

**Summary report of the**

**Annual meeting of the  
European Evaluation Network (EVA) for Maize**

**2–3 June 2022  
Belgrade, Serbia**



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This first in-person project meeting took place on 2–3 June 2022 in Belgrade, Serbia, in connection with the XXVth EUCARPIA Maize and Sorghum conference which happened in the days before. Network partners who were not able to travel to the meeting participated remotely through a virtual connection. The agenda of the meeting is attached as Appendix 1 and the list of participants as Appendix 2.

## **1. Welcome and introduction**

On behalf of the local organizers, the Maize Research Institute Zemun Polje, Violeta Andjelkovic welcomed all participants to Belgrade and the EVA meeting. She expressed her wish that the preceding days of scientific presentations and discussions during the EUCARPIA meeting would inspire the project discussions.

The EVA Coordinator, Sandra Goritschnig, opened the meeting, welcoming online participants as well as several observers who had attended the EUCARPIA meeting and were interested in learning more about the EVA Maize network. She thanked V. Andjelkovic for her help in organizing the meetings back to back and also for the opportunity to present the EVA Maize network during a session of the EUCARPIA meeting.

After a round of introductions, S. Goritschnig noted that the agenda of the meeting had been adjusted to allow the majority of discussions to happen before lunchtime on 3 June, as some participants had planned an early departure.

## **2. EVA networks – current status and workplan**

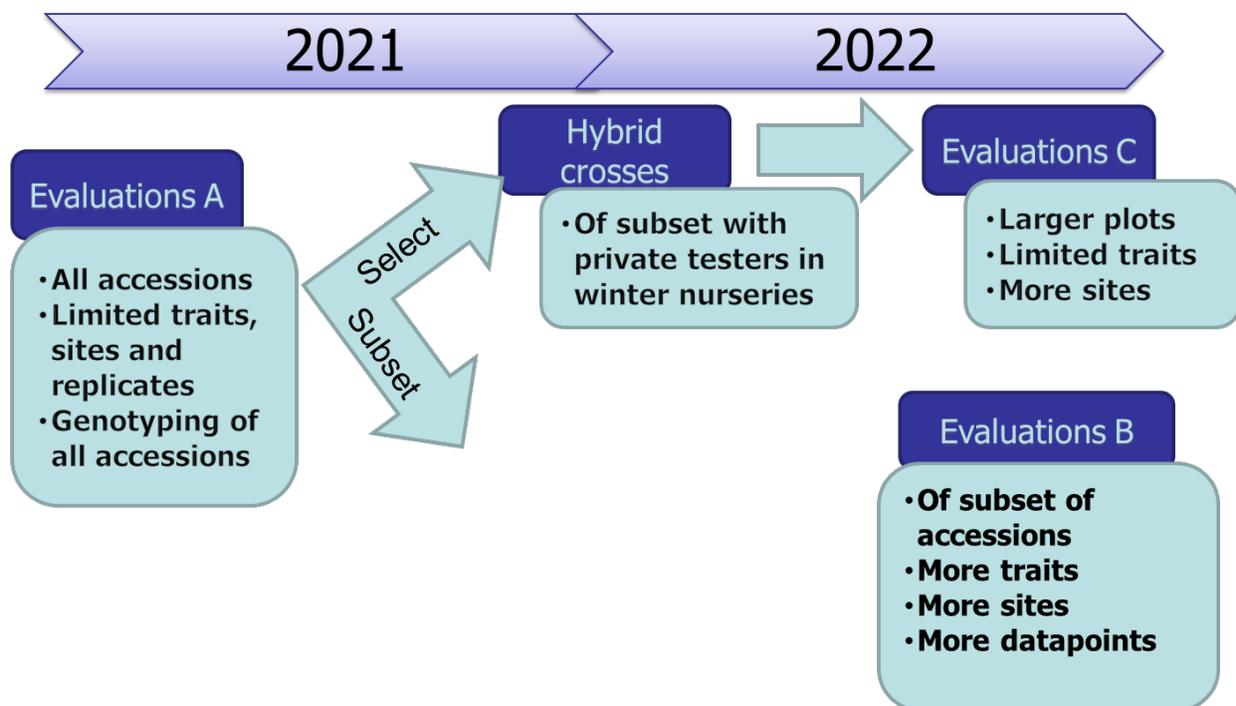
Chair: V. Andjelkovic

### **2.1 Overview of the current status of the ECPGR Evaluation Network EVA**

S. Goritschnig provided an overview of the status of all currently active EVA networks. She reminded partners of the [website of the EVA Maize network](#) and the project extension until November 2023, granted by the German donor to compensate for COVID-19-related delays and difficulties. The EVA Maize network currently counts 18 partners from nine countries, of which eight are breeding companies.

