European Cooperative Programme for Plant Genetic Resources
ECP/GR

Implementation of the ECPGR European Evaluation Network (EVA) on wheat and barley and vegetable crops (carrot, lettuce and pepper), with the addition of a Maize component and improved access to existing barley, wheat and maize evaluation data

GenR 2019-2

EVA
European Evaluation Network

Final technical report

July 2019 – March 2025

Federal Ministry of Agriculture, Food and Regional Identity

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1. Background

The Development and implementation of a European Evaluation Network (EVA) was included as an objective of ECPGR for Phase X (2019–2023), with the intention to promote the use of plant genetic resources for food and agriculture (PGRFA) and generate standardized evaluation data of genebank accessions and landraces for inclusion in the EURISCO database.

During several workshops, funded by the German Federal Ministry for Food and Agriculture (project GenR 2018-3), the EVA network projects were developed and formalized into a project proposal, which was accepted for funding in June 2019.

With project GenR 2019-2, the German Federal Ministry for Food and Agriculture supported the implementation of ECPGR-driven European Evaluation Networks (EVA) on wheat, barley, carrot, lettuce and pepper. After a successful meeting of the ECPGR Maize Working Group (WG) in December 2019, an extension of the project was requested and granted to establish a maize network and incorporate existing data on wheat, barley and maize into EURISCO. The project was amended through no-cost extensions to compensate for delays caused by COVID-19 and to finalize activities, extending the duration of the project until March 2025. Additional budget was approved, which allowed the inclusion of additional activities and expansion of the network to legumes in 2023. The final total budget of the project amounted to 1,053,275 EUR.

The project applied a public–private partnership (PPP) approach involving genebank managers, public and private breeders, fostering partnerships and strengthening the link between conservation and use of PGRFA.

This final activity report summarizes the outputs in all activities towards project objectives over the whole project duration.

2. Objectives of the project (amended in December 2019 and November 2022)

- Kick-start the implementation of the European Evaluation Networks on barley and wheat, on maize and on vegetables (carrot, lettuce and pepper) under the coordination of the ECPGR Secretariat
- Formalize the evaluation network consortia through the signature of Letters of Commitment by the partners and finalize specific Cooperation Agreements
- Improve the functionality of the EURISCO documentation system to enable dedicated intranet platforms for each consortium, to display and analyze data for the partners under a 3-year embargo
- Perform evaluation of cereals and vegetables:
  i. Wheat and barley: at least 150 European genebank accessions per year per crop (minimum 100 plots per site) in possibly 20 sites each of the three macro zones (northern, central and southern Europe), for two years, for a total of at least 3,000 cereal accessions evaluated
  ii. Maize: Perform evaluation for biotic and/or abiotic stresses of between 100–250 European genebank accessions per year, in possibly ten sites suitable for each of two maturity categories ('mid-late' and 'late'), for two years, for a total of at least 200 and up to a maximum of 500 accessions evaluated
  iii. Carrot: 20 accessions per year evaluated in possibly ten environments with two replicates for each environment (including lab screening for three *Alternaria* species and *Mycocentrospora acerina*), and field traits (diseases, morphology, harvest and quality traits), for a total of 60 accessions evaluated
  iv. Lettuce: between 20 and 50 accessions per year evaluated in possibly ten environments (including lab screening for three *Bremia* strains and morphological characterization), for a total of between 60 and 150 lettuce accessions evaluated
  v. Pepper: between 100 and 200 accessions evaluated for two years in possibly ten environments (including lab screening for TSWV, ToBRFV and *Verticillium* resistance/tolerance and field evaluation)
- Use jointly agreed evaluation protocols (experimental setup, scoring methodology) and data collection standards (ontologies) for data collection
- Genotype all the accessions selected for evaluation
- Implement a genotyping SNP viewer for the different crops evaluated in the EVA network where possible
- Facilitate analysis of evaluation data generated in all EVA networks
- Include the phenotypic + genotypic data derived from the projects in EURISCO
- Facilitate inclusion of evaluated accessions into AEGIS
- Include existing characterization and evaluation data into EURISCO from at least 100 accessions of wheat and barley and ca. 100 accessions of the European maize core collection
- Contribute to the preparation of the ECPGR Jubilee Video
- Prepare a promotional video on EVA for public outreach.

3. Project outputs towards its objectives

During its five years of implementation, the project has provided substantial contributions to the establishment of the European Evaluation Network, which, during the 17th ECPGR Steering Committee in 2023, was positively received and included in the ECPGR regular programme as a valuable initiative, enabling basic support for future activities. Below follows a summary of the project achievements towards the stated objectives.

