European
Cooperative
Programme
for Plant
Genetic
Resources
ECP/GR

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

22 November 2021
90:00 – 13:30, online MS Teams

Federal Ministry
of Food
and Agriculture

Summary report of the meeting

The meeting took place on 22 November 2021, 9:00 to 13:30, on MS Teams. The agenda of the meeting is attached as Appendix 1 and the list of participants as Appendix 2.

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 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/maize 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 EVA maize network currently had 18 partners from nine countries, including 11 genebanks and research institutes and 7 breeding companies. The Cooperation Agreement had not yet been signed by all partners; as soon as this is completed a compiled document with all signature pages would be made available on the network 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.

Based on a survey among partners and discussions conducted in 2020, a workplan had been developed (outlined in Figure 1), which foresees evaluation of accessions sets divided into three steps: 1) an initial characterization of all accessions in a set conducted in fewer locations and with fewer replicates (Evaluation A), 2) a selection of a subset of accessions based on Eval 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 company testers, for evaluation of relevant agronomic traits (Evaluation C). The setup of this workplan requires that genotyping information is available before, or at the same time, as results from Evaluations A, as both inform the following Evaluations.

Project funds were available for multiplication and hybrid production of up to 750 accessions in total, or three sets of 250 accessions. Due to Covid-19 restrictions, however, the first two sets of accessions were smaller, leaving some unused funds which could potentially be used for other activities within the project, e.g. lab tests by public sector partners. A budget revision to accommodate this would need to be discussed in the group and accepted by the donor.

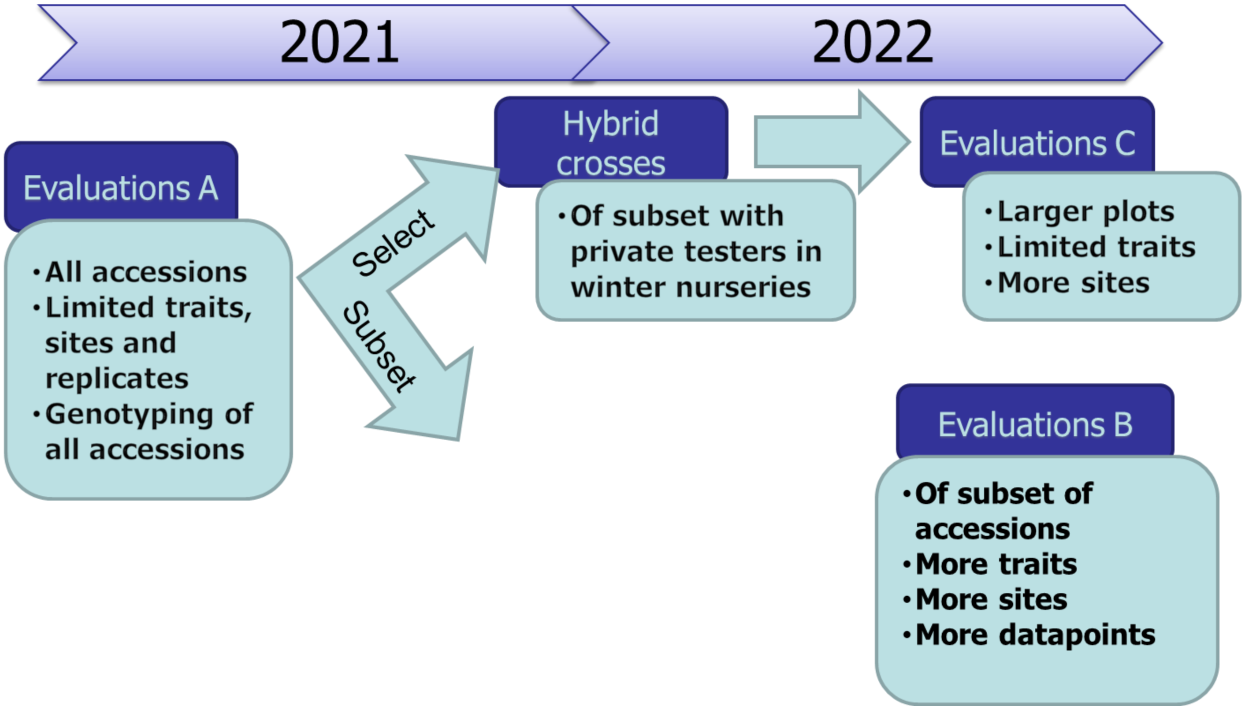

Figure 1. Schematic workplan of the EVA-Maize Network. Evaluations are conducted in sequential format, with production of hybrid populations outsourced to winter nurseries of network partners.