### **2.2 Review of EVA Maize network work plan 2019–2023**

Partners were reminded of the agreed work plan and timeline for the different planned activities between 2019 and 2023. The work plan (Figure 1) foresees three-step evaluations of accession sets: 1) an initial characterization of all accessions in a set conducted in a few locations (Evaluation A), 2) a selection of a subset of accessions based on Evaluation A and genotyping information for which in-depth evaluation for agronomic traits, biotic and abiotic stresses are conducted in more locations and with more plants and replicates (Evaluation B) and 3) generation of hybrid populations from the subset using private testers provided by company partners, for evaluation of relevant agronomic traits (Evaluation C). The setup of this work plan requires that genotyping information is available before, or at the same time, as results from Evaluations A, as both inform the following Evaluations.



**Figure 1.** Schematic work plan of the EVA-Maize Network. Evaluations are conducted in sequential format, with production of hybrid populations outsourced to winter nurseries of network partners.

Due to the timing of the work plan, the in-depth evaluations (B and C) of set 3 are scheduled for 2024, after the end of the current project. However, given that evaluations are contributed by partners in kind and with an intention of continuing the network activities after 2023, this was considered acceptable.

The first set of accessions consisted of 218 accessions from five genebanks, of which 86 were selected for hybrid production and 127 for in-depth evaluations in 2022. The second set, which is currently in the field for a first round of evaluations (Evaluations 2A) consists of 224 accessions from eight genebanks. A further set of accessions is currently in multiplication by participating genebanks, or could be made available from existing stocks for 2023. Genebanks were reminded to record the flowering time of their accessions to estimate the FAO maturity important for matching accessions with appropriate trial locations.

Evaluations ongoing in 2022 include Evaluations 2A in 13 trial sites across Europe, covering 3–5 different environments per accession; Evaluations 1B in 18 trial sites across Europe, covering 1–11 environments per accession and Evaluations 1C in 12 trial sites across Europe, covering 4–6 environments per hybrid population.

### 3. Overview of EVA materials

Chair: V. Andjelkovic

Genebanks presented the materials they had selected for the EVA Maize network, highlighting their main criteria for selection and any multiplication activities in the project.

Beate Schierscher-Viret (Agroscope, Switzerland) had selected 100 accessions of the Swiss collection, including 80 local varieties and 20 inbred lines showing good adaptation to cold conditions. She highlighted that even newly collected accessions were still very diverse. During the 2021 multiplication season, 21 descriptors were collected on the materials, improving the phenotypic database of the collection.

Hrvoje Šarčević (University of Zagreb, Croatia) presented the genebank system in Croatia, which is decentralized and includes *ex situ* and field collections from several public institutes and universities. The planned activities of the Croatian genebank in the period 2021–2027 are in line with the recently published *Plant Genetic Resources Strategy for Europe* and are listed in the National Programme for the Conservation and Sustainable Use of Plant Genetic Resources for Food and Agriculture in the Republic of Croatia. The Croatian plant genetic resources database lists ~4,400 accessions of plants related to original and traditional agricultural plants that are threatened to disappear. The maize collection, managed by the University of Zagreb, holds 253 accessions including 90 local inbred lines and 160 landraces collected from different regions across Croatia. Especially in the southern parts of Croatia, hot and dry conditions prevail. For the EVA Maize network, a total of 50 accessions have been selected for multiplication and evaluation, and the University of Zagreb contributes also to Evaluations 2A.

Carlotta Balconi (CREA-CI, Italy) presented the materials provided from the maize collection held in Bergamo, which is the largest in Italy with more than 5,700 accessions. For the EVA Maize network, the focus was put on 600 Italian landraces collected across Italy starting from 1950. In the first set, 42 accessions were selected; 19 of them had previously been included in the ResGen project, which collected 400 accessions across Europe with the goal to maximize diversity, while balancing the contributions of participating countries, creating the European Union Maize landraces core collection (EUMLCC). The other 23 landraces were selected based on recent experimental activities showing their diversity. CREA is not performing multiplications in 2022 but may have additional accessions available for a third set, which have not yet been genotyped.

