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

27 May 2020
12:30 – 16:30, online MS Teams

Federal Ministry
of Food
and Agriculture

Summary report of the meeting

The meeting substituted for an in-person project meeting on 27-28 May 2020 in Paris, France, and took place on 27 May 2020, 12:30 to 16:30, on MS Teams. The agenda of the meeting is attached as Appendix 1 and the list of participants as Appendix 2.

A number of preparatory documents had been made available to the project partners in advance of the meeting on MS Teams. These included presentations on ECPGR and the EVA networks and on EURISCO and its role within EVA.

1. Welcome and introduction

The EVA coordinator Sandra Goritschnig opened the meeting, reminding participants of the expected outcomes of the meeting and highlighting the available documents. She explained the functions of the virtual meeting platform used. Participants introduced themselves to the group in a round table.

2. General discussion of the project

2.1 Overview of the ECPGR Maize Working Group

Violeta Andjelkovic (Maize Research Institute Zemun Polje (MRZIP), Serbia), Chair of the ECPGR Maize Working Group (WG) reflected on the history of the Maize WG. She noted that European genebanks store more than 60,000 maize accessions recorded in EURISCO, many of which, especially in southeastern Europe have not been systematically investigated and characterized. Only limited activities in some countries have been done to collect, conserve, document and make available to users these maize genetic resources (GR). Work to identify duplicates and to provide evaluation data would be very beneficial for their further utilization. During a EUCARPIA Maize and Sorghum Conference in 2015 the need for a formal establishment of an ECPGR Maize WG was agreed, and supported by the Executive Committee of the ECPGR. The Maize WG was officially established in early 2019, at the beginning of ECPGR Phase X, and held its first meeting in December 2019. During this meeting, attended by 25 participants from genebanks and research institutes working on maize GR, the proposal for the extension of the EVA project to include a Maize Network was conceived and successfully submitted to the German Ministry of Food and Agriculture as donor.

The main objectives of the Maize WG involve improving the documentation and conservation of maize national collections and promoting their characterization, evaluation and use in breeding and research. Work is also planned on the development of standardized minimum descriptors for improved data comparability and of standardized regeneration protocols, and on genotyping projects to characterize accessions and detect duplicates. Violeta Andjelkovic highlighted the overlap of these objectives with the goals of the EVA project and noted that one of the expected outcomes of the meeting would be a list of traits and descriptors important to breeders.

She noted that today's meeting would be the first opportunity for representatives from genebanks and breeding companies to directly interact and discuss the goals and suggested activities within the EVA Maize Network. She hoped that despite the novelty of this network and the difficulties related to the ongoing Covid-19 pandemic a feasible workplan for EVA Maize in 2020 would be defined during this meeting, and also expressed her hope for an in-person meeting in the near future. She wished all participants a fruitful meeting and expects this network to grow with new members from genebanks and breeding companies.

2.2   Review of project proposal and current activities in the EVA Maize Network

Since most participants were new to the concept of EVA, the EVA coordinator reviewed the principles of the EVA networks, highlighting the intention of creating self-sustaining cycles of selection, multiplication, evaluation and analysis of maize accessions from European genebanks. She outlined the activities and outcomes proposed for the EVA maize project as well as the projected timeline until November 2022, noting that delays in establishing the network and limitations to activities in 2020 may be compensated for through an extension of the project duration.

She highlighted the main expectations for this meeting, which were to provide updates on genebank activities, receive feedback from breeding companies on interests and priorities, and to review and further develop a technical project proposal.

2.3   Genebanks present their ongoing activities with maize

Genebank representatives presented their maize collections, ongoing activities and potential contributions to the EVA Maize Network.

Ulrike Lohwasser (IPK Gatersleben, Germany) informed of their diverse collection of ca. 1,500 maize accessions originating from more than 40 countries (although only 51 accessions from Germany) and mainly consisting of landraces. The IPK usually regenerates 25-30 maize accessions annually, however, due to restrictions because of Covid-19 no regenerations are done in 2020. She presented the IPK regeneration protocol and noted that characterizations were done using adapted versions of the UPOV and IBPGR descriptors.

