Annual meeting of the
European Evaluation Network (EVA)
for Wheat and Barley
21 October 2021
9:00 – 16:00, online MS Teams

Federal Ministry
of Food
and Agriculture

Summary Report of the Meeting

The 2nd Annual Project meeting of the EVA Wheat and Barley network took place on 21 October 2021, 9:00 to 16:00, on MS Teams. The agenda of the meeting is attached as Appendix 1 and the list of participants as Appendix 3.

1. Welcome and introduction

The EVA Coordinator, Sandra Goritschnig, opened the meeting, reminding participants of the expected outcomes of the meeting and highlighting the shared documents folder of the network where partners could find all relevant templates and reference documents.

2. Review of Project progress in 2020/2021

2.1   Review of project workplan and general update

The EVA Coordinator presented a general update on the EVA project. The EVA website had been updated, partners were invited to visit it at https://www.ecpgr.cgiar.org/european-evaluation-network-eva/eva-networks/wheat-and-barley and provide feedback. Partners were informed of an additional no-cost extension of the project until November 2023, granted by the German donors in February 2021, and intended to compensate for delays in the implementation of the project due to Covid-19, including the lack of opportunity for strategic discussions during in-person project meetings. The Cooperation Agreement had been signed by all 48 networks partners from 21 countries and a compiled document with all signature pages made available on sharepoint. The EVA-EURISCO intranet, the platform to store and display phenotypic data collected in the EVA network,was nearing completion and was presented during the meeting.

The original workplan was reviewed and the time overlap between activities related to different evaluation cycles highlighted. The project funded by the German government provides for two cycles of evaluations of up to 1,500 accessions in total (~150-200 accessions per crop per geographic zone), including the development of the EVA-EURISCO intranet and genotyping of all evaluated accessions. The 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 in 2022 and evaluations in 2023-2024, was also presented during the meeting in more detail.

2.2   Highlights from 2020/2021 trials

During the first round of evaluations, a total of 1,153 accessions were evaluated by 32 organizations at around 100 evaluation sites in 16 countries across Europe. The numbers of evaluation sites ranged from nine sites for durum wheat, which was only evaluated by partners in the Southern Zone, to 35 sites for winter wheat, which was evaluated across all zones. It should be noted that 70 winter wheat accessions from the German genebank were evaluated in all zones.

Partners were reminded to provide their evaluation data to the EVA Coordinator as soon as possible, using the provided data templates and including relevant metadata on their experiments (e.g. GPS coordinates of field site, experiment start and end dates, field setup, sowing density, treatments as necessary). GPS coordinates will be used to extract weather data from appropriate databases during data analysis. Comments should be used to provide non-standard observations or notes on the trial. It was also highlighted that only permitted scoring values, as provided by the standard protocols and data collection templates, should be used, and that a guidance document on the data collection templates was available on the project sharepoint. Feedback on the

templates, and especially the requested metadata field, was welcomed. Partners were also invited to report on problems and challenges during their trials and to provide suggestions to improve the workflow and project management.

It was noted from around 50 evaluation data sheets provided so far, some diseases were not scored by any partners, while other more prevalent diseases were scored almost always, and that morphological data were not scored in all trials. Some partners considered these less relevant than the disease scoring, but it was noted that information on precocity, plant height and tendency for lodging were important in assessing disease severity (especially for Fusarium) and adaptation to different environments, as well as for selecting pre-breeding materials. It was suggested that data on plant height could be collected from fewer locations, but that data on maturity of the material could be interesting from multiple locations across all geographic zones. Several partners reported that due to unfavorable conditions, their trials did not have high disease pressure or did not allow good scoring of agronomic traits, resulting in incomplete or missing datasets.

Partners discussed options to increase the amounts of data on different diseases, also with a view to collecting enough data from different environments and replicates to enable genome-wide association studies (GWAS). Some partners relied on natural infections in their trials, while others used artificial inoculation, especially for rusts and Fusarium. Albrecht Serfling (JKI) pointed out that the standard protocols included guidance on conducting artificial infections for specific diseases, and suggested that leveraging the expertise of breeders who can perform these should be emphasized in order to be able to collect sufficient high-quality data. Some partners noted that trials with artificial inoculation use a different setup than natural infections and would require additional material or be done in special fields. The use of appropriate, locally adapted check varieties was recommended to control for different environments.