Alain Charcosset (INRAE, France), presenting on behalf of Anne Zanetto, noted that the 80 accessions selected from the French genebank were also included in the ResGen project. Overall, the French collection of maize includes ~1,200 accessions (263 of which are of French origin), and all have been genotyped.

Ana Maria Barata (BPGV-INIAV) reported that the Portuguese collection holds 2,710 maize landraces collected across Portugal, and characterization data for 1,683 have been collected during regular multiplication activities and made available in EURISCO in 2022. Portugal is also participating in a seed longevity experiment at the Svalbard Global Seed Vault, and has provided seeds of five maize accessions that will be screened for germination ability over 100 years. INIAV has provided 37 accessions to the EVA network, which have also been part of the ResGen project and had been collected across Portugal.

Natalija Kravic (MRIZP, Serbia) presented the Serbian collection, which holds 5,860 maize accessions including more than 2,000 local landraces. In total, 95 accessions have been selected for the three sets of the EVA project, including both local landraces from the western Balkans as well as introduced populations. The local landraces were selected based on previous characterizations, as potential sources of drought tolerance, with good agronomic performance and a high level of diversity. The introduced populations were selected based on abiotic stress trials under hot and dry conditions and exhibited good agronomic performance in temperate

climates. Here, the intention is to enhance EURISCO by adding this international germplasm to the database.

Danela Murariu (Suceava genebank, Romania) reported that their maize collection consists of more than 5,000 accessions, the majority of which are local landraces, mainly collected in the mountainous regions in Romania. There are only few landraces collected from the plains, because of potential contamination with commercial hybrids in this agronomically active area. The 50 accessions selected for EVA are representative of all regions of Romania, with early maturity and resistance to low temperatures.

Pedro Revilla (CSIC, Spain) recalled that the Spanish national genebank has the most diverse maize collection in the old world, with more than 3,000 accessions. The MBG (CSIC) in Pontevedra holds almost 300 populations and 258 inbred lines. For EVA, 180 Spanish accessions had been selected, representing large diversity in geographic origin, use and maturity ranges. He explained that the selection criteria for this set were availability, geographic diversity, diversity of uses and interest; and then explained how they considered each selection criteria. He also highlighted that their research station is equipped to evaluate biotic and abiotic stress resistance under controlled conditions.

Pedro Mendes-Moreira (ESAC, Portugal) noted that four of the five maize accessions provided by his institute have previously been published<sup>1</sup>. They have not been added to EURISCO yet, but will be included in the database as one output of the project.

Claude Welcker (INRAE) was impressed with the diversity of maize germplasm used in the EVA network and suggested including historical data where available to get a complete picture.

## 4. Review of experiments and preliminary data

Chair: V. Andjelkovic

### 4.1 Summary of genotyping results

Stephane Nicolas (INRAE, France) presented results from genotyping of 416 EVA accessions, following the same protocol as in a recently published study analyzing worldwide landraces (Arca et al, 2021a<sup>2</sup>). Briefly, maize populations were sampled using 15 plants and the DNA was genotyped using 50k SNP arrays. He noted that the Illumina array used for the genotyping will only be available until the end of 2022 and reminded partners to provide any missing materials to INRAE for genotyping before then.

The resulting data was used to predict allelic frequencies allowing comparison of landraces with a modified Roger's distance matrix. Further analyses investigated hierarchical clustering, Multidimensional Scaling (MDS) and structure analyses using Admixture. The data indicated a strong variation of diversity among the analyzed accessions. Analysis pointed out some accessions, especially from Swiss origin, with very low genetic diversity, which was expected

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<sup>1</sup> <https://www.mdpi.com/2071-1050/11/21/6081/htm> and <https://link.springer.com/article/10.1007/s10722-006-9168-3>

<sup>2</sup> Arca et al 2021a: <https://doi.org/10.3389/fpls.2020.568699>

since they were inbred lines and not landraces. Interestingly, some EVA landraces extended the genetic diversity of the worldwide panel described in the previous study (Arca et al., 2021b<sup>3</sup>).