FORMALIZING SIX EUROPEAN EVALUATION NETWORKS

The project was coordinated by a dedicated EVA Coordinator as part of the ECPGR Secretariat, Sandra Goritschnig, with temporary support for data management aspects by Research Specialist Filippo Guzzon. With the project start in 2019, the EVA Network started with the implementation of four networks, on wheat and barley and on three vegetable crops (carrot, lettuce, pepper), building on existing national and regional public–private partnerships for these crops. Through amendments of the project, the implementation of two additional EVA networks was made possible – EVA Maize starting in 2020, and EVA Legumes, starting in 2024.

The project website (https://www.ecpgr.org/eva) was regularly updated with network-specific content. All publications generated by the EVA networks are also available on the website[1].

Members for the different networks were invited via contacts of relevant ECPGR crop WGs and through an open call issued by Euroseeds among its member companies, resulting in geographically diverse crop-specific EVA Networks, with mixed and complementary expertise and capacity and a balanced representation of public and private sector partners. While some partners have ended their participation during the project, due to shifting priorities or capacities, outreach and communication activities have also attracted new partners.

Cooperation agreements were established for all networks, outlining the rights and responsibilities of network partners and signatures collected from all participating organizations. With the recent extension of the EVA networks to grain legumes, the six crop-specific networks currently count 125 partners from 37 countries (Table 1, Figure 1).

Table 1. Overview of membership of six crop-specific EVA networks as of 31 March 2025.

	All Networks	EVA Wheat Barley	EVA Carrot	EVA Lettuce	EVA Pepper	EVA Maize	EVA Legumes
Partner Institutes	125	45	16	10	25	24	49
Countries	37	21	8	7	16	13	23
Public sector partners	77	23	8	6	20	16	38
Private sector partners	48	22	8	4	5	8	11

[1] https://www.ecpgr.org/eva/documents-and-links/publications

Figure 1. Map of partners in the six crop-specific EVA Networks, showing their wide distribution across Europe.

DEVELOPMENT OF THE EURISCO-EVA INFORMATION SYSTEM

The EURISCO-EVA intranet, with a web-based user interface and visualization, search and filter functionalities was developed by IPK and finalized in 2022. It uses the same backbone as the public EURISCO information system, thus facilitating data exchange between the two platforms. The features of the EURISCO-EVA intranet were described in a paper published in *Genetic Resources*[2], which also includes screen shots of the interface (Figure 2).

[2] Kumar, S., Guzzon, F., Goritschnig, S. and Weise, S. (2024). The EURISCO-EVA Information System, an innovative approach to the data management of multi-site crop evaluation data. *Genetic Resources*, 5(10), pp. 117–125. https://doi.org/10.46265/genresj.IHXU5248

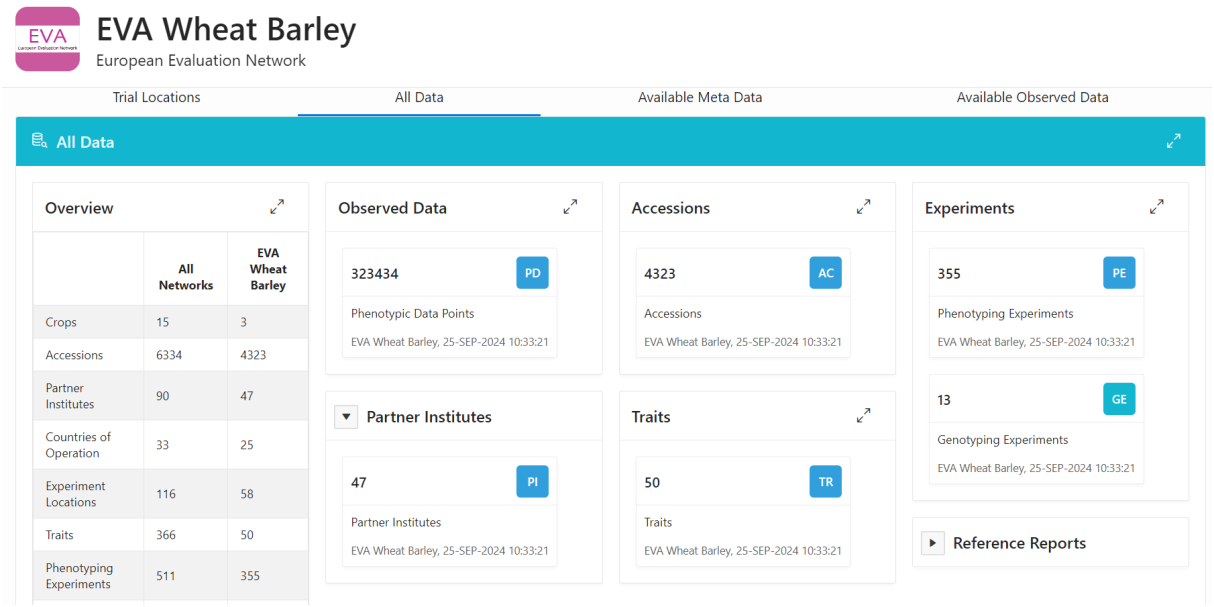

Figure 2. Screenshot of the EURISCO-EVA intranet user interface, showing the homepage for the EVA Wheat and Barley network with overview statistics of the network on the left and the shortcut cards leading to reports for metadata and phenotypic data. Additional tabs provide access to pre-filtered data and metadata reports tabs (taken from Guzzon et al, 2024).