Partners were asked to provide information on possible artificial inoculations that they could provide for different diseases and a survey will be distributed among network partners to collect this information. Given the number of environments available for evaluations of the different crop types, a minimum number of trials per disease should be planned and partners' commitment for these received.

Some partners noted that they had received seeds late for sowing, especially for winter crops, and that this, in some cases, affected scoring maturity (due to lack of effective vernalization). Multipliers noted that they did their best to provide seeds in time but, given the extremely short time window between harvesting and sowing of winter crops, this was not easy. It was noted that sending seeds to partners would be prioritized based on their sowing dates, and partners were thus reminded to provide this information as precisely as possible. Some partners noted that the seed amounts provided for the first set was not always sufficient for two years given their field setup. Some partners had harvested seeds from the first replicate and would be using these seeds for the second replicate, others had requested additional seed from Multipliers. Multipliers confirmed that the material sent was intended for two years, given the information provided by partners on required seed amounts, so this information should also be clarified by all evaluating partners. Partners were also reminded that all seed exchange in the network should be under the conditions of the Multilateral System of the ITPGRFA, using their Standard Material Transfer Agreement. Genebanks, multipliers and evaluators were reminded to archive copies of SMTAs for material shared by or with them.

Partners commented on the scoring protocols provided for the network. For some diseases, such as yellow rust, the scoring scale maxes out at ~70%, which may affect the precision of GWAS. Specifically, some partners use percentage ratings for disease scoring, which provides more fine-grained differentiation of disease severity. The protocols for the different traits will be reviewed based on a survey among network partners and adjusted as necessary, keeping in mind that the main purpose of the protocols is to allow consistent scoring across different trials and thus effective comparison of disease data from different trials and environments.

2.3   EURISCO – EVA intranet

Suman Kumar (IPK, Germany) provided a live demonstration of the EURISCO-EVA intranet platform, a database intended to store and visualize the phenotypic data collected in the EVA trials. A beta version of the platform had been commented on by some partners and feedback will be incorporated in the next iteration. It is expected that the intranet will be accessible for the EVA Wheat and Barley partners at the beginning of 2022.

The EURISCO-EVA intranet stores relevant metadata information on partner organizations, trials, evaluated accessions and traits. Phenotypic data can be filtered using simple searches and visualized in graphs. Pivoted tables allow comparison of accessions based on scores for different traits. Genotypic data will not be stored on the intranet, due to storage limitations, but metadata will be displayed, as well as links to the public repository where the data will be hosted. The platform should provide intuitive access to the different datasets and guidance material will be developed to assist partners in its use. Trainings for the use of the platform will also be provided as necessary.

The EURISCO-EVA intranet will be available to store data for the EVA networks as long as they are operational, and as long as ECPGR continues to support EURISCO. Data from the project will ultimately be included in the EURISCO database and thus publicly available.

Partners appreciated the efforts in developing this database platform, looking forward to being able to soon use it. The intention was to curate the phenotypic data of the 2021 trials so they could be uploaded to the EURISCO-EVA intranet by the end of the year. Several open questions that needed to be clarified were whether individual datapoints for each replicate should be recorded separately, how the quality and completeness of the datasets would be validated before upload and whether only primary data should be stored in the database or also whether curated and analysed data could be made available on the platform and how this information should be integrated. It was noted that most analysis would be stored in tables, thus it should not be too difficult to display that kind of data.

2.4   Update from genotyping

Delfina Barabaschi (CREA-GB, Italy) presented the progress in genotyping of the first set of accessions and an outlook for the second set, which is funded by the current project budget.

The selected technology for genotyping are high density Illumina Infinium SNP-arrays from TraitGenetics, providing 25k SNPs for wheat or 15k SNPs for barley, at a rate guaranteed for two batches of sixteen, 96-well plates. Eight hundred and forty-six wheat and 658 barley samples were included in the first set and, for most, the genotyping had been completed and data made

available. Only a few samples failed and will be repeated in the next batch of genotyping. Initial analysis of genotyping results for samples from the Nordic zone indicated that they were less diverse, with 75% and 78% useful SNPs, respectively for barley and wheat. Indeed, most materials for this zone are indicated as breeding material or advanced/improved cultivar. On the other hand, results from the Southern zone, where a higher percentage of accessions were identified as traditional cultivar/landrace, 87% and 85% of SNPs were useful, respectively for barley and wheat. Genotyping of durum wheat resulted in 52% of useful SNPs, this number was expected for material from a different Triticum species. The genotyping of accessions from the Central zone was ongoing.