Genetic grouping and hierarchical clustering had been used to guide the selection of appropriate testers to produce hybrid populations for Evaluations 1C (e.g. no flint tester was used for landraces assigned to European Flint). The majority of clearly assigned accessions are of the Italian Flint, Northern Flint or Pyrenean-Galicia group, however, most of the accessions were admixed (membership in a group < 0.6).

For further analysis, it was proposed to include the generated data in a PhD project investigating the contribution of landraces to the genetic diversity of modern breeding germplasm, supervised at INRAE GQE. This would extend the results in Arca et al, 2021b, adding a study on the comparison of landraces and inbred lines. Several additional analysis approaches were proposed, including using a different bulk genotyping method (e.g. single primer enrichment technology (SPET)), given that the current one will no longer be available in 2023. To deeper characterize the genetic diversity of maize landraces, INRAE GQE-Le Moulon built a new proposal called 'MineLandDiv' with eligible partners from EVA to apply to the ERA-NET SusCrop call. Finally, the combination of phenotypic and genotypic data generated in the network will be used to predict different traits interesting to participating breeders and breeding companies.

## **4.2 Overview of trials from 2021 (Evaluation 1A)**

During 2021, a first evaluation cycle (Evaluation 1A) was conducted on 218 maize accessions in between four and six environments per accession. Network partners presented preliminary results from their trials, focusing on traits evaluated, presenting characterization and biotic stress trial results and noting lessons learned and suggestions for upcoming trials.

V. Andjelkovic presented preliminary results from the MRIZP trial in Serbia, in which 103 accessions of mostly mid-late maturity had been characterized. In addition to the common checks used across all trials, several local checks had been included. In the analysis she noted variability of the different traits, especially when comparing averages of material from different geographic origins.

Cyril Bauland summarized the evaluations conducted by INRAE in France. Because the trial site is optimized for silage maize, no grain was harvested and characterized and the main traits scored are flowering time, plant height and lodging. Due to bird damage, fewer than expected plants per accession could be scored, but a correlation between genetic populations and bird damage was observed.

C. Balconi summarized results from evaluations conducted in Bergamo, Italy. The experiment was conducted on 54 accessions from Italy, Romania and Spain with two replicates, and observations were collected on plant architecture, plant morphology and yield traits. Some low germination reduced the number of plants per plot. Large variation was observed for many of the traits, and even some variability within plots of the same accession, especially for Spanish landraces. She noted some difficulty scoring stalk rot severity, as this was a new trait and some accessions had limited numbers of plants. Furthermore, she suggested adjusting the evaluation scales for some traits (e.g. ear husk cover and ear damage), which at the moment only have few

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<sup>3</sup> Arca et al 2021b: <https://www.biorxiv.org/content/10.1101/2020.09.30.321018v1>

allowed score values. It was also suggested to include additional pictorial guidance for traits such as ear husk cover in the standard protocol.

D. Murariu presented results from their trials on Romanian and Spanish materials in 2021, where they collected a number of morpho-physiological and agronomic descriptors and also scored for resistance to natural infection with *Fusarium verticilloides*. Like other partners, they observed a diverse range of values for the different characteristics. She noted that their grain yield estimates use 18% moisture content in the calculation, and this will have to be adjusted to compare to other trial results.

Alexandre Strigens reported on the trial conducted at DSP in Delley, Switzerland on early maturing accessions. A hailstorm in June 2021 caused significant damage to the trial and, together with wet conditions in May–July, promoted common smut (*Ustilago maydis*) infection. They observed a large range of flowering dates in the early material and noted a correlation between flowering date and grain moisture.

Thomas Presterl reported on the disease trials conducted by KWS in France, Germany and Italy, focusing on Northern Corn Leaf Blight (NCLB) and *Fusarium* artificial infection. They also observed a large range in flowering time, but also diversity in disease resistance which could be used for selection. The infections will be repeated on promising materials during Eval1B in 2022.

Rosa Ana Malvar reported on the trial conducted in Pontevedra, Spain in 2021, which used a 2-block design with all available accessions grouped by precocity. The conditions of the trial were considered optimal, and all traits were scored according to the protocol. All except the Romanian early maturing accessions had a good variation in flowering time and some accessions showed good yield under the growing conditions in Pontevedra. All traits were highly variable and initial multivariate analysis identified principal components explaining most of the genetic diversity of the material.

