessions for geographical zones**

In order to facilitate project planning, participants were divided into groups according to their geographical zones and discussed in separate breakout sessions topics including 1) material available for the two batches of evaluations, 2) traits, standard descriptors and protocols, 3) field and experimental design, 4) data collection and management, 5) roles, responsibilities and evaluation capacities of partners, 6) work planning and next steps as well as other open questions. Results from these discussions were reported back to the main meeting.

### **3.2.1 Breakout session – Nordic zone**

This session was chaired by Ahmed Jahoor (Nordic Seed). In an initial general discussion, several open questions concerning the selection of accessions were addressed.

Simon Orford (JIC) provided additional explanation on how their lines were selected and indicated that a number of additional wheat landraces from potential Nordic origin (UK, Poland and the USSR) could be provided. He indicated that the six lines provided from each Watkins population should be sufficient to cover all possible alleles in the landraces. He also cautioned that even though their material is indicated as spring wheat, there have been incidents where the material had required vernalization.

The accessions in multiplication at the moment were selected by NordGen and reviewed by several breeding companies. Preference was given to the material of Nordic origin. In addition, some accessions had been provided from the genebanks in Estonia, Lithuania and Latvia. It was indicated that for additional rounds of evaluation more material could be selected from the various genebanks. The group highlighted the decision to give preference to the material from Nordic genebanks, for which SSDs have been generated and are being multiplied. Only winter wheat would be delayed as the multiplication will only start in autumn 2020.

Current multiplication activities would make spring material available for evaluation in spring 2021, and winter material for evaluation in autumn 2021. Yield for the multiplications is expected at 300-400 grams per accession and depending on field setup partners estimated that ca. 20 g would be needed per evaluator. Partners were invited to select additional accessions of spring wheat and spring barley for the second batch of evaluations (ca. 20 per partner/genebank).

All project partners were invited to indicate their capacity for evaluation of the different crops. The corresponding data were collected in a template document available to the entire network. In total, partners committed to providing 8-9 evaluation sites for spring barley and spring wheat as well as 5 evaluation sites for winter wheat. Several companies expressed interest in evaluating winter barley, which had not initially been included in the crop types for the Nordic zone. It was clarified that the geographic zones should not be considered very strict and that material multiplied in other zones should be made available for partners if they wished to evaluate it. In this respect, partners from the Nordic zone wished to evaluate winter wheat from IPK currently being multiplied by JKI, if sufficient seeds were available.

The partners discussed which traits they would be able and interested to evaluate. Partners agreed to evaluate disease resistances as well as several traits of agronomic interest (e.g. earliness/heading, overwintering, lodging, protein content), where possible. Disease traits of interest were resistance to yellow or brown rust, leaf blotch, Septoria and powdery mildew for

spring and winter wheat as well as powdery mildew, barley rust, net blotch, spot blotch and Ramuleria for spring barley. Some partners indicated that they would be evaluating in disease nurseries with smaller plot size and also suggested that artificial inoculation could be considered.

The group noted that the experimental protocol and field design would need to be specified before starting the evaluations and nominated participants to the Phenotyping Task Force, which was proposed to address these issues. Lene Krusell (Sejet Plantbreeding), Marja Jalli (LUKE Finland) and Janni Hedensvang Jørgensen (Nordic Seed) would focus on plant pathology traits while Pernilla Vallenback (Lantmaennen) and Mara Bleidere (Institute of Agricultural Resources and Economics (AREI), Latvia) would provide their expertise on agronomic traits.

Gintaras Brazauskas (Lithuanian Research Center for Agriculture and Forestry) inquired how the results and generated data could be used in publications and it was clarified that this would need to be specified in the cooperation agreement.

### **3.2.2 Breakout session – Central zone**

Discussions in the Central zone were led by Albrecht Serfling (JKI). Partners discussed a number of practical issues related to the evaluations and data management, including 1) how rating methods can be implemented so that reliable results from each of the locations can be uploaded into the database; 2) which rating scales should be used; 3) how many ratings should be done in each evaluation (replications, different time points); 4) which diseases should be evaluated.