2.2 Highlights from 2021

During 2021, a first evaluation cycle was conducted on 218 maize accessions in between four and six environments per accession. Several genebanks regenerated maize accessions for the next evaluation cycle. Genotyping of all accessions was performed by INRAE. Partners shared their experiences from the first evaluations with the participants, highlighting any problems with the trial or the provided protocols and data collection templates.

2.2.1 Preliminary data from Evaluations 1A (set 1) in 2021

Violeta Andjelkovic (MRIZP, Serbia) reported that their trial had not experienced any major problems, except that the current setup provided too little material for determination of moisture content and proposed to increase the number of rows or plants in a plot to ensure sufficient material was available for evaluation of all relevant traits. She also reported some difficulty with scoring early vigor and suggested that the scoring protocol for this trait should be clarified. Furthermore, because of phytosanitary restrictions, import to and export from Serbia could be delayed and more seeds should be provided by partners where possible to allow phytosanitary testing during import and so that material is already available for generation of testcross populations. Additional comments on criteria for the selection of future accessions sets were brought up for the general discussion.

Rosa Ana Malvar (CSIC, Spain) presented the trials conducted in Pontevedra, one of two sites where all accessions were evaluated. Variability was observed for all traits, except tassel type, and ear samples had been collected for further characterization, during which the ears will also be photographed. It was noted that some accessions may have been previously misclassified according to their precocity data.

Bettina Kessel (KWS, Germany) provided feedback on their trials conducted in Germany, France and Italy, which focused on biotic stresses (Fusarium ear rot and NCLB). She noted that the indicated maturity rating of some accessions did not fit with the selected trial site. For Fusarium ear rot, they performed artificial inoculation, using F. verticilloides and F. graminearum, as the two strains have a different geographic distribution and infect maize of different precocity. The accessions showed good variation for all traits in the different locations, even for NCLB resistance, corresponding to different races of the fungus. She suggested that NCLB should be evaluated in more locations in order to identify the most resistant material against multiple races. Owing to its low heritability Fusarium ear rot should be evaluated with at least two replicates per location. Additional clarification was requested on how to use the data template effectively.

Danela Murariu (Suceava Genebank, Romania) reported on the trials conducted on 51 accessions in Romania, collecting data for more than 20 traits. During the growing period, the trial experienced some extreme weather, including very low temperatures in May affecting emergence of plants as well as extensive rain and hail in July. Their trials identified several accessions with cold tolerance or resistance to F. moniliforme. The only problem experienced during this trial were some inconsistencies between protocol and scoring scale in the data template for the trait “early vigor”.

B. Kessel pointed out that F. moniliforme is the old name of F. verticilloides and suggested that the Fusarium data from the different trials and different strains be compared, and resistant accessions tested again in suitable multiple locations with the different strains.

Carlotta Balconi (CREA-CI, Italy) reported on the trial conducted on 54 accessions in Bergamo, Italy. She highlighted that for the majority of accessions, the germination was low and fewer than the expected 30 plants grew to maturity, suggesting that more seeds should be provided initially to ensure enough material was available for evaluation. They noticed large variability in some traits for Spanish and Romanian landraces and took pictures of ears at harvest. Some landraces were also multiplied during this evaluation and could be used in future trials. They experienced some difficulty scoring stalk rot with the provided protocol, suggesting that it should be revised. In addition, some traits showed little variation, also because allowed scores did not include intermediate values; thus it was suggested to increase the range of allowed values for several traits.

Alexandre Strigens (DSP Delley, Switzerland) reported on their trial on early maturity accessions in Switzerland, noting that several accessions were much earlier than predicted from their maturity rating. Plant vigor was good for their trial but a hailstorm in late June resulted in a number of snapped stalks and lodged plants and heavier than normal infection with smut fungus. Ears had recently been harvested and associated traits were being collected. He pointed out that Switzerland, being outside the EU, seed distribution could be impacted, and also agreed with the suggestion that more seeds should be included in shipments from/to Switzerland. He further suggested to revise the protocol for smut fungus, to include descriptions where the fungus was observed and also to include more intermediate values in the scoring scale.

Alain Charcosset (INRAE, France) presented the French trials in Ploudaniel, where also the full set of 218 accessions was evaluated. They experienced uncommon bird damage in their field, resulting in reduced plant density but were able to evaluate flowering time, plant height as well as a rough estimate of resistance to some diseases. He noted that the range of flowering time was very high among accessions, with 45 days between the earliest and latest accessions, but it was highly correlated between the trials where all materials were evaluated. Preliminary analysis of the phenotypic data was done to inform the selection of accessions for hybrid production.

2.2.2 Preliminary results from Genotyping

Stephane Nicolas (INRAE, France) presented preliminary results from genotyping of 416 EVA accessions, following the same protocol as in a recently published study analysing worldwide landraces (Arca et al, 2021: https://doi.org/10.3389/fpls.2020.568699). Briefly, maize populations were sampled using 15 plants and the DNA genotyped using 50k SNP arrays. 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, principal components (PC) and structural analyses.