#### **4.3 Ongoing evaluations in 2022 (Evaluations 1B, 1C, 2A): experimental design and evaluated traits**

Partners involved in evaluations ongoing in 2022 reported on their current status.

R. Malvar outlined the experimental setup for their in-depth evaluations Evaluation 1B on a subset of 52 accessions from the first set, which will be tested in separate trials for cold tolerance and biotic stresses with artificial inoculations with *Fusarium verticillioides* and *Sesamia nonagrioides* over two years.

V. Andjelkovic noted that some of the mid-late material from the first set was selected for in-depth evaluation in 2022 (Evaluation 1B), with a focus on assessing drought tolerance. Since there is no specific protocol to evaluate abiotic stress, yield and other agronomic traits will be used as a proxy. For example, drought stress can lead to small kernels, reducing the 1,000 kernel weight. Due to early drought conditions in 2022 plants were still small. Environmental data are available for the trial site and will be collected over the duration of the experiment.

C. Bauland recalled the methods used to define the subsets for hybrid production and Evaluation 1C. Hybrid production was split among four partners and two majority groups, generating 107 populations of early maturity and 29 populations of mid-late maturity, and was conducted in winter nurseries in Chile. Production overall was successful, with only a few missing hybrids, which in

the experimental setup were replaced by filler hybrids. Experimental trials were designed as two complete blocks with subtrials for each tester to minimize competition between them. Populations were randomized manually in each subtrial to avoid the same neighbours in replications. The commercial checks included in the trials were grouped as they are mainly included to provide control for the precocity of the material.

Due to some delays in shipping, hybrid populations produced by DSP could not be distributed in time to evaluation sites. However, A. Strigens had been able to identify additional locations in Switzerland and Austria where these could be evaluated. In the trials originally planned, the missing populations were replaced by filler hybrids.

N. Delic noted that the mid-late maturity testcross populations will be evaluated in three locations in Serbia, covering different microclimates, as well as one location in France. Considering the distance between the Serbian sites it may be difficult to score flowering time in all locations.

#### **4.4 Discussion**

Partners noted the heterogeneity with which the data had been analyzed and presented by the different researchers and discussed how the data analysis should be organized to ensure comparability of the different trials. Some partners noted that within the project the phenotyping and data analysis undertaken by public institutions should be budgeted and not expected as in-kind contributions, considering the financial limitations that most public institutions are facing.

Partners noted that grain yield was reported using different grain moisture levels in the calculations. The standard protocol defines the level for calculation at 10%, thus partners should ensure that they record grain yield at the same moisture percentage. Furthermore, since grain yield of testcrosses is scored differently, the standard protocol should be updated to include this method. V. Andjelkovic highlighted the importance of using a standardized experimental protocol, since yield is dependent on the plant density in the evaluation plots.

For the analysis of the biotic stresses, it will be important to consider the different pathogen races used in the trials or present naturally at different locations as well as to collect weather data for the different trial sites.

### **5. Outlook**

Chair: A. Charcosset

#### **5.1 Dissemination and exploitation of results**

Participants discussed what outputs they expected from the analysis of the generated data. It was generally agreed that the data analysis and valorization will be very important. Given the diverse approaches used by partners it would be critical to see how data from individual trials could be combined in a global analysis. All raw data will be made accessible through the EURISCO-EVA intranet. It was suggested that each trial is first analyzed individually, using standard statistical analysis tools, and that a global analysis could then follow for suitable trials and traits. This global analysis was considered an important output of the project. The integration of data for a publication should also be coordinated and could focus on the analysis of some interesting traits in all trials.

Companies were equally interested in describing the diversity of the maize germplasm through global analysis of the landrace phenotyping and genotyping data as well as the agronomic performance of the testcrosses. It was emphasized that, although in the long term the intention should be to add diversity to farmers' fields through breeding using genebank materials, the main focus was not on the overall diversity but on specific traits important for adaptation to climate change. The expectation was that materials could be used to maintain or enhance the diversity of existing breeding pools with a limited number of accessions.

C. Balconi suggested writing a paper on the EVA networks for the *Genetic Resources* journal, focusing on the participatory aspects of the project and the expected outputs and benefits for participating partners.