The EURISCO-Intranet has also been expanded to include the possibility to display genotypic data in the form of a SNP Viewer, DivBrowse[3], developed by IPK and available for the networks. Although the system does not support direct linkage between phenotypic and genotypic data, it provides a useful graphical interface to visualize and analyze genotypic data.

The intranet is available exclusively to partners to upload, visualize, filter and download datasets. Standard data templates to collect phenotypic data alongside relevant metadata on accessions and experiments were created and are being used by partners to record their evaluation data. By March 2025, data from 456 trials have been collected in the database, totalling 630,735 individual datapoints (Table 2). Data curation and management of the metadata stored in the database have been assisted by the EVA coordination, supporting the data completeness in the database.

Table 2. Status of data available in the EURISCO-EVA intranet database (as of 31 March 2025).

	All Networks	EVA Wheat Barley	EVA Carrot	EVA Lettuce	EVA Pepper	EVA Maize	EVA Legumes
Crops	15	3	1	2	1	1	7
Accessions	5,566	3,555	67	367	261	1,018	298
Experiment Locations	125	59	14	6	11	30	5
Traits	319	46	139	25	27	55	27
Trials with Data available	456	296	27	19	18	90	6
Phenotypic Data Points	630,735	367,352	95,875	11,730	26,171	126,493	3,114

[3] Patrick König, Sebastian Beier, Martin Mascher, Nils Stein, Matthias Lange, Uwe Scholz, DivBrowse—interactive visualization and exploratory data analysis of variant call matrices, *GigaScience*, Volume 12, 2023, giad025, https://doi.org/10.1093/gigascience/giad025

EVALUATION ACTIVITIES OF THE EVA NETWORKS

Experimental work planning in the crop-specific networks was done in consultation with scientific leads within each network, and taking into account priorities and capacities of the participating partners. In general, it follows a scheme (Figure 3), whereby network partners contribute to the joint evaluations as material providers, by performing regeneration activities or evaluation trials (in field, greenhouse or laboratory, according to specific requirements), contributing to genotyping activities and finally data collection, joint data analysis and dissemination.

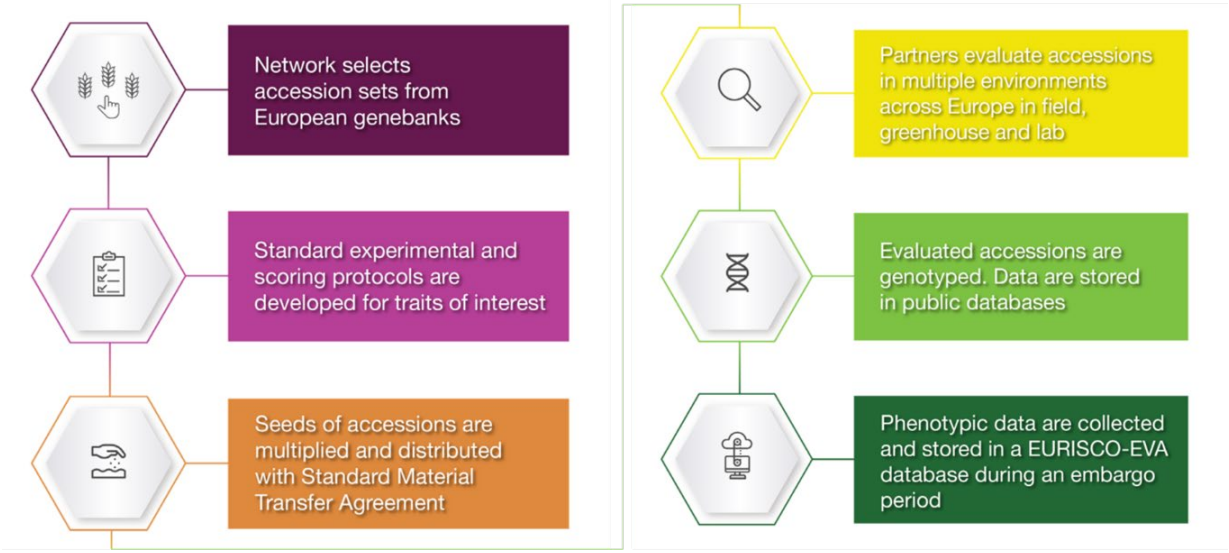

Figure 3. Schematic overview of evaluation activities in EVA networks.