The samples for the second batch of genotyping would include the accessions of the second set, except for those that were already added to the first batch to fill plates. It can thus be expected that there will be fewer samples and it was noted that they should be rationalized between zones, to fill plates and economize. Final sample counts will be available when the information on spring crops from the Nordic and Central zones were completed.

Several important points were mentioned for the data analysis, for discussion in the breakout sessions. Given the different crop types in the geographic zones, as well as different environmental conditions and prevalent diseases, it was suggested to create three groups responsible for analyses of genotypic and phenotypic data from the three geographic zones. CREA-GB offered to take the lead for the Southern zone and called on partners in the other zones to step forward as leads for data analysis. Data management and storage, as well as dissemination within the network, were reiterated as important discussion points.

Finally, it was noted that it would be good to create additional overlap between the different accession sets. For effective GWAS, it would be beneficial to include at least two sets in the analysis, however, they were only evaluated in parallel for one year. Given that pathogen presence/attack could be very different from one year to the next, it was suggested to create additional overlap by including ~5% of accessions from the first set also in the third year of evaluations to bridge the different accession sets.

It was noted that the problem of comparing different accessions sets is known to breeders who use common checks to provide the link between the different sets during analysis. The proposal to use 5% of accessions from set 1 also in the evaluations in 2023 could be considered and would be discussed further.

3. Ongoing activities

3.1 Outlook for Evaluations on Set 2 of accessions

The EVA Coordinator presented a summary of accessions in set 2, noting that winter crops in the Nordic and Central zones have already been distributed, as well as all crops for the Southern zone, as these are sown starting in September. Spring barley and spring wheat in the Nordic and Central zones will be processed and distributed before the end of 2021 and partners were reminded to confirm their capacity for evaluations of set 2 in a shared file, and to clarify any changes in contact information as well as seeds needed for their trials. In total, around 100 evaluation sites were again expected to be used in this next round of evaluations.

3.2 Horizon2020 project AGENT

The Horizon2020 project Activated Genebank Networks (AGENT)[1] (www.agent-project.eu) was interacting with the EVA Wheat and Barley network, providing materials and genotyping for a third evaluation set. Nils Stein (IPK, Gatersleben), the project Coordinator for AGENT, provided an overview of the project to partners.

The project builds on work done at IPK and intends to improve the available information on materials stored in genebanks. For example, the Genesys database contains ~250,000 entries for barley, but the majority has little information associated with it, making a selection of interesting accessions difficult. Holding institutes typically have few data associated with their genetic resources, usually limited to passport and some characterization & evaluation (C&E) data collected during multiplications and much of that data has not yet been digitized. Therefore, in a pilot study, the entire barley collection of IPK Gatersleben (~20,000 accessions) was sequenced at low density to define the diversity available in the collection[2]. Using this data, IPK analyzed the composition of their collection and estimated that around 30% of it may constitute duplicate entries, identified as accessions with less than 0,05% genetic difference in pairwise comparisons. The genotyping data was also linked with historic C&E data to do a GWAS analysis that was able to identify known flowering loci. Genotyping of genetic resources in genebanks will be an indispensable tool to improve the management of collections and, through linkage with phenotypic data collected by genebanks, allow further analysis and use of the material.

Results from the pilot study at IPK were used to develop AGENT as an international collaboration of 14 genebanks and five bioinformatics centres from 17 countries to build a genebank network that would expand on this concept. The project was funded by H2020 with sevenmillion Euros for a duration of five years and started in May 2021. The project focusses on wheat and barley as pilot crops and is organized around a central core around EURISCO as the main crop database, to which data is provided from the bioinformatics and data management work packages. The genebanks support this core by providing accession collections for wheat and barley, while stakeholders such as the EVA Wheat and Barley network, contribute additional evaluation data.