In their published study, they had identified seven genetic groups highlighting clear geographical trends with latitude and longitude, indicating that structure was driven mostly by adaptation and isolation by distance. Using these data as a structure, the EVA accessions were assigned to the different genetic groups according to genetic similarity, where possible. Overall, the landraces displayed large genetic diversity, except for some accessions provided by the same genebank. PC analysis highlighted some landraces that extended the genetic diversity observed in the published set. The genotyped accessions included already phenotyped accessions as well as those still in the pipeline and would inform selection of the next set of accessions.

Together with preliminary phenotypic data on flowering time, hierarchical clustering was used to select landraces for hybrid production, using their assignment to the seven genetic groups to guide the choice of « testors » to produce hybrids and also to eliminate redundancy between landraces by removing landraces genetically close based on their MRD distancesv from the subsets.

During the discussion, C. Balconi proposed to include other accessions from the Italian collection in the EVA materials to extend the variety from the Italian flint material that was already provided. A. Charcosset commented that the first sets were selected with speed and constraints faced by genebanks due to Covid, but the criteria for a third set could be optimized with a view to maximising diversity of the overall set to allow a global analysis of all evaluated accessions. In this regard, there would be a need to balance the contributions from genebanks to eliminate bias towards certain accession types. He also noted the low diversity observed in some landraces, which could be explained by low diversity in the field or the multiplication protocol applied to these accessions, and thus suggested to review the multiplication process for these accessions to identify potential bottlenecks of diversity. Finally, INRAE also involved some student researchers to work on combining the phenotypic and genotypic data and these results would be presented during the next meeting. S. Goritschnig reminded participants that funding within the current project provided for multiplication and genotyping of up to 750 maize accessions, thus there is room to identify a balanced third set for multiplication in 2022.

Genebank partners were reminded to ensure the material included in multiplications and sent for evaluations was also included in the genotyping pipeline and sent to INRAE for this purpose.

2.3 EURISCO – EVA intranet demo

Suman Kumar (IPK, Germany) provided a live demo 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 would be incorporated in the next iteration. It was expected that the intranet would be accessible for the EVA maize partners at the beginning of 2022.

The EURISCO-EVA intranet stores relevant metadata information on partner organizations, trials, evaluated accessions and traits. Phenotypic data could be filtered using simple searches and visualized in graphs. Pivoted tables allow comparison of accessions based on scores for different traits. The platform should provide intuitive access to the different datasets and guidance material would be developed to assist partners in its use. Trainings for the use of the platform would also be provided as necessary.

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

Partners appreciated the efforts into developing this database platform, looking forward to being able to use it soon. One comment on improving the displayed data was to provide the link between the different data points and to be able to draw distributions as well as correlations and principal component analyses from the existing data. Visualization of the data was currently limited to some data combinations but these functionalities can be extended based on user feedback.

Pictures of accessions can be uploaded to the database and R. Malvar (CSIC) confirmed that she would be taking pictures of the ears and kernels for the first set of accessions during the final phenotypic scoring. Partners were reminded to include standard colour scales when taking photographs, in order to facilitate comparisons.

Genotypic data would not be stored on the intranet due to storage limitations, but metadata would be displayed, as well as links to the public repository where the data will be hosted. Additionally, options to store analysis results of the genotyping on the EURISCO-EVA platform would be explored.

Partners were reminded to provide raw data for their trials to facilitate the statistical analysis in the database and to use one data file per experiment to prevent mix-ups of data. S. Goritschnig noted that the intention was to curate the data from the 2021 evaluations and include them in the database over the coming months so that these were available on the platform when it was rolled out to partners in spring 2022.

3. Outlook for activities in 2022

3.1 Update and outlook on Evaluations1C (set 1C)

During a meeting in early October, the network had discussed the selection of the subset of accessions for production of hybrid populations by partners in their winter nurseries. Minutes of the meeting were available for project partners on the sharepoint.

For the selection, several parameters were taken into account: 1) accessions were assigned to genetic groups as described above based on available genetic data, 2) redundancy was minimized by avoiding selection of genetically close accessions and maximize genetic diversity in the selection, 3) phenotypic data from Evaluations 1A were used to select accessions with flowering times in a suitable range for the testers.

The choice of tester was also done based on the genetic data and partners RAGT, Lidea Seeds and DSP Delley selected to use an Iodent tester to be crossed with flint-type material of relatively early maturity. MRIZP selected to focus on dent-type materials of later maturity, which would be crossed with several testers. In total, for this subset 1C 86 accessions were selected from the original 218, of which 36 would be crossed with more than one tester, creating some overlap to provide links between different testers used. Thus 107 populations, with a predicted FAO rating of 200-400 and 29 populations with FAO>300, would be produced. Information on the selected accessions and matched testers was made available on sharepoint. Populations would be produced in winter nurseries in Chile and seeds were expected to be available for distribution to evaluators in March 2022.