Outputs of the different networks are summarized in detail below.

EVA Wheat and Barley

The EVA Wheat and Barley network[4] is divided into three geographic zones (Nordic, Central and Southern zones), with three priority crop types per zone, according to environmental conditions: spring, winter or facultative types. For each crop type and zone, up to 150 accessions were included in each of two sets, for a total of 1,664 wheat, 1,521 barley and 370 durum wheat accessions evaluated between 2021 and 2024 (Table 3).

Accessions were sourced from 31 genebanks, exploiting existing SSD collections (from IPK, CREA-GB, CNR and AGENT project partners) and other European holding institutes (Table 4). They were multiplied as SSDs (which were created if not yet developed) by partners in the three zones (Nordic zone: Nordic Seed; Central zone: JKI; Southern zone: CREA-GB) and distributed to evaluation partners, using SMTA[5]. Within AGENT, regeneration in the Southern Zone was done by AGENT partner CREA-CI.

[4] https://www.ecpgr.org/eva/eva-networks/wheat-and-barley

[5] https://www.ecpgr.org/fileadmin/templates/ecpgr.org/upload/AEGIS/FOR_WEB_FINAL/AEGIS_SMTA.pdf

Table 3. Overview of distribution of evaluated accessions and recorded evaluation trials (2021–2024) per crop type and geographic zone in the EVA Wheat and Barley Network, provided within GenR 2019-2 and the H2020 project AGENT.

	Accessions					Evaluation trials			
	Nordic	Central	South	AGENT	total	Nordic	Central	South	Total
Winter barley		263		150	413		39		39
Winter wheat	153	250		348	751	34	51		85
Spring barley	184	173		301	658	33	20		53
Spring wheat	348			115	463	37			37
Barley			300	150	450			23	23
Bread wheat			300	150	450			22	22
Durum wheat			300	70	370			37	37
Total	**685**	**686**	**900**	**1284**	**3555**	**104**	**110**	**82**	**296**

Between 2020 and 2024, the EVA Wheat and Barley network collected useful data from 296 field trials in 59 locations (Tables 2, 3). Some additional trials were discarded, as conditions prevented the production of usable data (e.g. missing pathogen pressure, trial failure due to pests or adverse environmental factors). Nevertheless, an average of 90, 99 and 146 data points were collected per accession for barley, wheat and durum wheat, respectively, primarily on biotic stresses, but also on morphologic and agronomic traits of interest (Figure 4).

Genotyping data for 1,222 barley, 1,264 soft wheat and 358 durum wheat accessions have been generated using Infinium barley and wheat SNP arrays, respectively. This data has been formatted for display in a SNP viewer in early 2024. The accessions in the 3rd set obtained from the AGENT project were genotyped within AGENT using GBS (barley) and DartSeq (wheat) approaches, and their genotyping data have been made available to EVA project partners as well as through a public SNP viewer within the AGENT data portal[6].

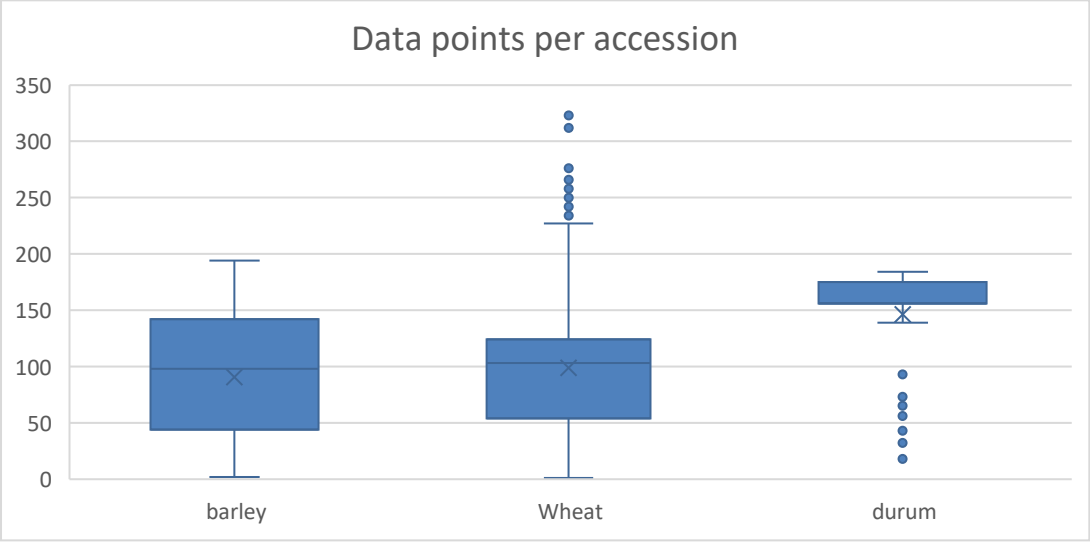

Figure 4. Distribution of individual data points collected for barley, wheat and durum wheat accessions in 2021–2024.