The AGENT project uses several approaches to improve our knowledge about genetic resources in different genebanks. In a first approach, genebanks use sets of 50 standard commercial varieties in evaluations at their locations, and the resulting data will be used to assess the presence of European mega environments (similar to the geographic zones in EVA), which could be used for integrated data analysis from genebanks in these environments. A second approach aims at identifying "bridging collections" at genebanks, which include up to 150 putative duplicate accessions that are also conserved at other partner genebanks. Historic data of these accessions, which are also genotyped, could then be used in integrated analyses of environments. Identification of putative duplicates is aided by analyzing passport data in EURISCO but is not straightforward.

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[2] Milner, S.G., Jost, M., Taketa, S. et al. Genebank genomics highlights the diversity of a global barley collection. Nat Genet 51, 319–326 (2019). https://doi.org/10.1038/s41588-018-0266-x.

Finally, genebanks identified "precision collections" of wheat and barley, containing up to 500 accessions with a high potential of uniqueness within their overall collections, or being representative for the country of the holding institute. This approach aims at maximizing the diversity of material genotyped in this project, similar to the efforts done in the BRIDGE project at IPK or the "Seeds of discovery" project at CIMMYT. These precision collections are also phenotyped by their genebanks for agronomic traits plant height, flowering time and 1000 kernel weight. The accessions in the precision collections were propagated as SSDs and genotyped using GBS for barley and DartSeq for wheat. Some genebanks will evaluate their own collections for a limited set of biotic stresses and several genebanks collaborate on evaluating abiotic stress traits on a selected subset of the material. All data will be used in an integrated way, also to assess prediction of suitable materials using FIGS (Focused Identification of Germplasm Strategy) within the global collection which contains around 7,000 accessions of wheat and ~5,000 accessions of barley.

Overall goals of the AGENT project were to establish a proof of concept for actively collaborating genebank networks, which could also be translated to other crops and extended to other world regions. Improved genebank management, using standard protocols and data flows, will help to make historic data accessible and to generate new data, enabling genebank curators to assess the quality and composition of their collections. The project also manages its data according to the FAIR principles (making data Findable, Accessible, Interoperable and Reusable), developing data management tools to this end with an emphasis on EURISCO.

The EVA Coordinator added information on the interaction between the EVA Wheat and Barley network and AGENT. Through the funding provided by AGENT, a third set of SSD accessions would be multiplied and evaluated over two years, starting in 2023. This extension would allow the project to progress sufficiently to allow strategic discussions for its continuation after the end of the current projects. It was highlighted that six of the AGENT genebanks were also partners in the EVA Wheat and Barley network, having signed the cooperation agreement.

The precision collections identified by the AGENT partner genebanks include approximately 6,000 bread wheat and 4,000 barley accessions, which could feed into the EVA evaluations. Some genebanks contributed wild relatives of wheat and barley, which were excluded from the selection of the third set. Agroscope (Switzerland) is also creating a precision collection of Triticum spelta. No durum wheat collections were planned within AGENT.

The bread wheat and barley accessions selected from the AGENT precision collections for the different geographic zones of EVA Wheat and Barley were chosen based on availability of GPS coordinates of their origin, matched with the EVA geographic zones, and availability of sufficient seeds from the SSD step. Selection of a third durum set depended on limited resources from AGENT, a selection provided by ICARDA (International Center for Agricultural Research in the Dry Areas) and accessions from the first set which were not yet included in EVA. Winter crops for the Nordic and Central zone and all crops for the Southern zone were already distributed to multipliers. As for the second set, the spring crop lists will be finalized and distributed to multipliers by the end of 2021.

Another goal of the AGENT project was to extend the range of stakeholders utilizing available genetic resources. An Italian organic farmers' network, "Rete Semi Rurali", has thus joined the EVA Wheat and Barley network and will be evaluating sets of 50 accessions each of bread wheat, durum wheat and barley under organic conditions in nine farms across Italy, starting in 2023. Matteo Pettiti (Rete Semi Rurali, Italy) introduced his farmers' cooperative to the meeting

participants. Their traits of interest focus on agronomic traits relevant for organic farming, including early vigor and ground coverage, and simplified data collection methods appropriate for their decentralized network would be developed. Suggestions for potential diseases and scoring methods were invited. One partner proposed to evaluate seed-borne diseases. Lab analyses were considered outside the scope of their activities, as the farms were not equipped to perform these and would thus focus on on-field evaluations. Given the structure of their farmers network and evaluation sites, as well as the trial setups, the data generated may not be as standardized as that generated by the breeding companies in their trials.