## **5.2 Discussion on the continuation of network activities after the end of the current project (Nov. 2023)**

Participants were generally positive to continue their collaboration after the end of the current project in November 2023, also given that the current work plan already foresees activities in 2024. One priority would be to invite new genebanks to the project, to extend the diversity of the material under investigation. Greece and Turkey could be considered, also based on some connections made with researchers and companies during the EUCARPIA meeting. The EVA coordinator will contact relevant representatives to establish their interest.

Given the need for financial support for the network activities in the future, with a focus on budget for genotyping, data analysis and meetings, a variety of options were suggested, including exploring funding options from different countries, applying to the ECPGR Working Group grant scheme with a relevant activity and other international project calls.

## **6. Data management**

Chair: S. Goritschnig

S. Goritschnig presented the standardized data collection template, which had been developed in parallel with the EURISCO-EVA intranet, to be used by all EVA networks for direct upload of phenotypic data into the database. Several iterations of the template had been circulated at various times, but the current version should be considered the final one compatible with the automatic uploader. The template consists of two files, Part I providing indications and metadata for the experiments and Part II being the template to be filled with data, which appeared clear and appropriate to the participants.

Stephan Weise, calling in remotely, presented the upload process and responded to questions from the audience. During a hands-on session, partners provided feedback on the portal, which will be communicated to the EVA developer for implementation. Accession metadata in the database can also include pictures and partners agreed to include photos of maize accessions, depicting ears after harvest, ears after storage and kernels.

S. Goritschnig reminded partners that the EURISCO-EVA intranet was designed to only hold raw phenotypic data, although an extension for SNP viewing may be feasible. Genotypic data and analysis results will be shared via project-specific platforms and ultimately deposited in public

repositories. S. Weise will evaluate if files can be attached to trials, which would help for instance to store initial statistical analyses and some additional metadata.

R. Malvar noted that the design of sub-blocks can not be defined in the current template using the field layout. It was suggested to use the 'Remarks' field in the experiment metadata to include relevant information or consider uploading the field design as a picture to the documents folder.

S. Nicolas informed that all genotyping data would be permanently stored in an INRAE database (<https://thalia.moulon.inra.fr/>) and can be made available to partners for download. The curated dataset and analysis could be made available for publication via <https://data.inrae.fr/>, where the data would receive a DOI and before publication an EVA project space could be created in the INRAE cloud for exclusive access to network partners.

## 7. Data analysis

Chair A. Charcosset

Continuing from earlier discussions, partners brainstormed on suitable data analysis approaches.

### Statistical analysis:

Most trials had used two replicates in two blocks and where only one replicate was evaluated, internal checks had been used to account for error variance.

It was agreed that the data of each experiment should first be analyzed by the partner who conducted the trial and/or the randomization. For trials with two blocks (replicates) models should be in the form

$Y = \mu + B + RC + G + E$ , where

B = block effect (can be fixed or random)

RC = random field effects (row column or autoregressive, possibly subblocks)

G = fixed entry effect (landrace or check)

E = random error term

This will help to evaluate the precision of the trials before going for more global analyses. A threshold for data quality should be based on estimates of least means.

For global analyses, R. Malvar kindly volunteered to conduct this analysis for the trials evaluating landraces per se (Evaluations A and B), while C. Bauland would do the analysis for all hybrid testcross trials (Evaluation C). Results for the first set may be available for presentation at a meeting in January 2023.

### Selection of accessions for Evaluation 2C:

Given the difficulties in distributing seeds to winter nurseries in 2021, partners agreed to select the subset 2C for hybrid production earlier this year, by mid-September at the latest. As before, the selection should be based on the integration of flowering and plant height data and genotyping results of set 2 accessions. Therefore, all relevant data should be received by early September so that they can be used for selection. Furthermore, to facilitate shipping of accessions to the winter nurseries, C. Bauland agreed to collect seeds of all accessions at INRAE Le Moulon and coordinate the seed shipments to Chile.

MRIZP will again be responsible for the production of hybrids of mid-late maturity (> FAO 400).

## Genotyping

Partners were reminded to send accessions not yet genotyped to INRAE by mid-June, to ensure the data analysis would be done before September 2022. Some partners expressed interest in genotyping their testers for hybrid production, in order to assess the genetic distance between landraces and testers. Some partners already have genotyping data for their testers and would confirm whether that could be shared within the consortium.