[6] https://agent-project.eu/agent-data-portal

Table 4. Wheat, barley and durum wheat evaluated by the EVA Wheat and Barley Network, by holding institutes. AEGIS status is reported for accessions used as parents of SSDs.

Holding Institute Code	Evaluated accessions (3,555 total)			Part of AEGIS (1,508 total)		
	Barley	Wheat	Durum	Barley	Wheat	Durum
AUT001	39	19	0	0	0	0
BGR001	20	32	18	0	6	8
CHE001	33	240	2	33	191	0
CZE122	196	72	0	96	63	0
DEU146	404	292	0	296	157	0
ESP004	91	68	111	0	0	0
EST019	6	15	0	6	14	0
GBR247	0	235	0	0	0	0
ISR003	0	0	3	0	0	0
ITA382	71	0	200	0	0	0
ITA383	0	74	0	0	30	0
ITA436	99	25	0	99	19	0
LBN002	0	0	12	0	0	0
LTU001	5	5	0	5	0	0
LVA009	7	6	0	7	6	0
POL003	9	79	0	0	2	0
PRT001	39	28	24	0	0	0
ROM002	73	157	0	0	0	0
ROM007	7	0	0	7	0	0
SVK001	256	0	0	242	0	0
SWE054	166	317	0	81	140	0
total	**1,521**	**1,664**	**370**	**872**	**628**	**8**

The EVA Wheat and Barley Network met in person twice, in Freising, Germany, in November 2023 and in Fiorenzuola d'Arda, Italy, in January 2024, as well as multiple times virtually, to review progress and work planning, discuss results and challenges, as well as future strategies[7]. The close collaboration between EVA Wheat and Barley and AGENT was also reflected in reciprocal progress reporting at their respective project meetings.

For data analysis a Task Force was established with representatives from the three zones, which analyzed the data of the first two accession sets, using a common analysis pipeline. This involved statistical analysis of the phenotypic trials, assessing the quality of the data and genetic and environmental effects, analysis of the genotyping data and the population structures of the evaluated crops and finally association studies to identify regions within the genome that may be linked to specific traits. These marker trait associations (MTA) are useful for breeders as they facilitate selection of useful breeding lines, but they require confirmation via additional experiments before they can be successfully applied. The results were presented to the network at various occasions and made available on the project SharePoint, including information on significant marker-trait associations, their genomic locations and possible linked genes, as well as a list of promising material containing interesting (combinations of) useful alleles.

The AGENT project has generated a number of bioinformatics tools that will be useful for the EVA Networks, especially the EVA Wheat and Barley, since datasets generated by AGENT

[7] https://www.ecpgr.org/eva/eva-networks/wheat-and-barley/eva-wheat-and-barley-project-meetings

can be used to preselect new materials and data analysis pipelines could be applied to EVA datasets linked to AGENT materials.

EVA Maize

The EVA Maize Network[8] was established after the first meeting of the ECPGR Maize WG in December 2019[9] and comprised 18 partners in nine countries. Membership has been expanded through collaboration with two projects coordinated by INRAE, France: MineLandDiv and the ECPGR Grant scheme activity MALANIRS, starting in 2024. The network now includes 24 partners from 13 countries, of which eight breeding companies.

The EVA Maize workplan was implemented as a two-step evaluation process, whereby several partners performed initial characterization of a full set of accessions, from which a subset was selected based on agreed criteria for production of hybrid populations in winter nurseries and in-depth evaluation of both landraces and hybrids in the following year. In this step-by-step approach, multiplication and generation of hybrids of the same accessions were planned for sequential years. Evaluation of the third set was finalized in 2024.

Three sets of accessions combining 612 maize accessions from nine partner genebanks have been genotyped using a 50k SNP array and included in field evaluations. In addition, 360 test crosses were generated from 228 accessions in the three sets and using different commercial testers from private partners for evaluation of combining abilities (Table 5).

Table 5. Number of accessions provided by European genebanks for evaluation in EVA Maize, as well as the number of accessions used in test crosses and flagged as AEGIS accessions in EURISCO. [1)] partner MBG-CSIC provided material from four different Spanish genebanks.