Partners welcomed the information on the AGENT project and its contribution to the EVA network. One question concerned the protocols used for the evaluation of biotic and abiotic stresses by the genebanks, especially on what trait would be scored as a proxy for drought stress. Another important issue that would need to be clarified was the data sharing between AGENT and EVA, for example to what extent data generated within either project will be available for the other project. It was noted that access to data should be governed by collaboration agreements and it was highlighted that the EVA Wheat and Barley network cooperation agreement had been signed by six AGENT partners. Lorenzo Maggioni (ECPGR) noted that, at the moment, AGENT provide accessions and genotypic data to EVA Wheat and Barley, and that the EVA embargo would apply to the results from the evaluations generated within the EVA networks. Thus, there is an exchange of data that is expected between the two projects and a discussion on how to manage access to data, including how to apply the embargo, will be necessary.

Noam Chayut (John-Innes-Centre, UK) offered durum wheat SSDs held by their genebank, that could be added to a future set of accessions. He reiterated the necessity to be clear about the access to data generated in the evaluations. It was noted that these discussions were already started in the first annual project meeting and that an embargo on the data was necessary to provide an incentive for the private sector partners, but that this would not mean that exploitation of the data through publications was not possible during this timeframe. Further discussion on this topic will be necessary and perhaps best done during an in-person meeting.

4. Breakout sessions - Data analysis:

Meeting participants were invited to join crop-specific discussions on approaches for data analysis, led by Luigi Cativelli (CREA-GB, wheat) and Martin Mascher (IPK, barley). Suggested topics for the discussions were: data curation and management, methods of data analysis, possible GWAS approaches/integration with genotyping analysis, possible stand/alone genotyping diversity studies. A main outcome of the discussions was to identify analysis Lead(s) among partners for the different crops and geographic zones.

4.1   Barley breakout discussions

The main goal of the data analysis was identified as GWAS to identify novel resistances and associated markers, using the large amounts of phenotypic data generated by the evaluators integrated with the available high quality genotypic data. Most common fungal diseases (e.g. powdery mildew and rusts) occur as different strains across Europe and this could provide interesting differential data for the same disease in different locations. This aspect may also need to be taken into consideration for GWAS analysis, which could identify different QTLs for different regions/different strains. Another potentially interesting analysis could be of accessions from different geographic origins and their response to different diseases, similar to the FIGS approach

used for genotypic prediction in AGENT. In general, interpretation of the analyzed data would only be possible after the second year of evaluations, starting in 2023.

It was clarified that the tasks associated with the analyses of phenotypic data could be divided into three parts: 1) data curation, 2) quality control (QC) and 3) data analysis. Data curation and QC will be very important, and appropriate management of the data is a prerequisite of the downstream GWAS analysis. Data curation should ensure that the phenotypic data provided follows the agreed scoring scales, includes sufficient metadata information on the trial and uses the correct data template to allow upload to the EURISCO-EVA intranet, used for data storage and visualization. Additional QC should happen after upload, for example some morphological traits are correlated across locations, these could be used to control for outliers and potential mix-ups in the trials, while disease traits can show large variation between sites.

Breeders called on the research institute partners to volunteer to lead the data analyses of phenotyping, genotyping and joint analysis for the three geographic zones as there was only limited overlap within accession sets for the different crops. Appropriate statistical analyses to assess the repeatability of the experiments and inclusion of common check varieties in all environments will be important to assess the relevance of the phenotypic data.

Alessandro Tondelli (CREA-GB) volunteered to lead the data analysis of barley for the South zone. Volunteers from the Nordic and Central zones will need to be identified.

It was noted that the pipelines developed for the analysis could be adapted to all crop types. Thus, if no volunteers for barley can be identified, perhaps the partners who volunteer for wheat would be interested in also analyzing the barley data. Alternatively, additional experts in quantitative genetics groups could be invited to collaborate in the EVA consortium. Another suggestion was to identify partners who could take on parts of the analysis workflow to make this a truly joint effort. It was highlighted that the pipelines for the GWAS analysis could be developed already, but the interpretation of the results should only be done after the second year of evaluations. A working group could be set up to manage these tasks across crops and geographic zones.