Based on the populations that would be available for evaluation in 2022, the offers for evaluations were reviewed to match the sites and populations in terms of maturity. The target was to evaluate each population in five locations with two replicates and partners noted their preferred capacity in terms of maturity and trial size.

Nenad Delic (MRIZP, Serbia) offered to evaluate 24 hybrids each for maturity groups 400 and 500 in up to four locations with up to two replicates, with more locations possible if fewer replicates were needed. The offered locations represented diverse microclimates and thus provided a good variety of environments. This would mainly cover the hybrids produced in their own winter nursery, but seeds could also be forwarded to other partners if enough were available.

Amelie Le Foll (MAS Seeds, France) offered to evaluate hybrids of a higher maturity in one location in Southern France, but noted they may be flexible to also offer a location more suitable for early material in central France.

Carole Derue (Lidea Seeds, France) had originally offered a location in France with a focus on lower maturity material, but could possibly split into two locations to also accommodate higher maturity populations, if necessary.

Alexandre Strigens (DSP Delley, Switzerland) offered an early maturity trial, also Stephane Melkior (RAGT, France). Alain Murigneux (Limagrain, France) was not present at the meeting but had previously indicated that they were flexible in their trial location to best suit the project.

Based on feedback received from the partners, a matrix would be generated to maximize the numbers of trial sites per population, based on a proposal developed by Cyril Bauland (INRAE). S. Melkior suggested that the seed distribution could be centralized, perhaps by INRAE, but this would need to be confirmed. Partners were also invited to comment on the proposed traits for evaluation and associated protocols and scoring templates, which would be updated in time for the trials.

3.2 Update and outlook on Evaluations 1B (set 1B)

As outlined in the workplan, a subset of the accessions evaluated in 2021 would be evaluated more in depth for further traits in additional locations and with more replicates in 2022. Overall, the combination of different approaches and trials would generate large amounts of data for the accessions and offer a complete picture of their characteristics. The selection of the subset could be aligned with that used in hybrid production (set 1C) to maximize genetic diversity in the set but the set could also include additional lines of interest based on available phenotypic data. It was noted that a pitfall of the selection based on genotype groups was that it favoured small clusters, while larger clusters have fewer representative accessions. To facilitate the selection of interesting accessions not included in set 1C, the available genotypic and relevant phenotypic data would be combined for all accessions, and used to identify very early or very late accessions that were not suitable for hybrid production, as well as those with other interesting characteristics that may be useful to further evaluate. This would also help to identify any bias which may have been created in the initial selection.

Seven partners had offered to contribute to these evaluations and their trial offers were compared with the available accession subset.

Bettina Kessel (KWS) confirmed that KWS would be able to repeat the same material for disease traits as in 2021 Evaluations 1A to generate more statistically significant data and noted that the Fusarium trials should be done with two replicates, requiring a larger amount of seeds to be distributed. Numbers of individual trials would be adjusted to better match maturity of the materials to the trial sites. As these trials would be in addition to the next set 2 of accessions for Evaluations 2A, the following selection was agreed: NCLB trials would be done on all previously resistant accessions included in the set for hybrid production, plus any outstanding accessions that were not included in that set. As Fusarium trials involve a larger workload associated with artificial inoculations, it was agreed that from the set1B for hybrid production, only the best and worst accessions in terms of Fusarium resistance would be selected from different maturity groups for a smaller validation experiment to verify the results from 2021 in addition to accessions with promising Fusarium resistance not included in set 1C and accessions selected for Evaluations 2A. (see also section 3.3). It was also noted that early material would be inoculated with F. graminearum and later material with F. verticilloides, as these strains were more relevant for different maturity types.

Franck Chopin (Bayer Seeds, France) offered three sites in Germany, France and Hungary, which could accommodate the subset 1C plus extra accessions and noted that they would need to receive a final list of set 1B by mid-January 2022 to be able to plan their trials and receive the seeds by March 2022.

R. Malvar (CSIC) confirmed that they would do artificial inoculation field trials for F. verticilloides on 50 accessions which could be selected similar to the set for KWS. Their protocol used inoculation of the kernel and required replicates over two years to ensure statistical significance. A second trial was proposed on 50 accessions with artificial inoculation with corn borer (Sesamia nonagrioides), also over two years.