Carlotta Balconi (CREA Bergamo, Italy) noted that the Italian maize genebank is involved in activities around the promotion of utilization of local varieties and contributes to maize breeding activities. CREA Bergamo houses the largest maize collection in Italy, with ca. 5,700 accessions, including 600 landraces from Italy, which had been collected from all over Italy since the 1950s and all of which are included in the AEGIS European Collection. In projects aimed at valorizing the genetic variety, they have characterized accessions for their nutritional and safety characteristics, as well as biochemical composition, with a special interest in maize used for polenta. CREA is involved in a number of national and international research programmes, including participatory breeding initiatives. In terms of their contribution to the EVA project CREA is currently multiplying 23 Italian landraces from their collection. In addition, 19 Italian landraces that are part of the GENRES 088 project, in which they are involved together with INRAE in France (A. Charcosset) are being regenerated and genotyped and could be included in the EVA list of accessions. She closed by emphasizing CREA's commitment to the EVA Maize Network and their interest to create synergies within the network.

Danela Murariu (Suceava Genebank, Romania) presented activities on maize GR in Romania, where 5,695 maize accessions, mostly from Romania, are preserved in different institutes across the country. The collection comprises mainly local landraces and inbred lines, with a large amount of accessions collected in mountain and submountain regions higher than 500 m above sea level. Genebank materials are well documented in their national database with passport data and information on characterization and conservation. Suceava genebank regenerates 50 – 60 maize accessions annually. Within several national projects, morphological, biochemical and molecular characterization datasets have been generated, resulting in the identification of 200 accessions that are resistant to cold, 100 accessions with high protein content and 85 accessions resistant to Fusarium.

Ana Maria Barata (Banco Português de Germoplasma Vegetal (BPGV-INIAV), Portugal) reported that within their cereals collection, INIAV conserves about 2,700 local maize landraces, accounting for 37% of all cereals in the genebank. The landraces were collected mostly in the central and northern parts of Portugal and the Algarve, the main growing areas of maize. All accessions are documented in EURISCO and characterization data for ca. 1,700 accessions are being prepared for inclusion in EURISCO. Multiplication and characterization of accessions are annual activities of the genebank, using standard protocols and key descriptors (revised in 2008). Portugal is part of the Maize Mediterranean collection and has also included 17 accessions within the Maize European core collection. All accessions are documented in the INIAV database and INIAV is actively involved in promoting the valorization of local maize landraces among farmers and consumers.

Pedro Mendes Moreira (Instituto Politécnico de Coimbra, Portugal) presented his institute's activities in relation to maize GR, which include characterization and evaluation of traits as well as socioeconomic studies, food technology and sensory evaluation aimed at valorization of local landraces among all stakeholders, following a transdisciplinary and multi-actor approach. They are involved in several Horizon2020 and participatory breeding projects, conducting field trials and collection missions. Within the EVA project the institute is multiplying five maize accessions in 2020.

Natalija Kravic (MRIZP, Serbia) informed about ongoing activities. The Serbian maize genebank collection contains 5,800 accessions and ranks among the largest maize collections in Europe, conserving 2,217 local landraces from the western Balkans, which have been classified into 16 main and two derived agroecological groups, according to natural classification based on morphological traits, origin and evolution. For the EVA project, 25 maize populations were selected for multiplication, including 15 local landraces and 10 introduced populations. The local landraces were selected based on information on drought tolerance, maximum genetic diversity and heterotic pattern. The introduced populations are also part of the drought tolerance core collection and were selected because of their stability and higher grain yield in managed stress environment trials.

Pedro Revilla (Misión Biológica de Galicia (CSIC), Spain) presented the activities of the Spanish Maize working group, which maintains the Spanish maize collection in five national centres situated in the north of Spain and in the Canary Islands, covering three main climatic areas: humid Spain, dry Spain and Canary Islands (semi-tropical). In total, almost 3,000 accessions make up the collection, with a high genetic variability. However, it should be noted that there is a significant level of redundancy within the collections. He noted that the most interesting collection could be the 120 populations of semi-tropical maize conserved in the Canary Islands, which have never been studied in detail. The Spanish national collection is made up of 90 varieties based on morphological, agronomic and molecular characterization data as well as on previous knowledge of breeders. Twenty-four varieties of the national collection belong to the European Union Maize Landrace Core Collection (EUMLCC) made in the framework of the project GENRES 088 and these are thought to be representative of the genetic variability present in Spain. The CSIC is multiplying 62 maize populations in 2020, and they are also involved in a number of trials in diverse locations and equipped for biochemical, physiological and molecular analysis.