Partners agreed to limit disease rating to one collection time point at the developmental stage recommended by the protocol in order to minimize the efforts for each evaluation partner. Natural infection was preferred by breeders over artificial inoculations, therefore only naturally occurring diseases will be rated (mostly rusts, Zymoseptoria, powdery mildew and some other leaf spot diseases can be expected). It was noted that protocols are available from the German Evaluation programme EVA II for each of the diseases evaluated. These protocols will be made available from JKI and can be adapted to all zones. In addition, data collection templates from the EVA II project could be adapted for the EVA networks and will be shared with the TF on phenotyping and data collection.

Partners also agreed to integrate rating data of physiological characteristics (plant height, differences of developmental stages) into the database. It was suggested that a simple rating scale should be available for all partners and included in the protocol. This could be a logarithmic scale which is already used by many breeders and institutions. The EURISCO coordinator emphasized that the scales and methods should be aligned in all three geographical zones in order to ensure their comparability.

Partners discussed how many seeds are needed for each evaluation and have to be dispatched by JKI. They noted that the number of seeds (between 60 and 100) depended on the methodology of sowing employed by the evaluator. This should be recorded in the table “available evaluation sites”. One hundred seeds for each of the partners was considered a sufficient amount for one evaluation.

Partners suggested that evaluation data should be uploaded into the database at the end of the year of rating at the latest and a deadline should be clearly defined for all evaluators. The EURISCO EVA intranet could implement sending of automatic reminders.

It was suggested to generate Standard Material Transfer Agreements (SMTAs) automatically from the accession list available in the database, and evaluators were reminded that material exchange would need to be accompanied by an SMTA. The EVA coordinator indicated that she would assist in the coordination of SMTAs and the data management.

There are different interests and capabilities of partners to evaluate accessions in the Central zone. It was suggested that at least 50 of 150 genotypes should be evaluated at each location. JKI as distributor of seeds will take care of a consistent division of genotypes, so that statistical analysis from different environments can be performed after evaluations.

### **3.2.3 Breakout session – Southern zone**

Discussions in the breakout session for the Southern zone were led by Luigi Cattivelli (CREA) and focused on getting agreement on traits of interest and standard experimental protocols for traits to be evaluated in 2020-21 and 2021-22. Partners were invited to note whether their evaluation sites are hot spot areas for diseases of interest.

Not all of the potential seven evaluation partners were present at this meeting. Among partners present, three will evaluate all three crops (*T. aestivum*, *T. turgidum* and *H. vulgare*), while two companies will only evaluate durum wheat. The group thus felt the need to extend the network both in the number of evaluators and the geographical distribution of evaluation sites (e.g. in Spain and Turkey).

Partners discussed the experimental design of the field plots and agreed that the preferred approach would be to use a randomized block design and sow two rows of 25 plants in two replicates for each accession, as this could be done with machine sowing. Alternatively, one row of 50 plants could be sown. It was highlighted that susceptible reference cultivars should be included at regular intervals, which would help to spread natural infections.

It was noted that wheat and barley landraces can grow very tall, so the protocol should specify that only little fertilizer should be used to minimize lodging. Partners also requested that protocols for disease scoring should include pictures and scales and recommended that scoring should take place regularly, following plant development.

Among disease resistance traits, partners showed interest to evaluate Net form of net blotch (NFNB, *Pyrenophora teres* f. *teres*), Spot form of net blotch (SFNB, *Pyrenophora teres* f. *maculata*), Scald (*Rhynchosporium commune*), Powdery mildew (*Blumeria graminis* f. *hordei*), Leaf rust (*Puccinia hordei*), Spot blotch (*Bipolaris sorokiniana*) and Fusarium head blight (*Fusarium* spp.) on barley. *Septoria nodorum*, *Parastagonospora nodorum*, Leaf rust (*Puccinia triticina*), Yellow rust (*Puccinia striiformis* f. sp. *tritici*), Brown rust (*Puccinia recondita* f.sp. *tritici*) and Fusarium head blight (*Fusarium* spp.) were identified as wheat diseases of interest. In addition to disease resistance traits, partners agreed to score also phenological traits such as heading date and plant height and to provide meteorological data of the evaluation sites.