C. Balconi (CREA-CI) noted that in their location, F. verticilloides was predominant and in their artificial inoculation trials, they also preferred to do kernel inoculation mimicking insect damage, as it was less work intensive. Scoring could be based on visual examination or mycotoxin content, and would depend on the numbers of accessions evaluated. KWS used the silk channel infection protocol as they don’t usually rely on presence of insect damage. B. Kessel also noted that from their experience, the visual scoring and mycotoxin content were highly correlated for artificial inoculations. C. Balconi noted that it may be useful to implement both protocols as they could be complementary, representing primary and secondary infection pathways. Partners agreed to share their inoculation protocols so a standard protocol can be developed.

A. Strigens (DSP Delley) confirmed that their trials would focus on the subset 1C selected for hybrid production. If this could be split into early and later maturity varieties, he could evaluate sets of 40 accessions in two locations, or alternatively do the whole set in one location only, preferably under cold conditions, which could be complementary to the other trials.

S. Melkior (RAGT) confirmed that they could offer a trial for the 86 accessions in subset 1C in Brittany, France with prevailing colder conditions and artificial inoculation with NCLB.

A trial matrix will be created for Evaluations 1B to match selected accessions and available trial sites and shared with partners in January to facilitate trial planning and seed distribution. The standard protocols for the different traits will be reviewed and amended as necessary, missing trait scoring protocols will be developed in time for the spring evaluations.

3.3 Update and outlook for Evaluations 2A (set 2)

In 2021, ~200 accessions were multiplied by partners in Croatia, France, Portugal, Serbia, Spain and Switzerland; in addition, the French genebank at INRAE has stocks available for 80 additional accessions. Most of these have been genotyped and included in the presented results and any remaining ones have been sent to INRAE for genotyping. Genebanks were reminded to provide missing information on collection sites and FAO maturity ratings, where available, to allow assignment of accessions to matching trial locations.

The second set 2 will be selected from these available accessions, taking into account available harvested seed and maturity group, with the aim to ensure maximum diversity in the evaluated set, based on available genetic information. Partners were asked to provide feedback on their contributions for the second set in a workplan excel file, similar to the one for the first round. In addition, it was noted that some accessions multiplied and genotyped in the first round were also still available to be included in this set.

A. Charcosset noted that it would be advisable to create a balance of origin within the material so that all countries are appropriately represented. While important traditional maize growing countries should be given extra weight, attention should be taken not to have certain countries overrepresented in the EVA set. Thus, using the available genetic data, closely related accessions from the same genebank could be eliminated to enhance the overall diversity in the set for evaluation.

S. Goritschnig noted that the second set would again be matched to available evaluation sites using a matrix as last year and a final number in the set adjusted as necessary. The second set of accessions includes material from different countries as compared to the first set. Italy offered to provide Italian landraces from available stocks to be included in the second set. Anne Zanetto (INRAE) confirmed that the 18 landraces multiplied in France this year were part of the ResGen88 project and had already been genotyped. Portugal could potentially provide accessions from their available stocks, depending on whether 2000 seeds are available. Unfortunately, Portugal will still not be able to multiply in 2022.

One other aspect to consider in the selection of set 2 would be the focus of the project, which is currently split in interest groups between drought tolerance and cold adaptation. This would depend on the origin of material.

3.4 General discussion

V. Andjelkovic requested company partners to provide direction for the selection of the final set of accessions, in terms of kernel type and maturity ratings. Taking the three sets together all accessions from participating genebanks should be included in the evaluations, but care should be taken especially for the final set to select appropriately according to the needs and priorities of the breeders. For example, the majority of accessions for hybrid production were selected from early material, thus if only MRIZP is interested in evaluating late maturity dent type materials then the sets should also be split accordingly. A. Strigens noted that the selection of early material for hybrid production in Chile was also based on the fact that seeds usually arrive later in spring and if evaluated in the same year would have to be of early maturity. Alternatively, hybrid production in the summer in Europe could use later materials as the seeds would be available in time for early sowing. He also noted that around 20 accessions from the Swiss genebank were indeed inbred lines, which could explain the lack of diversity between them. A. Charcosset noted that the intention was to sample the diversity present in the different genebanks and thus create an overall EVA set with maximum diversity, including different kernel types and maturity ratings and carrying target traits such as drought tolerance.

Another suggestion was to split the remaining sets into early and late materials, to facilitate evaluation across different sites and ensure that all maturity types are included in in depth evaluations. The selection of early materials in this first hybrid subset 1C was done also for practical reasons, as noted by A. Strigens and S. Melkior.

Genebanks were invited to propose accessions for multiplication of a third set in 2022. This set could include up to 340 accessions, as the genotyping budget still had this amount available. Partners were reminded to aim for a diverse set of accessions, in terms of origin and genetic relatedness, to ensure that the overall panel of EVA accessions was as diverse as possible. V. Andjelkovic noted that accessions from the Serbian genebank were historically from former Yugoslavia and so could have been collected in different regions. S. Goritschnig reminded partners that EURISCO relied on data provided by national coordinators, which was not always complete. Therefore, one of the overall goals of EVA was also to raise awareness of the importance of complete data and improve information in EURISCO.