Beate Schierscher (Agroscope, Switzerland) introduced the activities of the Swiss genebank on maize GR. Among the 410 maize accessions conserved at the genebank are 209 local landraces collected since 1941 in the maize growing valleys of Switzerland. The genebank's maize breeding

programme started in 1930 working on silage and grain maize, but was privatized in 1994 and is now done by Delley Seeds and Plants Ltd, who are present in the meeting as a potential industry partner of EVA. A number of projects have been conducted as part of the FAO Global Plan of Action (GPA) to inventorize, conserve and document their maize collection, with agronomic and molecular data available on their website.

Alain Charcosset (INRAE - Génétique Quantitative et Évolution, France) presented on behalf of Anne Zanetto the French maize genebank which conserves 1,600 landrace populations and 3,200 inbred lines in two locations. The national collection of 458 accessions, which can be exchanged within the Multilateral System (MLS) of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), is comprised of 258 French landraces, 114 Caribbean landraces and a number of synthetic and inbred lines. Multiplication of accessions is done in collaboration with breeding company partners within the Promaïs network, most of which were also present at the meeting. A. Charcosset provided additional background on the European project GENRES 088, in which a European core collection from six countries was evaluated and characterized, and noted that the EVA Maize Network provides the unique opportunity to expand on previous work. INRAE will be contributing to the EVA project with the provision and regeneration of accessions and SNP genotyping.

2.4   Round table discussion

During a round table, company representatives were invited to provide feedback and indicate their expectations in relation to the use of maize GR stored in European genebanks. They were also asked to indicate their main interests and priorities that could be addressed through participation in the EVA Maize Network.

Participants appreciated the information given by genebanks and expressed their general support for the network, but several companies indicated that they had open questions and concerns about some aspects of the project. It was noted that due to time constraints the project proposal had been written without input of breeding companies, and that there was some flexibility to adjust the project plan to better meet the needs of breeders.

Several participants requested additional information about the exchange of and access to genetic resources. Lorenzo Maggioni (ECPGR Secretary) clarified that all material used in the EVA project would be exchanged under the Multilateral System (MLS) of the ITPGRFA, using the Standard Material Transfer Agreement (SMTA), which provides free access to said material for research and breeding purposes as long as it and derived material continue to be available under the same conditions.

Other questions addressed the selection of accessions by the genebanks, the criteria of selection and how this would apply to the future evaluations. It was noted that due to limitations caused by the Covid-19 pandemic, the first set of accessions currently multiplied by genebanks would not reach the desired 250, but this would hopefully be compensated in additional sets and through use of winter nurseries, and would be discussed in more detail during the development of the technical project plan.

One partner suggested to use the EVA Network to develop a core collection in order to better understand the material present in the large genebank maize collections and to focus the evaluations on these. He also noted that it may be worthwhile to consider building the EVA Maize Network on the example of Promaïs, where breeders are successfully working together with the French genebank at INRAE to maintain and regenerate maize populations.

Several participants noted that the selection of material would affect which environments are suitable for evaluations, as there can be great differences in the earliness of the genetic resources and also in the climatic environments. One partner noted that their potential evaluation sites would be more suitable for early material, however, the project proposal indicates a preference for mid-late and late accessions. It was suggested that great attention be given to adaptation of material to certain environments when selecting the material as it would not make sense to evaluate semitropical landraces in northern Europe. Adaptation preferences in the proposal were suggested based on comments from participants during the Maize WG meeting in Belgrade (December 2019) and would necessarily be adjusted to suit the environments in which evaluations would take place.

The possibility to evaluate hybrid progeny from test crosses was generally welcomed. The selection of appropriate testers was considered important as they depend on the heterotic group of the accession.

The choice of traits and standard protocols is important in the implementation of the network. It was noted that genebanks in their characterization often follow guidance developed by CIMMYT and IPGRI, using their standard descriptors. The EVA coordinator clarified that other EVA networks, especially those for vegetable crops, use the standard descriptors in addition to standard protocols for other traits of interest. These protocols are developed with input from network partners and provided for use by all evaluators in the crop-specific network. One partner considered that the network should focus on evaluation of qualitative traits (such as disease resistance or cold tolerance) as these would be more straightforward to score and compare than quantitative traits and could use standard protocols. Another related question inquired whether genebanks use the same regeneration protocols for their populations.

One participant expressed his concern about their participation in the network as a smaller breeding company with fewer resources. It was clarified that the network would ideally involve both large and small companies according to their capacity and in order to provide synergies and benefits to all partners in the network.

One participant noted the challenge of the network to account for the genetic diversity within populations throughout the project, considering the genotyping, selection of parents for crosses as well as the evaluations themselves in different environments.