CREA agreed to distribute instructions for planting and protocols as well as the data collection template developed by the phenotyping TF to evaluation partners before the planting time (ca. September 2020).

As durum wheat will be used only in the Southern zone, it was suggested that a different genotyping technology than for the other crops could be used, if agreeable for the companies. Advantage for the companies would be the fast and effective identification of markers for diseases and the markers and the source of resistance would be contained in the material already made available. This should be further discussed by the genotyping TF.

### **3.3 Conclusions from breakout sessions and general discussion**

The discussions in the separate breakout sessions of the geographic zones identified a number of common open questions that need to be addressed with some urgency.

In summary, partners agreed that ca.100 seeds per accession would be sufficient for one evaluation; however, the field design should be normalized among partners and clearly defined (including randomization design). Inclusion of susceptible varieties as disease markers and diffusers was considered very important, the identity of these would, however, depend on the region and therefore need to be adapted accordingly. Standard protocols should include information on field design, rating scales (preferably with pictures) and appropriate controls and diffusers for different locations/regions.

It was suggested that additional information needed to be collected from evaluators, including coordinates of their evaluation sites, size of the site (and capacity in terms of numbers of accessions that can be evaluated at the site), crop evaluated at the site, required amounts of seeds (depending on plot design, sowing mechanism and number of sites) as well as information on which diseases are typically important at evaluation sites. It was noted that a number of EVA network partners would be able to do evaluation on sites in multiple zones and therefore the distinction between the geographic zones should be considered more fluid. Companies should be invited to indicate whether they have capacity to evaluate in multiple zones. Similarly, even though crop accessions had been initially selected based on geographic zones, partners should have the possibility to evaluate accessions from all zones.

It was agreed that a Task Force for phenotyping and data collection should meet as soon as possible to discuss the highlighted issues and define the standard protocols, propose standard field layouts, develop data collection templates and agree on a standard coding system for accessions. Volunteers for this TF were identified in the Nordic zone, other partners should indicate their availability as soon as possible.

Some partners suggested that a steering committee could be convened to provide guidance and advice to the network consortium and make decisions that would be necessary to maintain the cohesion of the project and avoid creating three separate autonomous geographical sub-projects. The committee would be convened by the Secretariat or by request of any of its members to discuss relevant issues, such as strategies for phenotyping, genotyping or data analysis, criteria for the selection of accessions, coverage of the evaluation sites, issues with the consortium agreement or budget revisions. Proposed members of the committee were Frank Ordon (alternate Albrecht Serfling), Luigi Cattivelli (alternate Delfina Barabaschi), Ahmed Jahoor (alternate Jihad Orabi), Jochen Reif or Nils Stein, Szonja Csörgő (Euroseeds, for legal issues); Stephan Weise (EURISCO, for documentation issues), ECPGR Secretariat.

The EVA coordinator reviewed the draft cooperation agreement, clarifying that it had been modified from the version included in the EVA establishment document to be more specific for

each network. Some partners noted that in its current form the cooperation agreement is too detailed and needs to be simplified.

An important aspect of the consortium agreement and the EVA network is the embargo period applied to data generated in the project. Several partners from public institutions questioned whether some data, especially genotyping data, should be made publicly available immediately outside the embargo. The ECPGR Secretary clarified that the embargo is necessary and important as an incentive for breeding companies, noted the interconnection of phenotyping and genotyping data and cautioned about reopening this discussion. Some partners concurred, noting that a change in how the embargo applies might affect the willingness of companies to participate in the project. Several breeding companies suggested that genotyping data without the associated phenotypic evaluation data could be made publicly available and used by academics. This view was supported by public institutions which noted the need to consider their in-kind contributions and suggested that options to publish data would need to be provided. It was agreed that a compromise would need to be found. The consortium agreement should provide additional details about application of the embargo period and consortium partners would need to agree with publications generated from project data.

## **4. Timeline and next steps**

Based on decisions made in the meeting the following activities will be coordinated:

### **4.1. Cooperation agreement**

Based on comments in the meeting, the agreement will be revised with the input of legal advisors and the steering committee. Main points are to simplify and generalize the description of tasks and to clarify the issue of the embargo period. This agreement needs to be ready and signed by all partners before evaluation trials begin.