As concerns the discussion on availability and data sharing, it was noted that partners have access to the generated data within the consortium and, according to the consortium agreement, were allowed to publish with the consent of the other partners. Sharing data with other projects, such as AGENT, will need to be further discussed, issues clarified and perhaps appropriately formalized. It should be highlighted that the needs of both public and private partners should be considered, public partners relying on publications to secure funding and private companies needing some advantage in a competitive market. It was further highlighted that the AGENT project could potentially contribute further sets of genotyped wheat and barley accessions for evaluation by EVA, as the third set included only a subset of the precision collections.

4.2   Wheat breakout discussions

The wheat group identified volunteers for global management of the data analysis (including quality control of phenotypic data as well as GWAS) for the Central (JKI) and Southern zones (CREA-GB). A volunteer for the Nordic zone will still need to be identified. It was emphasized that data analysis leads need to be identified now, to assign clear responsibilities for the workflow.

Data curation and QC were also highlighted as important stages in the analysis, as well as collecting all relevant metadata including field layouts, which could be important for some

analyses. It was proposed that the EVA Coordinator could lead the data curation to ensure all datasets were complete for upload into the database. Further QC would then use an initial statistical analysis to assess consistency, data distribution and identify outliers and potential mix-ups.

It was emphasized that a first QC on the data from the first year of trials should be done to inform the evaluations of the replicate trials in the second year. Thus, all data should be available on the EURISCO-EVA intranet by the end of 2021, and a report on the QC presented to the consortium during webinars in early March 2022 to highlight any issues or problems that were identified, and partners could therefore avoid repeating them in the next evaluations. It would also help with sorting datasets according to their usefulness for GWAS.

It was not considered necessary to use the same analysis pipelines in the three sub-regions, which could be done independently, but the partners working on the analysis should regularly exchange experience and problems, possibly within the context of a working group. However, analysts should be able to directly interact with data providers to ensure quality of the data and to clarify any questions.

Useful data were those with differential scoring in trials, datasets were all datapoints in a trial show the same scoring were not useful and should be discarded from the analysis. Careful analysis of the datasets, however, could find evidence of rare alleles, if only few plants show resistance. This data would not be useful for GWAS, but partners could independently carry out different follow-up experiments (e.g. biparental analysis) at the discretion of each partner. Furthermore, as noted in the barley group, analyses may need to consider data subsets (especially for specific races of the pathogen) as well the entire set (depending on the quality of the data).

Another point made during the discussions was the intention to increase the number of trials with artificial inoculum of certain diseases to improve the data on those. Several partners indicated that they would be willing to share inoculum, or could perform artificial inoculation, and a survey will be created to collect this information. Including two to three inoculated trials in each zone would add strength to the collected data and benefit the consortium.

The EVA Coordinator agreed to manage the initial data curation, noting that partners will be contacted to clarify or provide missing metadata as necessary. Field layout information should also be included where available and the data collection templates provides columns where that data can be recorded.

5. General discussion

The EVA Coordinator reminded participants of next steps for the project which would ensure the long-term continuation of the EVA Wheat and Barley network. Current funding for the project was guaranteed until 2024, through the German project and AGENT, but a fourth set of accessions would need to be identified and SSDs ready for multiplication by summer of 2022 to allow continuation of the overlapping rolling circle evaluations. It was highlighted that the AGENT precision collections could provide additional material for bread wheat and barley, and these would already be genotyped SSDs. Durum wheat accessions would need to be identified, but JIC could provide SSDs from their collection, if agreed. It was further outlined that the funding currently provided for project coordination, development of the EURISCO-EVA intranet, multiplication and

genotyping of accessions and includes limited travel funds, which will be used to organize an in-person meeting for strategic discussions in 2022. Funding options for a project extension should be explored, including external funding options, as well as an option for network partners to contribute funds to the budget.

Tanja Gerjets (GFPi, Germany) commended the network for its achievements so far, noting that the project was still in its early steps, but seemed to be well on track. She reminded partners of the initial intention stated in the project to ultimately become self-sustained evaluation networks, using the project funding to kick start activities. She noted, however, that the possibility to tap into national programmes and funding options should be further explored.