Taken together, the participants welcomed the possibility to contribute to a European evaluation network for Maize, but agreed that the details of the project would require further work and discussion.

ECPGR Secretary Lorenzo Maggioni reminded participants of the intention of the EVA networks to promote the cooperation of private companies and public institutes to jointly valorize the existing genetic diversity in European genebanks through effective partnerships. By generating good genotypic and phenotypic evaluation data, these genetic resources would become more valuable for breeders and would be more useful as they become valorized in breeding programmes. He highlighted the principles of the EVA network which are included in the document on the Establishment of the EVA networks[1], namely to operate on a pre-competitive level and on material that would remain available under the terms of the MLS of the ITPGRFA.

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[1] Document on the Establishment of the European PGRFA Evaluation Network (EVA) available at: https://www.ecpgr.cgiar.org/fileadmin/templates/ecpgr.org/upload/EVA/Establishment_of_European_PGRFA_Evaluation_Network.pdf

He further elaborated on the MLS, noting that all material shared with the SMTA could be freely used in research and breeding, as well as in the development of commercial products as long as these are again available under the MLS. The producer of material that does not remain in the MLS would be required to contribute financially to the Access and Benefit Sharing fund of the ITPGRFA. He also informed that ongoing discussions at the international level may result in modifications to the SMTA, to perhaps simplify the agreement and to address access to genetic sequence information.

In response to questions from participants about what each partner is expected to contribute to the network, L. Maggioni reminded that the project funded by Germany until November 2022 includes a budget for the genotyping and multiplication of accessions as well as the production of test crosses. Evaluations of an agreed number of accessions are expected to be contributed in kind by partners, and in return all network partners would receive priority access to all generated data within a special EVA intranet environment during a specified embargo period. Details of the expected commitments and benefits, including access to data and confidentiality aspects would be included in a cooperation agreement, which all network partners are expected to sign.

3. Development of detailed evaluation protocol

Alain Charcosset (INRAE, France) led the discussion, presenting a draft technical evaluation protocol which should provide guidance to all evaluation partners on the activities associated with the EVA Maize Network.

3.1 Genetic material

The intention of the project is to multiply up to 750 accessions over three evaluation sets, however, the number of accessions for phenotyping could be reduced to a minimum number of 100 accessions per set. The selection of the material should consider phenology appropriate for the evaluation environments, based on the FAO standards, and project partners would need to discuss and agree on which and how many different phenologies should be evaluated by the network. Types of material for evaluation could include landraces (with preference given to those considered typical or representative for each country), first generation inbred lines of landraces or more advanced inbred lines or breeding populations, and the choice would be made by all evaluation partners. Combining different types of material would enable comparisons of more advanced lines with the original landraces they were generated from, but an emphasis should be placed on evaluating landraces (a suggestion was to include 80% landraces and 20% inbred lines).

It was further suggested to incorporate material from previous projects, for example the maize core collection generated within the GENRES 088 project, which has already been characterized for some traits. Additional evaluation data as well as generating hybrid lines for evaluation within the EVA Maize Network could add value to this collection. The proposed 750 accessions should thus be sourced at about equal proportion from all participating genebanks and could include several accessions from the GENRES 088 core collection. The Italian genebank confirmed that they are including 19 accessions from the GENRES 088 collection in their 2020 multiplication activities.

Next steps within this part of the project would be to define a list of ca. 750 accessions, using a template developed also for other EVA networks, including available passport and existing

genotyping data, which would be included in the three sets for evaluation over the course of the current project. One genebank representative cautioned that seed amounts in the genebanks should also be taken into account in the selection.

One partner recommended that the overall goals of the project and traits chosen for evaluation should inform the selection of accessions by the genebanks in order to increase the probability to identify interesting and novel material for breeders for traits of specific interest to them. Participants were reminded that the intention is to generate data on accessions for which little or no prior information is available. However, including accessions with some background information on specific traits agreed as important by partners could be interesting and important and a compromise should be reached between these two aspects of the evaluation.

The Chair of the Maize WG reminded participants of the original project plan which had included multiplication activities in 2020. Since capacities for multiplication are limited, a selection of maximum 25 accessions per genebank per year was proposed and the criteria for these selections are up for discussion in this meeting and should be aligned with the interests and priorities of the breeders. In addition, due to the Covid-19 pandemic and restrictions imposed by governments, not all activities could continue as planned and therefore an extension of the project beyond 2022 is a possibility to be discussed with the donor.