Holding institute	# accessions evaluated	# of accessions used in test crosses	# AEGIS accessions
CHE001	88	32	0
ESPxxx[1)]	151	60	0
FRA015	80	25	0
HRV041	50	17	0
ITA386	54	24	54
PRT001	42	16	0
PRT053	5	4	0
ROM007	51	10	51
SRB001	91	40	0
total	**612**	**228**	**105**

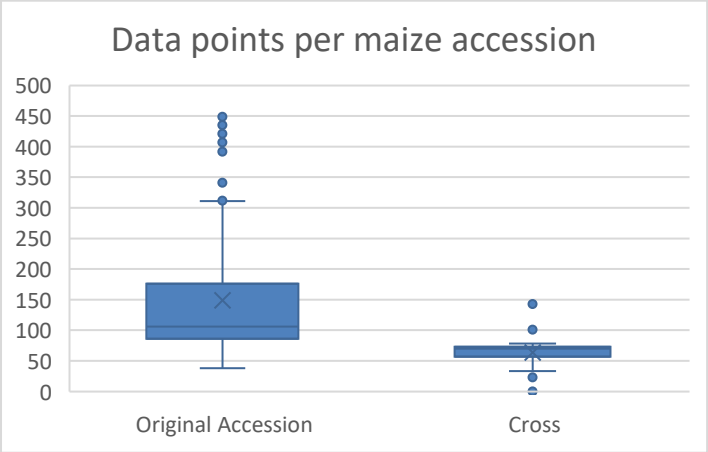

Figure 5. Distribution of individual data points collected for original maize accessions and test crosses in 2021–2024.

[8] https://www.ecpgr.org/eva/eva-networks/maize
[9] https://www.ecpgr.org/working-groups/maize

Between 2021 and 2024, the EVA Maize network conducted 90 trials (63 on per se accessions and 27 on testcross populations) and data have been uploaded to EURISCO-EVA, totalling 126,493 datapoints (Table 2), corresponding to on average 148,6 and 63,5 datapoints for per se accessions and testcrosses, respectively (Figure 5). Priority traits included phenological, morphological and agronomic traits as well as relevant abiotic and biotic stresses, including cold and drought stresses, Northern corn leaf blight (NCLB) and *Fusarium*.

Data analysis is being led by R. Malvar (CSIC, phenotypic data of original accessions), C. Bauland (INRAE, phenotypic data of testcrosses) and S. Nicolas (INRAE, genotyping data). Results have been presented at various occasions and included in two recent publications. Two other publications describing the EVA Maize populations in relation to the sets included in MineLandDiv and other projects are in preparation.

The EVA Maize network has met in person three times, as well as virtually throughout the project[10], engaging also with the MineLandDiv and MALANIRS projects, which provide a framework for continued collaboration of the EVA Maize Network. Both developed additional accession sets which expand the maize collections available for the network's evaluations. Genotyping and other phenotypic experiments add value to the accessions and provide important data for the selection of sets for multilocation trials by company partners. These evaluations will be possible as in-kind contributions as long as sufficient material is available. Future regenerations, as well as the development of testcross populations, may require additional funding.

EVA Carrot

The EVA Carrot Network[11] conducted extensive field evaluations of 62 carrot accessions and landraces from four European genebanks (Table 5), including appropriate controls, which were finalized in 2022. The network selected for this project accessions for which sufficient seeds were already available, and around 40 carrot accessions have been regenerated by project partners to feed into a second set of evaluations. Twelve partners conducted 27 trials to evaluate basic morphological and agronomic characterization in field trials, complemented by biotic stress trials under different conditions (lab, greenhouse), testing for major pathogens affecting carrot. Experiments in the lab conducted by JKI (Quedlinburg) increased the available data set with detailed morphological data for individual plants and disease assays under controlled conditions, and these data can be applied to Genome-Wide Association Study (GWAS) analysis as they were collected on genotyped individuals. Material of these accessions was also sampled for analysis of volatile compounds by Gas Chromatography – Mass Spectrometry (GC-MS) techniques, and data analysis by JKI is ongoing, including GWAS.

Table 6. Number of accessions provided by European genebanks for evaluation in EVA Carrot including those flagged as AEGIS accessions in EURISCO.

Holding Institute	# accessions evaluated	# AEGIS accessions
GBR006	25	6
SWE054	9	4
FRA250	15	0
ESP027	13	0
Total	62	10

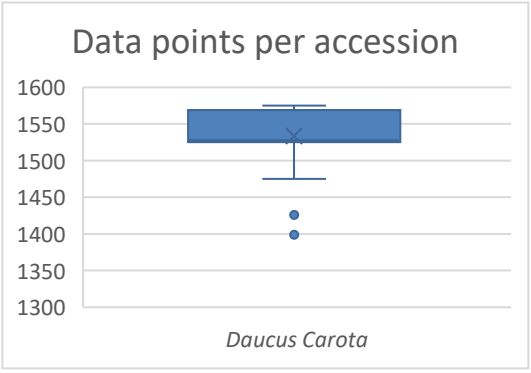

Figure 6. Distribution of individual data points collected for carrot accessions in 2020–2022.