Some breeding companies disagreed with them funding the project, noting that they significantly contribute in-kind to the screening of the genetic diversity, which is valuable and should be continued. However, high quality data analysis was essential for private companies to be able to use the generated data and select suitable material for their breeding programmes. It was highlighted that the apparent oversight of not including funding in the project specifically for data analysis and relying on volunteers to do this task, may jeopardize the whole project. The project was of high value and its great advantage was that it encompasses a diverse group of stakeholders with different expertise to jointly work on the evaluation of genetic resources. However, due to the large number of actors involved, it was difficult to curate and manage the data appropriately. Data analysis should be done by participating research institutes with the relevant expertise, and perhaps creating a longer-term solution through funding of a PhD position should be considered. It needs to be ensured that the analyzed data was made available to all partners and thus there should be emphasis on putting a solution in place for this issue as soon as possible.

Lorenzo Maggioni (ECPGR) reiterated that data analysis was an essential part of the project and also highlighted the need to identify responsible persons with the right expertise and, if necessary, additional funding sources. It may be too early to discuss the options of continuing the network as a self-funded project, given that it is still in the proof-of-concept stage. If this option is selected, this would require private companies to provide additional funds to support the project activities.

Ahmed Jahoor (Nordic Seed, Denmark) highlighted the success of the Nordic PPP projects on wheat and barley, which have been ongoing for more than 10 years. In these projects, data are generated by the participating breeding companies and data analysis is provided by research institutes. This setup was working well, but it should be noted that it is a smaller network and includes financial contributions by the private partners.

Many breeding companies joined the network as it provided an opportunity to go beyond the standard screening of genetic resources, with its diversity in environments, partners and availability of extensive sets of phenotypic and genotypic data. This could be a basis to explore additional scientific questions, as well as potentially moving some interesting materials forward in breeding programmes. Funding options should be explored after a first analysis of data, as it will be easier to base discussions on preliminary results showing the success of the project and could be discussed during the in-person meeting in 2022. Particular emphasis should perhaps be given to secure funding specifically for data analysis.

Albrecht Serfling (JKI, Germany) highlighted that for JKI the most important aspect at the moment was to get reliable and comparable phenotypic data from the different locations, which would

inform the selection of material for breeding and provide scientific data for future projects looking at novel sources of resistance. Public research institutes depended on publications of their research to secure additional funding, but additional clarification may be needed on how the results can be exploited by the partners with different interests in the project. LAMMC and AREI could add expertise to the data analysis.

It was suggested that, in the long-term, the EVA network could work towards building/gathering expertise in phytopathology to tackle some of the more challenging biotic stresses that were emerging, such as Barley Yellow Dwarf Virus or Fusarium, as well as looking at more complex traits that can be emerging problems. Breeding companies have learned from previous PPP projects that the main benefit of the project was the generation of multilocation data from across Europe, and everyone should be interested in analysing this data.

6. Next steps and any other business

Based on the discussions during the meeting, a number of milestones and next steps were identified and are summarized in an action list in Appendix 2.

Mara Bleidere (AREI, Latvia) extended an invitation to the 13th International Barley Genetics Symposium, which will happen in Latvia at the beginning of July.

Partners agreed on scheduling an online meeting to review the data from the first year of evaluations in February 2022, with an in-person annual meeting for strategic discussions possible later in the spring.(~May 2022). Partners were reminded that travel funding was reserved for public sector participants and were invited to propose possible venues that could host a large meeting in multiple rooms, preferably in a location where material is grown.