To facilitate selection of this set and future subsets and to ensure timely seed distribution to partners, a calendar with deadlines will be created to guide logistics efforts.

Partners were reminded that the evaluations of set 3 as scheduled would go beyond the current project duration, and even though multiplication, hybrid production and genotyping would be covered by the project budget, the second year of evaluations would take place in 2024, and analysis would extend beyond the current project.

Next steps for the project would include finalizing the workplans for accession sets 1 and 2, and selection of set 3, based on discussions in the meeting. Actions related to that are summarized in the action list in Appendix 3.

4. Any other business

V. Andjelkovic repeated her invitation to network partners to attend the XXVth EUCARPIA Maize and Sorghum Conference, scheduled in Belgrade, Serbia from 30 May to 2 June 2022. It was suggested to hold an in-person project meeting adjacent to this conference, possibly using 1,5 days on 2 and 3 June, depending on the final programme of the conference and partners were asked to block these days in their calendars. Potential topics for this meeting could include a detailed review of protocols and templates, data analyses and long-term outlook for the EVA Maize network.

Meeting participants were invited to respond to an online survey to provide their feedback on the meeting and the project overall. Survey respondents were overall satisfied with the outcomes of the meeting and the progress made in the project. Topics that would require additional discussion were identified as how to involve all partners in the joint analyses of the generated data (genotyping and phenotyping) and to discuss a strategy for publication of results in line with the cooperation agreement and according to interests of both public and private partners. A clear plan and timeline was considered essential to streamline seed distributions to partners for the different activities. Some partners highlighted problems experienced in their work due to the Covid-19 pandemic, sometimes gravely affecting their project activities. Respondents were also strongly in favour of holding the next meeting in person, to facilitate interaction with partners.

Appendix 1. Meeting agenda

22 November, 9:00– 13:00 (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 2021	
9:05 – 9:15	Review of project workplan and general update	S. Goritschnig
9:15 – 9:45	**Highlights from 2021** - Preliminary data from Evaluations 1A (set 1) - Overview of multiplications for next round of evaluations	V. Andjelkovic R. Malvar B. Kessel D. Murariu C. Balconi A. Strigens A. Charcosset S. Goritschnig
9:45 – 10:15	Update from genotyping - Data from first batch - Plan for next batches	S. Nicolas
10:15 – 10:30	General discussion on first round of evaluations	All
10:30 – 10:45	EURISCO – EVA intranet demo	S. Kumar
10:45 – 11:00	Coffee break	
	Outlook for activities in 2022	
11:00 – 11:30	**Update and outlook on Evaluations 1C (set 1)** - Selection of accessions for hybrid production - Timeline for hybrid production - Review of traits for evaluations C - Discussion	S. Goritschnig/All
11:30 – 12:00	**Update and outlook on Evaluations 1B (set 1)** - Selection of accessions for in-depth evaluation of per se accessions - Review of traits and locations for Evaluations B - Discussion	S. Goritschnig/All
12:00 – 12:30	**Update and outlook for Evaluations 2A (set 2)** - Overview of available accessions - Review of traits and locations for Evaluations A - Genotyping of accessions - Discussion	S. Goritschnig/All

12:30 – 12:55	**General discussion** - Outlook for 3rd set of accessions (multiplications in 2022) - Wrap up of conclusions and agreements - Review of timelines and deliverables - Define next steps	All
12:55 – 13:00	Any other business - Next meeting	
13:00	Close of meeting	

Appendix 2. List of participants

Violeta Andjelkovic
Maize Research Institute Zemun Polje
Slobodana Bajica 1
11080 Belgrade - Zemun Polje
Serbia
Email: violeta@mrizp.rs

Carlotta Balconi
Consiglio per la Ricerca in Agricoltura e l`Analisi dell`Economia Agraria, Centro di Ricerca Cerealicoltura e Colture Industriali (CREA-CI), Sede di Bergamo
Via Stezzano 24
24126 Bergamo
Italy
Email: carlotta.balconi@crea.gov.it

Ana Maria Barata
Banco Portuguęs de Germoplasma Vegetal Instituto nacional de Investigação Agrária e Veterinária (BPGV-INIAV)
4700-859 Braga
Portugal
Email: anamaria.barata@iniav.pt

Jean Beigbeder
Pro-Mais – Euroseeds
Avenue des Arts 52
1000 Brussels
Belgium
Email: jeanbbd@wanadoo.fr

William Bourdoncle
Bayer – Crop Science
Borkener Straße 169
46325, Borken
Germany
Email: william.bourdoncle@bayer.com