### **4.2. Task Force for phenotyping**

Volunteers will be identified (max. 15 members, preferably representatives from each evaluation zone); Members will collect information relevant to phenotyping and data collection and meet virtually in June 2020 to work on standard protocols and data collection templates. Information needed for phenotyping TF: Photographs applicable for disease scales, sample protocols and description of disease scoring for all diseases, field trial setup options, data collection templates, control/diffuser accessions for each crop/disease in the various regions.

### **4.3. Task Force for genotyping**

Volunteers for this Task Force have been identified. The TF will meet virtually in late 2020 to develop an appropriate genotyping strategy, taking into account the discussions during this meeting, existing genotyping data for some of the accessions and budget considerations. Different genotyping options including quotations from appropriate commercial providers will be identified and discussed. Data analysis strategies should be outlined as these are important for selection of the genotyping method, detailed discussion on data analysis can be postponed to a later date.

### **4.4. Survey of evaluation sites**

Detailed information of the number and location of evaluation sites for the various crop types will be collected. In regions where a lack of evaluation sites is noted (target is up to 20 evaluation

sites per geographic zone), additional partners will be invited. This information must be available before seed distribution starts.

#### **4.5. Passport information on accessions**

Providers of GR material should provide as much information on the accessions they shared as possible (origin, existing characterization data, EURISCO identifier, etc.). A template to gather this information will be developed by the ECPGR Secretariat and EURISCO and shared with genebank curators to be filled by them.

#### **4.6. Seed harvest and distribution**

Multipliers will harvest seeds from multiplied accessions and assign them the agreed EVA code. Relevant information (amount of seeds harvested, passport data etc.) will be centrally collected (EVA coordinator) to facilitate and coordinate distribution to evaluators. Evaluators need to specify which crops they will evaluate in which sites and indicate the amount of seeds needed (estimate 100 seeds per evaluation) as well as contact details for seed delivery. All seeds exchanged within the EVA project will be distributed with an SMTA, all partners need to ensure they have the authority to sign this agreement. Control/diffusor accessions as defined by the phenotyping TF need to be added to the EVA list (with EVA code) and included in the distribution activities. Seed distribution should be completed before September 2020.

#### **4.7. Multiplication of accessions for second batch of evaluations**

Multipliers should clearly identify the accessions that have undergone SSD and will be multiplied during the 2020-2021 season to guarantee 150 accessions are available for each crop and zone for the second batch of evaluations starting in autumn 2021. Missing crop types (e.g. spring barley in Nordic zone) could be complemented from existing SSD collections (e.g. at IPK) and distributed to multipliers.

#### **4.8. Next meeting**

It was proposed to convene an online meeting (mainly targeted at evaluating partners) before sowing of the winter crop (in early September 2020), during which operational questions on field trials, standard protocols and data collection should be clarified.

#### **4.9. Additional discussions**

In a survey after the meeting, participants expressed the need for further clarification and discussions for several aspects of the project, including details of the experimental and evaluation protocols, timeline and other practical aspects of the workplan, as well as the embargo period, and whether genotyping data should be included. Most of these issues will be addressed within the Task Forces or the Steering Committee (see above).

## Appendix 1. Meeting Agenda

### PRE-MEETING DOCUMENTS

ppt	Background and overview of the ECPGR Evaluation Network EVA	L. Maggioni
Video/ppt	Update on current status and activities in EVA Network - Focus on Wheat/Barley component	S. Goritschnig
ppt	Overview and current status of EVA II project on wheat and barley	A. Serfling
ppt	EURISCO: ensuring integration of data in special intranet environment for EVA	S. Weise
ppt	Virtual visit to multiplication sites for EVA wheat and barley in Germany, Denmark and Italy.	A. Serfling/ A. Jahoor / L. Cattivelli
Documents	Drafts available for: <ul style="list-style-type: none"> <li>• Workplan 2020/2021</li> <li>• Roles and responsibilities of partners</li> <li>• Cooperation Agreement</li> </ul>	S. Goritschnig