3.2   Genotyping

The main objective of the genotyping, given the available budget, is to determine the main lines of diversity (structure among landraces, originality of landraces relative to inbred lines etc.) as well as to assist in predefining combination axes (testers to be excluded due to possible inbreeding depression). INRAE has been involved in genetic characterization of landraces using the Illumina 50k maize array and proposed to use this technology also in the EVA Network. A. Charcosset also informed that INRAE are presently evaluating an Illumina Infinium 25k array, which could be used instead of the 50k array (with approximately 17k common markers) to reduce the associated costs. Results from this internal evaluation would be available by September 2020 to inform the final decision on genotyping technology.

The proposed timeline accounted for the genotyping of material included in the multiplication (excluding material that has been previously genotyped), assembling the generated data (including the existing datasets), and using the data to inform generation of hybrid crosses and heterotic groups for the evaluation.

3.3   Traits

A. Charcosset presented a comprehensive list of proposed traits of interest for breeders in the EVA Maize Network, noting that this should be used to identify a manageable number of main target traits for the evaluations. He highlighted that the trait selection should take into account what material is evaluated (different traits evaluated on landraces versus test crosses), that accessions should be grouped based on phenology (as established from existing information and scored during multiplication) to ensure homogeneous trials in the environments and that this should result in a field network that is organized based on maturity groups. He also noted that the logistics of the test crosses should be discussed, including which testers to use and how to set up the test crosses to ensure appropriate representation of landrace diversity and production of sufficient seed of hybrid progeny for trials.

Traits were grouped by different categories and included descriptive traits for general characterization of the landraces (e.g. phenology, plant, ear and tassel architecture) as well as potential target traits for breeders (e.g. vigour, yield, disease resistance or adaptive traits). Partners were invited to indicate their priorities in order to agree on a manageable number of traits for joint evaluation, and to comment on what traits would be suitable for evaluation on landraces, hybrids or both.

Several participants indicated that they would need to discuss the proposal internally before being able to define priorities. One participant suggested to collect information from partners about their priorities and capacities in an anonymized survey and to discuss the resulting proposal in a follow-up meeting. This survey should also include questions to collect feedback on practical issues such as available environments and testers.

One partner commented that the phenology of the selected accessions would influence the choice of evaluation sites and should be taken into account and perhaps also indicated in the survey. Another question was whether disease resistance tests would be done under natural infection or under controlled conditions, and it was clarified that this would depend on the capacity of partners to conduct controlled experiments in kind and could also be surveyed. Standard descriptors for the traits in the list have been defined and should be used by evaluators using standard protocols and could be added to the trait list in the survey as much as possible.

3.4   Use of Testers

Concerning the open question on which testers to use for hybrid production, a common one or company-specific ones, a consensus would need to be found. It was noted that, given the variability of the genetic material, a range of different testers would be needed.

Hybrid seed production could be done at genebanks using common known testers or by private companies using their own testers. It was noted that the latter option would be easier to manage logistically but might make data analysis more difficult and require the inclusion of extra controls. However, as a benefit to the companies, this would provide them with data relevant for their own breeding programmes right away. This approach has been successfully applied in the Promaïs network, where partners have created and evaluated hybrid populations from their own internal testers.

It was clarified that the intention for the EVA network was that hybrid seeds from test crosses should be distributed to all evaluators for evaluation, and that all generated data would be shared with all network partners.

One company representative suggested that seeds from crosses with internal testers could be shared for the evaluation, as long as the identity of the tester and associated genetic information would not be shared. One participant commented that while it would be preferable to use internal testers and to evaluate those crosses only in company environments, this might again make the comparison of evaluations difficult and would require further discussion. One partner noted that the selection of testers would depend on the phenology of the accessions and should be done based on known characteristics. It was agreed to include a question on the choice of testers and sharing of material in the survey, as it was linked with priorities in traits and available environments.

3.5   Timeline

A timeline for the practical activities was presented in order to coordinate the evaluations of landraces and hybrid progenies. It was again noted that due to the Covid-19 pandemic the activities in 2020 are reduced, but genotyping data for a first set of accessions would be available by the end of 2020. These data will be useful to identify the heterotic patterns and phenology of the landraces to coordinate evaluations and logistics of hybrid production. Participants were invited to consider contributing to multiplication and hybrid production in winter nurseries. They were reminded that project budget is available for such activities, noting that hybrid progenies generated using project funds should be available for evaluation by all project partners. A final proposal made by A. Charcosset was to consider generation of double haploid (DH) lines of the most interesting landraces in the project, and a question on whether that would be interesting to partners will be added to the survey.