Alain Charcosset
INRAE - Génétique Quantitative et Évolution Le Moulon - Université Paris-Sud - CNRS - AgroParisTech Ferme du Moulon
91190 Gif-sur-Yvette
France
Email: alain.charcosset@inrae.fr

Franck Chopin
Bayer Crop Science
Chateau Mercier
82170 Monbequi
France
Email: franck.chopin@bayer.com

Nenad Delic
Maize Research Institute Zemun Polje
Slobodana Bajica 1
11080 Belgrade - Zemun Polje
Serbia
Email: ndelic@mrizp.rs

Carole Derue
Lidea Seeds
117 avenue de Vendôme
41000 Blois
France
Email: carole.derue@lidea-seeds.com

Amelie Le Foll
MAS Seeds
Route de Saint-Severa
40280 Haut-Mauco
France
Email: lefoll@maisadour.com

Gwenaëlle Gossart
Lidea Seeds
117 avenue de Vendôme
41000 Blois
France
Email: gwenaelle.gossart@lidea-seeds.com

Brigitte Gouesnard
INRAE, UMR AGAP
Bâtiment Arcad
10 rue Arthur Young
34000 Montpellier France
Tel: (33) 4 32 72 23 20
Email: brigitte.gouesnard@inrae.fr

Colin Guillaume
MAS Seeds
1 Route de Saint-Sever
40280 Haut-Mauco
France
Email: guillaume@maisadour.com

Bettina Kessel
KWS SAAT
Grimsehlstrasse 31, Postfach 1463
Einbeck
Germany
Email: bettina.kessel@kws.com

Natalija Kravić
Maize Research Institute Zemun Polje
Slobodana Bajica 1
Belgrade
Serbia
Email: nkravic@mrizp.rs

Suman Kumar
Leibniz Institute of Plant Genetics & Crop Plant Research (IPK) – Gatersleben
Stadt Seeland
Corrensstrasse 3
Germany
Email: kumar@ipk-gatersleben.de

Ulrike Lohwasser
Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3
06466 Seeland OT Gatersleben
Germany
Email: lohwasse@ipk-gatersleben.de

Giuseppe De Luise
Consiglio per la Ricerca in Agricoltura e l`Analisi dell`Economia Agraria, Centro di Ricerca Cerealicoltura e Colture Industriali (CREA-CI),), Sede di Bergamo
Via Stezzano 24
24126 Bergamo
Italy
Email: Giuseppe.deluise@crea.gov.it

Rosa Ana Malvar
Mision Biologica de Galicia, CSIC
Apartado 28
Pontevedra 36080
Spain
Email: rmalvar@mbg.csic.es

Stephane Melkior
RAGT 2n
ZA Route de Dax
40300 Port de Lanne
France
Email: SMelkior@ragt.fr

Danela Murariu
Suceava Genebank
B-dul 1 Mai nr. 17
720224 Suceava
Romania
Email: dmurariu@suceava.astral.ro

Rita Redaelli
Consiglio per la Ricerca in Agricoltura e l`Analisi dell`Economia Agraria, Centro di Ricerca Cerealicoltura e Colture Industriali (CREA-CI), Sede di Bergamo
Via Stezzano 26
24126 Bergamo
Italy
Email: rita.redaelli@crea.gov.it

Pedro Manuel Reis Mendes Moreira
Departamento de Cięncia Agronómicas
Politécnico de Coimbra – Escola Superior Agrária de Coimbra
3045-601 Coimbra
Portugal
Email: pmm@esac.pt

Hrvoje Šarčević
Faculty of Agriculture; University of Zagreb
Svetosimunska 25
Zagreb 1000
Serbia
Email: hsarcevic@agr.hr

Beate Schierscher-Viret
Agroscope
Route de Duillier 50
1260 Nyon 1
Switzerland
Email: beate.schierscher-viret@agroscope.admin.ch

Alexandre Strigens
Delley Semences et Plantes SA
Route de Portalban 40
1567 Delley
Switzerland
Email: strigens@dsp-delley.ch

Alessio Torri
Consiglio per la Ricerca in Agricoltura e l`Analisi dell`Economia Agraria, Centro di Ricerca Cerealicoltura e Colture Industriali (CREA-CI), Sede di Bergamo
Via Stezzano 26
24126 Bergamo
Italy
Email: alessio.torri@crea.gov.it

Anne Zanetto
INRAE - Centre de Montpellier
Batiment ARCAD. Rue Arthur Young
34000 Montpellier
France
Email: anne.zanetto@inrae.fr

ECPGR Secretariat

Vanessa Bryant
The Alliance of Bioversity International & CIAT
Via San Domenico 1
00153 Rome
Italy
Email: v.bryant@cgiar.org