### 5 MAY, 9:00– 16:30 (Venue: MS Teams)

9:00 – 9:30	Connecting to MS Teams – technical assistance if needed	
	<b>Welcome</b>	
9:30 – 9:35	Welcome and introduction of platform and available files/tools	S. Goritschnig
9:35 – 9:45	Introduction of participants	All
	<b>Development of detailed project workplan</b>	<b>Chair: L. Maggioni</b>
9:45 – 10:00	Review of project proposal and new developments	S. Goritschnig
10:00 – 10:30	Review of current activities in the EVA network wheat/barley <ul style="list-style-type: none"> <li>- Selection of accessions and SSD populations</li> <li>- Multiplication of accessions</li> </ul>	N. Chayut / J. Reif / A. Börner A. Serfling/ A. Jahoor / D. Barabaschi
	<b>Discussions on Workplan</b>	
10:30 – 11:15	<ul style="list-style-type: none"> <li>• Workplan: <ul style="list-style-type: none"> <li>- Agreement on genotyping protocol and data analysis pipeline</li> <li>- Confirmation of roles and responsibilities of each project partner (multiplication and evaluation)</li> </ul> </li> </ul>	D. Barabaschi S. Goritschnig

11:15 – 12:15	<b>Breakout sessions I</b> <b>Evaluation round 1:</b> Agreement on traits of interest and standard experimental protocols for traits to be evaluated in 2020/21 Field design and confirmation of evaluation sites for each crop type Roles and responsibilities Work plan timeline	All in geographical breakout sessions A. Jahoor – Nordic zone A. Serfling – Central zone L. Cattivelli – Southern zone
12:15 – 13:30	<b>Lunch break</b>	
13:30 – 14:45	<b>Breakout sessions II</b> <b>Evaluation round 2:</b> Agreement on accessions for multiplication in 2020/21 and proposal for traits of interest to be evaluated in 2021/22 Other open questions	All in geographical breakout sessions A. Jahoor – Nordic zone A. Serfling – Central zone L. Cattivelli – Southern zone
14:45 – 15:00	Reporting back from the breakout sessions	Volunteer from the three groups
15:00 – 15:15	<b>Break</b>	
15:15 – 16:00	Wrap up of conclusions and agreements reached in breakout sessions Review of cooperation agreement, timelines and deliverables Define next steps	S. Goritschnig
16:00 – 16:30	Discussion	All
16:30	Close of meeting	

**POST-MEETING DOCUMENTS (MADE AVAILABLE ONLINE AFTER FINALIZING)**

Documents	<b>Formulation of Cooperation Agreement for EVA Wheat and Barley</b>	
	Finalizing: <ul style="list-style-type: none"> <li>• Project workplan</li> <li>• Roles and responsibilities</li> <li>• Deliverables 2020/2021</li> <li>• Cooperation agreement</li> </ul>	S. Goritschnig with input from all
	<b>Practical guidance on experimental procedures</b>	
Documents/ videos	Evaluation protocols for traits of interest for field trials: <ul style="list-style-type: none"> <li>• Standard protocols</li> <li>• Video tutorials on practical evaluation</li> <li>• Template data collection form</li> </ul>	S. Goritschnig with input from all

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### Appendix 3. Acronyms and abbreviations

AGENT	Activated GEnebank NeTwork (Horizon 2020 project)
AREI	Institute of Agricultural Resources and Economics, Latvia
CREA	Council for Agricultural Research and Analysis of Agricultural Economics, Italy
DOI	digital object identifiers
ECPGR	European Cooperative Programme for Plant Genetic Resources
EURISCO	European Internet Search Catalogue
EVA	European Evaluation Network
EVA II	National Evaluation Programme for Plant Genetic Resources, Germany
GBS	genotyping by sequencing
GWAM	genome-wide association mapping
ICARDA	International Center for Agricultural Research in the Dry Areas
IPK	Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany
JIC	John Innes Centre, Norwich, UK
JKI	Julius Kühn-Institute, Quedlinburg, Germany
NFNB	net form of net blotch
SFNB	spot form of net blotch
SMTA	Standard Material Transfer Agreements
SNP	single-nucleotide polymorphism
SSS	single seed descent