INRAE (S. Nicolas et al.) proposed to conduct a genome-wide association study (GWAS) using the data from the global analyses mentioned above. To do this environmental GWAS effectively, geographical coordinates of collection sites of the landraces are needed and will be collected if not available yet in EURISCO. S. Goritschnig will provide a template to collect this missing information from genebanks.

## **8. Wrap-up of meeting**

S. Goritschnig summarized the main results of the discussions during the meeting and actions to be taken by participants (see action list in Appendix 3). She thanked all partners, including those connecting online for their active participation and especially local host V. Andjelkovic for her assistance with logistics.

A. Charcosset thanked participants for the discussions and expressed satisfaction with the progress made during the past days.

The next meetings will be held virtually and are planned for mid-September 2022 to discuss the hybrid production and in early 2023 to review initial data analysis results. Another in-person meeting may be possible in 2023, if necessary, but will be confirmed later.

## Appendix 1. Meeting agenda

### Agenda (20/05/2022)

Venue: Falkensteiner Hotel, Belgrade, Serbia. "Iolite" meeting room

THURSDAY 2 JUNE		
13:30 – 14.00	Registration	
	<b>Welcome and introductory session</b>	<b>CHAIR: V. ANDJELKOVIC</b>
14.00 – 14.10	Welcome by local host, ECPGR	<i>V. Andjelkovic</i> <i>S. Goritschnig</i>
14.10 – 14.20	Introduction of participants	<i>All</i>
	<b>EVA networks – current status and workplan</b>	
14.20 – 14.30	Overview of the current status of the ECPGR Evaluation Network EVA	<i>S. Goritschnig</i>
14.30 – 14:40	Review of network workplan 2019-2023	<i>S. Goritschnig</i>
	<b>Overview of EVA materials</b>	<b>CHAIR: V. ANDJELKOVIC</b>
14:40 – 15:30	Genebanks present on their collections and how they selected accessions for evaluation in EVA (~5 mins each)	<i>B. Schierscher-Viret</i> <i>H. Šarčević</i> <i>C. Balconi</i> <i>A. Barata</i> <i>N. Kravic</i> <i>D. Murariu</i> <i>P. Revilla</i> <i>A. Charcosset</i> <i>P. Mendes-Moreira</i>
<b>15.30 – 16:00</b>	<b>TEA/COFFEE BREAK</b>	
	<b>Review of experiments and preliminary data</b>	<b>CHAIR: V. ANDJELKOVIC</b>
16:00 – 16.20	Summary of genotyping results	<i>S. Nicolas</i>
16:20 – 17:00	Overview of trials from 2021 (Evaluation 1A) <ul style="list-style-type: none"> <li>- Traits evaluated</li> <li>- Characterization data</li> <li>- Preliminary results from disease trials</li> <li>- Lessons learned and suggestions for upcoming trials</li> </ul>	<i>V. Andjelkovic</i> <i>C. Balconi</i> <i>D. Murariu</i> <i>A. Strigens</i> <i>T. Presterl</i> <i>R. Malvar</i>
17:00 – 17:30	Ongoing evaluations in 2022 (Evaluations 1B, 1C, 2A): experimental design and evaluated traits <ul style="list-style-type: none"> <li>- In depth evaluations 1B</li> <li>- Testcross populations 1C</li> <li>- Preliminary evaluations of second set 2A</li> </ul>	<i>C. Bauland</i> <i>S. Goritschnig</i>
17:30 – 18:00	Discussion	<i>All</i>
<b>20.00</b>	<b>SOCIAL DINNER</b>	