4. Next steps

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

1. Meeting participants and other potential public or private entities will be invited to become Members of EVA by signing the Letter of Commitment and joining the EVA Maize Network.
2. Information on maize accessions currently being regenerated by genebanks and on additional material identified for a first set will be collected and shared with network partners.
3. Seeds of the first set of accessions will be distributed to INRAE for genotyping by 15 June 2020.
4. A survey will be prepared and distributed among network partners to collect information on their priorities with respect to traits (evaluated on accessions and/or test cross hybrids), genetic material (selection criteria, preferences for phenology, proportion of landraces versus inbred lines), choice of testers and availability of seed material, availability of evaluation sites, possibility to regenerate in winter nurseries, genotyping methodology and possibility of DH production. The survey should be shared by end of June and results collected by end of July 2020.
5. Another meeting will be scheduled in Autumn 2020 with network partners to discuss results of the survey and develop a final workplan.

Appendix 1. Meeting agenda

ppt	Background and overview of the ECPGR Evaluation Network EVA	L. Maggioni
ppt	Update on current status and activities in EVA Network - Focus on Maize component	S. Goritschnig
ppt	EURISCO: ensuring integration of data in special intranet environment for EVA	S. Weise
Documents	Drafts available for: • Proposal of traits selected • Criteria for selection of accessions • Project workplan and timeline • Roles and responsibilities of partners • Letter of Commitment • Draft Cooperation Agreement	S. Goritschnig

27 May, 12:30 - 16:30 (Venue: MS Teams)

12:30 – 13:00	Connecting to MS Teams – technical assistance if needed	
	Welcome	
13:00 – 13:05	Welcome and introduction of platform and available files/tools	S. Goritschnig
13:05 – 13:15	Introduction of participants	All
	General discussion of the project	**Chair: V. Andjelkovic**
13:15 – 13:25	Overview of ECPGR Maize Working Group	V. Andjelkovic
13:25 – 13:40	Review of project proposal and current activities in the EVA network Maize	S. Goritschnig
13:40 – 14:30	Genebanks present their ongoing activities with maize (~ 5 mins each) • France • Germany • Italy • Portugal • Romania • Serbia • Spain • Switzerland	A. Zanetto U. Lohwasser C. Balconi A. Barata; P. Moreira D. Murariu N. Kravic P. Revilla B. Schierscher-Viret

14:30 – 15:00	**Round table discussion**	A. Charcosset
	Expectations with respect to GenRes	
	Feedback and suggestions from industry representatives	
	Discussion on interests and priorities for partners	
15:00-15:15	**Break**	
	Development of technical project proposal	**Chair: A. Charcosset**
15:15 - 16:15	**Discussion on:**	All
	Targeted materials (landraces / inbred lines) and criteria for choice (within and between collections, checks, other)	
	Genotyping and use for preselection of materials to be phenotyped	
	Traits and environments of interest, modalities of testing (per se / hybrid)	
	Workplan 2020/2021	
	Roles and responsibilities of partners	
16:15 – 16:30	Wrap-up of meeting:	S. Goritschnig
	Review of cooperation agreement, timelines and deliverables	
	Define next steps	

Appendix 2. List of participants

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Appendix 3: Acronyms and abbreviations

AEGIS	A European Genebank Integrated System
CIMMYT	International Maize and Wheat Improvement Center
CSIC	Consejo Superior de Investigaciones Científicas, Spain
CREA	Council for Agricultural Research and Analysis of Agricultural Economics, Italy
DH	Double haploid
ECPGR	European Cooperative Programme for Plant Genetic Resources
EUCARPIA	European Association for Research on Plant Breeding
EUMLCC	European Union Maize Landrace Core Collection
EURISCO	European Internet Search Catalogue
EVA	European Evaluation Network
FAO	Food and Agriculture Organization of the United Nations
GR	Genetic resource
INIAV	Instituto nacional de Investigação Agrária e Veterinária, Portugal
INRAE	National Research Institute for Agriculture, Food and Environment, France
IPGRI	International Plant Genetic Resources Institute
IPK	Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany
ITPGRFA	International Treaty on Plant Genetic Resources for Food and Agriculture
MLS	Multilateral system
MRZIP	Maize Research Institute Zemun Polje, Serbia
SMTA	Standard Material Transfer Agreements
SNP	single-nucleotide polymorphism
WG	Working group