Appendix 1: Meeting Agenda

21 OCTOBER, 9:00– 16:00 (Venue: MS Teams)

8:45 – 9:00	Connecting to MS Teams – technical assistance if needed	
	Welcome	
9:00 – 9:05	Welcome and review of platform and available files/tools	S. Goritschnig
	Review of Project progress 2020/21	**Chair: L. Maggioni**
9:05 – 9:15	Review of project workplan and general update	S. Goritschnig
9:15 – 10:00	**Highlights from 2020/2021 trials** - Summary of data on different traits - Review of scoring protocols for different traits	S. Goritschnig/A. Serfling All
10:00 – 10:30	General discussion on first round of evaluations	All
10:30 – 10:45	Coffee break	
10:45 – 11:00	EURISCO – EVA intranet demo	S. Kumar/S. Weise
11:00 – 11:15	Update from genotyping - Data from first batch - Plan for second batch	D. Barabaschi
	Ongoing activities	
11:15 – 11:30	**Outlook for Evaluations on Set 2 of accessions** - Overview of available sites and accessions - Seed distribution deadlines - Discussion	S. Goritschnig
11:30 – 12:00	**Horizon2020 project AGENT** - Overview of the project - Interaction between AGENT and EVA wheat and Barley - Discussion	N. Stein S. Goritschnig All
12:00 – 13:00	**Lunch break**	
	Data analysis	
13:00 – 13:05	Introduction of Breakout sessions	S. Goritschnig
13:05 – 14:15	**Breakout session - Data analysis:** - Methods of data analysis - Possible GWAS approaches/integration with genotyping analysis - Possible stand/alone genotyping diversity studies - Identify analysis Lead(s) among partners	All in crop-specific breakout sessions **Barley:** M. Mascher (IPK) **Wheat:** L. Cattivelli
14:15 – 14:30	Reporting back from the breakout sessions	Volunteer from the three groups
14:30 – 14:45	Coffee break	

	Next steps	
14:45 – 15:00	**Long term planning for EVA Wheat and Barley** - Project's funding coverage - Selection of next accession set for SSD generation - Identification of sources for Durum wheat accessions	S. Goritschnig/All
15:00 – 15:45	**General discussion** - Wrap up of conclusions and agreements - Review of timelines and deliverables - Define next steps	S. Goritschnig/All
15:45 – 16:00	Any other business - Next meeting	
16:00	Close of meeting	

Appendix 2: Action list

#	Section	Task	Responsible	Due date
1	2.2	Provide data from evaluation trials 2021, using data collection templates	All evaluators	ASAP
2	3.1	Finalize spring crop lists for 2nd round of evaluations	S. Goritschnig	15.11.2021
3	4.1	prepare a data flow map between AGENT and EVA	S. Goritschnig	18.11.2021
4	2.2	Prepare Survey on capacity for trials with artificial inoculation and traits scoring scales	S. Goritschnig	30.11.2021
5	2.4	Finalize sample lists for second batch of genotyping	S. Goritschnig, D. Barabaschi, A. Serfling, J. Orabi	30.11.2021
6	3.2	Check standard protocols used by AGENT for biotic and abiotic stresses	S. Goritschnig	30.11.2021
7	3.2	Discuss Data sharing between AGENT and EVA during AGENT GA	S. Goritschnig/L. Maggioni	30.11.2021
8	2.2	Respond to survey on capacity for trials with artificial inoculation	All evaluators	31.12.2021
9	2.2	Update information on trial capacity and deadlines	All evaluators	31.12.2021
10	2.2	Archive copies of SMTAs used for seed exchange	All senders and recipients of seeds	31.12.2021
11	2.2	Review standard protocols and scoring scales	S. Goritschnig and A. Serfling	31.12.2021
12	3.1	Distribute seeds of spring crops to evaluators	J. Orabi, A. Serfling	31.12.2021
13	3.2	Finalize spring crop list for AGENT accessions and coordinate distribution to multipliers	S. Goritschnig	31.12.2021
14	4.1	Identify analysis leads for barley for Nordic and Central zones	S. Goritschnig	31.12.2021
15	4.1	Establish Data analysis working group, including analysis leads for different crops from all zones	S. Goritschnig	31.12.2021
16	4.2	Identify analysis lead for wheat in Nordic zone	S. Goritschnig	31.12.2021
17	5	Curate data from first evaluations 2021 and upload to EURISCO-EVA intranet	S. Goritschnig/S. Kumar	31.12.2021
18	5	Provide access to EURISCO-EVA intranet to all partners	S. Goritschnig/ S.Kumar	31.12.2021
19	5	QC analysis of first evaluations 2021 on EURISCO EVA intranet	Analysis leads for crops/geographic zones	28.2.2022
20	6	Organize virtual meeting on data analysis	S. Goritschnig	15.03.2022
21	6	Organize in person annual meeting, location tbd	S. Goritschnig	31.05.2022

Appendix 3: Participants list

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