**Venue: Falkensteiner Hotel, Belgrade, Serbia. “Iolite” meeting room**

<b>FRIDAY 3 JUNE</b>		
	<b>Outlook</b>	<b>CHAIR: A. CHARCOSSET</b>
09.00 – 09.20	Dissemination and exploitation of results	<i>S. Goritschnig</i>
09.20 – 10.30	Discussion on continuation of network activities after end of current project (Nov. 2023)	<i>All</i>
<b>10.30 – 11.00</b>	<b>TEA/COFFEE BREAK</b>	
	<b>Data management</b>	<b>S. GORITSCHNIG</b>
11.00 – 11.20	Review of data collection templates	<i>S. Goritschnig</i>
11:20 – 12:30	Hands-on session with EURISCO-EVA intranet	<i>S. Weise (remote)?</i>
<b>12.30 – 14.00</b>	<b>LUNCH</b>	
	<b>Data Analysis</b>	<b>CHAIR: A. CHARCOSSET</b>
14.00 – 14.45	Brainstorming and discussion on data analysis – questions to be addressed, approaches, possible contributors	<i>All</i>
14.45 – 15.30	Planning of data analysis work for 2022/23	
<b>15.30 – 16.00</b>	<b>TEA/COFFEE BREAK</b>	
16:00 – 17.00	Wrap-up of meeting	<i>S. Goritschnig/All</i>
17.00	<i>End of meeting</i>	

## Appendix 2. List of participants

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### Appendix 3: Action list

#	Activity	Action	Responsible	Due date
1	genotyping	Provide seeds of missing accessions (incl testers) to INRAE for processing	S. Goritschnig to coordinate	Jun-22
2	Evaluations	Update standard protocol and data collection template with new traits data as necessary	S. Goritschnig	Jun-22
3	Eval 1A	Include all phenotypic data in new data collection template and upload to EURISCO-EVA intranet	Partners responsible for trials 1A	Jul-22
4	Eval 1A	Initial statistical analysis of data from individual trials	Partners responsible for trials 1A	Jul-22
5	Eval 2C	Send seeds of set 2 accessions (early maturity) to INRAE (C. Bauland) to facilitate seed shipment to Chile	Genebanks	Jul-22
6	Eval 1A	Upload pictures to EURISCO-EVA (ears at harvest, after storage, kernels)	S. Goritschnig	Aug-22
7	Eval 2A	Provide preliminary data on flowering time and vigour	Partners responsible for trials 2A	Aug-22
8	genotyping	Provide PCA data and genetic grouping information for all genotyped EVA accessions	S. Nicolas/D. Madur	Sep-22
9	genotyping	Create a repository for genotyping data accessible to network partners	S. Goritschnig/S. Nicolas	Sep-22
10	Eval 2C	Meeting for Selection of subset 2C for production of hybrid populations	S. Goritschnig and evaluating partners	Sep-22
11	Eval 2C	Send seeds to Chile for hybrid production	C. Bauland	Sep-22
12	Accessions	Collect geographic origin data where missing	S. Goritschnig and genebanks	Nov-22
13	Eval 1B	Include all phenotypic data in new data collection template and upload to EURISCO-EVA intranet	Partners responsible for trials 1B	Nov-22
14	Eval 1C	Include all phenotypic data in new data collection template and upload to EURISCO-EVA intranet	Partners responsible for trials 1C	Nov-22
15	Eval 2A	Include all phenotypic data in new data collection template and upload to EURISCO-EVA intranet	Partners responsible for trials 2A	Nov-22
16	Data analysis	Initial statistical analysis of data from individual trials	Partners responsible for trials 1B, 1C and 2A	Nov-22

#	Activity	Action	Responsible	Due date
17	Data analysis	Virtual meeting to discuss analysis results of trials in 2021 and 2022 and next steps.	All	Jan-23
18	Eval 2B	Finalize selection of subset for Eval2B based on set 2C and phenotyping results of Eval 2A	S. Goritschnig	Jan-23
19	Eval 2B	Create trial matrix for subset 2B and evaluation sites	S. Goritschnig	Jan-23
20	Eval 2C	Compile list of hybrid populations and assign EVA ID	S. Goritschnig	Jan-23
21	Eval 2C	Create trial matrix for hybrid populations and evaluation sites	S. Goritschnig	Jan-23
22	Eval 3A	Finalize trial site commitments for Eval 3A trials on set3 in 2023	S. Goritschnig and evaluating partners	Jan-23
23	Accessions	Finalize set 3 based on Eval3A capacity and precocity of available material.	S. Goritschnig	Jan-23
24	Eval 3A	Create trial matrix for landraces and evaluation sites	S. Goritschnig	Jan-23
25	Evaluations	Provide deadlines for receipt of seeds for different evaluations	all evaluating partners	Jan-23
26	workplanning	Update information in workplan for set 2 and 3	all partners	Jan-23