[10] https://www.ecpgr.org/eva/eva-networks/maize/eva-maize-project-meeting
[11] https://www.ecpgr.org/eva/eva-networks/carrot

An average of 1,533 individual data points were collected for each carrot accession (Figure 6), and all collected data are available on the EURISCO-EVA intranet (see Table 1). Considering the large amount of primary data, it was agreed that they needed further curation before they could be made publicly available in EURISCO. For example, qualitative traits with homogeneous scoring from all trials should only be recorded once, to reduce the data volume. Furthermore, partners suggested entering the data into the CarrotOmics database (www.carrotomics.org), which would be more specifically targeted to carrot researchers and breeders. An analysis of formatting requirements will be conducted, and possible interactions with this project explored.

Genotyping was completed in 2021 for 66 carrot accessions (including relevant controls) using genotyping by sequencing (GBS) on ten plants per accession, as well as whole genome sequencing and a new SNP array (in collaboration with SGS TraitGenetics) on one plant per accession each. The data have been mapped to the carrot genome version (v3) and preliminary results showed that the three approaches created similar clustering of accessions. Comparing the three genotyping approaches will assist researchers in selecting cost-effective genotyping options for carrots, benefiting the whole research community. Further analysis and association with phenotyping results is still ongoing and is expected to result in several research publications.

Statistical analysis of phenotypic data has been coordinated by E. Geoffriau (Institut Agro, France), and two MSc students have contributed to the analysis using various statistical approaches and models to correlate the different environments and traits with the aim of describing the genetic diversity within the collection and G×E interactions for specific traits. Preliminary results identified: (1) which traits best capture genetic diversity, (2) which environments best differentiate certain traits, and (3) which traits correlate and are most stable in their expression across environments. These analyses form the basis of a draft scientific article, which complements the first publication of the EVA Carrot Network on preliminary results[12], which had already been presented at various occasions.

The EVA Carrot Network has met twice in person and multiple times online[13]. With the finalization of the current EVA project, the network has expanded to include additional partners, consisting now of 16 partners from eight countries, half of which are from the private sector. A new accession set of 50 carrot landraces has been selected, which will be evaluated by private sector partners starting in 2025.

EVA Lettuce

The EVA Lettuce Network[14] has ten partners from seven countries. It has conducted evaluations on two lettuce species, sourced from four European genebanks (Table 7). One hundred and seventy-eight (178) accessions of cultivated lettuce (*Lactuca sativa*) were screened in eleven field trials in five locations for agronomic and morphology traits, along three common controls. In parallel, and supported through an amendment of the project, 125 accessions of the lettuce wild relative *Lactuca serriola* were screened for resistance to five recent *Bremia lactucae* strains, identifying several lines with potential resistance to powdery mildew, which could be useful in breeding.

The network generated on average 15 and 41 data points per accession, for *L. serriola* and *L. sativa*, respectively (Figure 7).

[12] https://www.ecpgr.cgiar.org/resources/latest-news/news-detail/getting-to-the-roots-of-carrot-genetic-diversity

[13] https://www.ecpgr.org/eva/eva-networks/carrot/eva-carrot-project-meetings

[14] https://www.ecpgr.org/eva/eva-networks/lettuce

Table 7. Number of accessions provided by European genebanks for evaluation in EVA Lettuce including those flagged as AEGIS accessions in EURISCO.

Holding Institute	Accessions evaluated		AEGIS accessions	
	Lactuca sativa	*Lactuca serriola*	*Lactuca sativa*	*Lactuca serriola*
SWE054	2	74	2	53
FRA011	66	36	0	0
NLD037	36	9	11	5
BGR001	74	6	0	0
Total	178	125	13	58