Sandra Goritschnig
The Alliance of Bioversity International & CIAT
Via San Domenico 1
00153 Rome
Italy
Email: s.goritschnig@cgiar.org

Lorenzo Maggioni
The Alliance of Bioversity International & CIAT
Via San Domenico 1
00153 Rome
Italy
Email: l.maggioni@cgiar.org

Appendix 3: Action list

#	Activity	Action	Responsible	Due date
1	Eval 1A	provide list of accessions multiplied during Eval1A in CREA-CI trial	C. Balconi	Jan-22
2	Eval 1B	compile list of accessions for subset in Eval 1B (=hybrid subset 1C plus interesting accessions in terms of resistance and extreme maturity ratings)	S. Goritschnig	Jan-22
3	Eval 1B	finalize trial site commitments for in-depth *per se* trials in 2022	S. Goritschnig and evaluating partners	Jan-22
4	Eval 1B	create trial matrix for landraces and evaluation sites	S. Goritschnig	Jan-22
5	Eval 1C	compile list of hybrid populations and assign EVA ID	S. Goritschnig	Jan-22
6	Eval 1C	finalize trial site commitments for hybrid trials in 2022	S. Goritschnig and evaluating partners	Jan-22
7	Eval 1C	create trial matrix for hybrid populations and evaluation sites	S. Goritschnig	Jan-22
8	Eval 2A	finalize trial site commitments for Eval 2A trials on set2 in 2022	S. Goritschnig and evaluating partners	Jan-22
9	Eval 2A	create trial matrix for landraces and evaluation sites	S. Goritschnig	Jan-22
10	Evaluations	provide deadlines for receipt of seeds for different evaluations	all evaluating partners	Jan-22
11	genotyping	provide PCA data and genetic grouping information for all genotyped EVA accessions (including French accessions already genotyped through a different project)	S. Nicolas/D. Madur	Jan-22
12	Multiplication	provide list of accessions that could be provided for sets 2 and 3 from existing stocks (CREA and INIAV)	C. Balconi, AM. Barata	Jan-22
13	workplanning	Update information in workplan for set 2	all partners	Jan-22
14	Eval 1A	take pictures of ears	R. Malvar	Feb-22
15	Eval 1A	provide final evaluation data for Eval 1A trials in 2021 on sharepoint	evaluation partners	Feb-22
16	Evaluations	share inoculation protocols for Fusarium ear rot	B. Kessel, C. Balconi, R. Malvar, S. Goritschnig	Feb-22
17	Multiplication	select third set of maize accessions, with a view to maximum diversity and representativeness	genebanks	Feb-22

#	Activity	Action	Responsible	Due date
18	workplanning	include calendar with deadlines in MS Teams environment	S. Goritschnig	Feb-22
19	Eval 1A	upload pictures to EURISCO-EVA	S. Goritschnig	Mar-22
20	Eval 1A	upload data from Eval 1A to EURISCO-EVA	S. Goritschnig	Mar-22
21	Eval 1B	compile scoring protocol and data collection templates for traits in evaluations	S. Goritschnig	Mar-22
22	Eval 1C	compile scoring protocol and data collection templates for traits in evaluations	S. Goritschnig	Mar-22
23	Evaluations	review scoring protocol for plant vigor, stalk rot, smut fungus; include intermediate values for scores	S. Goritschnig	Mar-22
24	Evaluations	review data collection template and create templates for Evaluations B and C	S. Goritschnig	Mar-22
25	genotyping	ensure that all accessions included in multiplications and evaluation sets are in the genotyping pipeline or have data available	S. Goritschnig	Mar-22
26	genotyping	create a public repository for network genotyping data	S. Goritschnig/INRAE	Mar-22
27	data analysis	present student's results on data analysis during next in person meeting	A. Charcosset	May-22
28	meeting	next project meeting in person in Belgrade, Serbia	All	Jun-22

Appendix 4: Acronyms and abbreviations

CSIC	Consejo Superior de Investigaciones Científicas, Spain
CREA	Council for Agricultural Research and Analysis of Agricultural Economics, Italy
DNA	Deoxyribonucleic acid
ECPGR	European Cooperative Programme for Plant Genetic Resources
EUCARPIA	European Association for Research on Plant Breeding
EURISCO	European Internet Search Catalogue
EVA	European Evaluation Network
FAO	Food and Agriculture Organization of the United Nations
INIAV	Instituto nacional de Investigação Agrária e Veterinária, Portugal
INRAE	National Research Institute for Agriculture, Food and Environment, France
IPK	Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany
MRIZP	Maize Research Institute Zemun Polje, Serbia
NCLB	Northern Corn Leaf Blight
PC(A)	Principal Component (Analysis)
SNP	single-nucleotide polymorphism