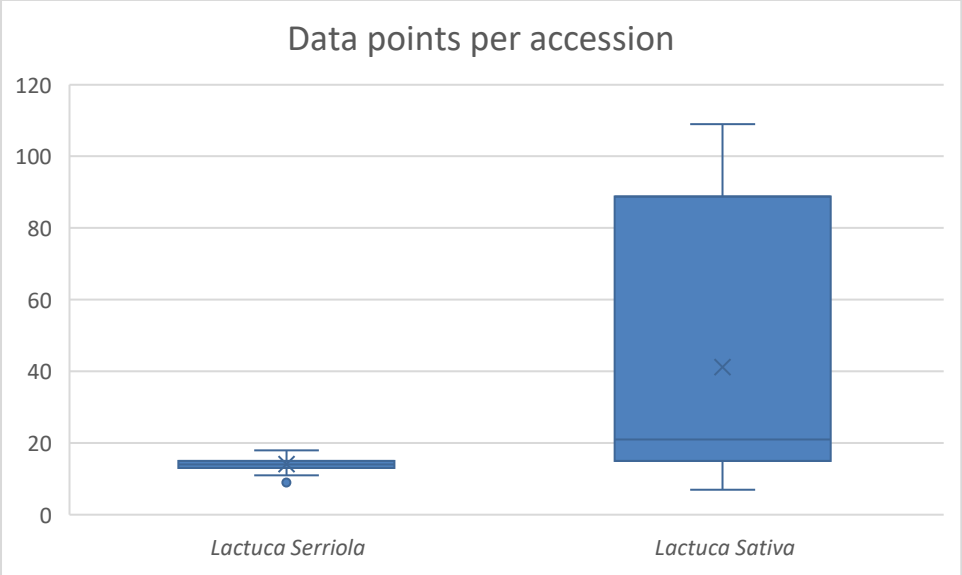

Figure 7. Distribution of individual data points collected for Lettuce accessions in 2021–2024.

Since there was at the time no available genotyping array for lettuce, the network teamed up with IGAtech to develop a new assay, using Single Primer Enrichment Technology (SPET). This method combines SNP genotyping and sequencing to allow for the detection of more than 80k SNPs across the whole genome, starting from a set of 40k probes designed based on existing SNPs.

This new method, along with a diversity analysis of the *L. sativa* panel, was published in the high-impact journal *Frontiers in Plant Science*[15] and has already been viewed and downloaded almost 6,000 times and has been cited by 11 other peer-reviewed publications, showing the significant impact of this work. It was also presented at various conferences. Additional communications and outreach for this work in particular, have been achieved through the production of a podcast about the article[16].

The genotyping dataset on *Lactuca sativa* was used in the first implementation of the SNP viewer, which was developed together with IPK and made available to network partners through a link with the EURISCO-EVA intranet. Public release of the SNP viewer will be coordinated with IPK.

The EVA Lettuce Network has met twice in person and multiple times online. New partners in Poland, Slovenia, Spain and the UK have been approached and may join the network for the next evaluation cycle.

[15] https://doi.org/10.3389/fpls.2023.1252777

[16] https://www.scipod.global/dr-sandra-goritschnig-dr-pasquale-tripodi-the-science-of-greens-using-genetic-insights-to-cultivate-better-stronger-lettuce/

EVA Pepper

The EVA Pepper network[17] had initially selected an accession set of 230 pepper accessions from eight genebanks. The start of their activities coincided with the emergence of the tomato brown rugose fruit virus (ToBRFV) as a spreading pest of *Solanaceae* species, presenting a problem for seed multiplication and seed distribution, as phytosanitary measures had to be stepped up. Of the accessions multiplied by ISI Sementi in 2020, 160 accessions were selected for multilocation field trials, with an additional 22 accessions provided for lab disease tests and genotyping. The original EVA collection was enlarged in 2024 by including 40 diverse *C. annuum* accessions from the G2PSol project and now represents material originating from 48 countries across the globe, sourced from 11 European genebanks (Table 8).

Table 8. Number of accessions for different *Capsicum* species provided by European genebanks for evaluation in EVA Pepper, including those flagged as AEGIS accessions in EURISCO.

Holding Institute Code	*Capsicum Annuum*	*Capsicum Baccatum*	*Capsicum Chacoense*	*Capsicum Chinense*	*Capsicum Frutescens*	AEGIS accessions
POL003	3	0	0	0	0	0
HUN003	4	0	0	0	0	0
FRA011	1	0	0	0	0	0
BGR001	2	0	0	0	0	0
NLD037	124	2	6	48	12	28
DEU146	25	0	0	3	0	21
PRT001	0	0	0	0	3	0
MKD001	1	0	0	0	0	0
SRB056	20	0	0	0	0	0
ITA391	5	0	0	0	0	0
ITA393	1	0	0	0	0	0
Total	186	2	6	51	15	49

Field evaluations were implemented on nine trial sites in five countries from 2021 to 2024, allowing all evaluating project partners to evaluate the full set of 160 accessions. The field data were complemented with lab tests for three pathogens (TSWV, *Xanthomonas*, ToBRFV) and data from 18 trials have been uploaded to EURISCO-EVA (Table 1).

An additional abiotic stress experiment was conducted by CNR Portici, using 192 accessions of the EVA collection, including mainly *Capsicum annuum* accessions to enable GWAS analysis. Preliminary results indicated that the collection could be clustered into differentially tolerant accessions, and follow-up experiments should be planned to confirm these results.

Overall, between on average 30 and 94 phenotypic data points were collected for the pepper accessions, with some only included in few lab trials if not sufficient seeds were available. (Figure 8).

[17] https://www.ecpgr.cgiar.org/eva/eva-networks/pepper

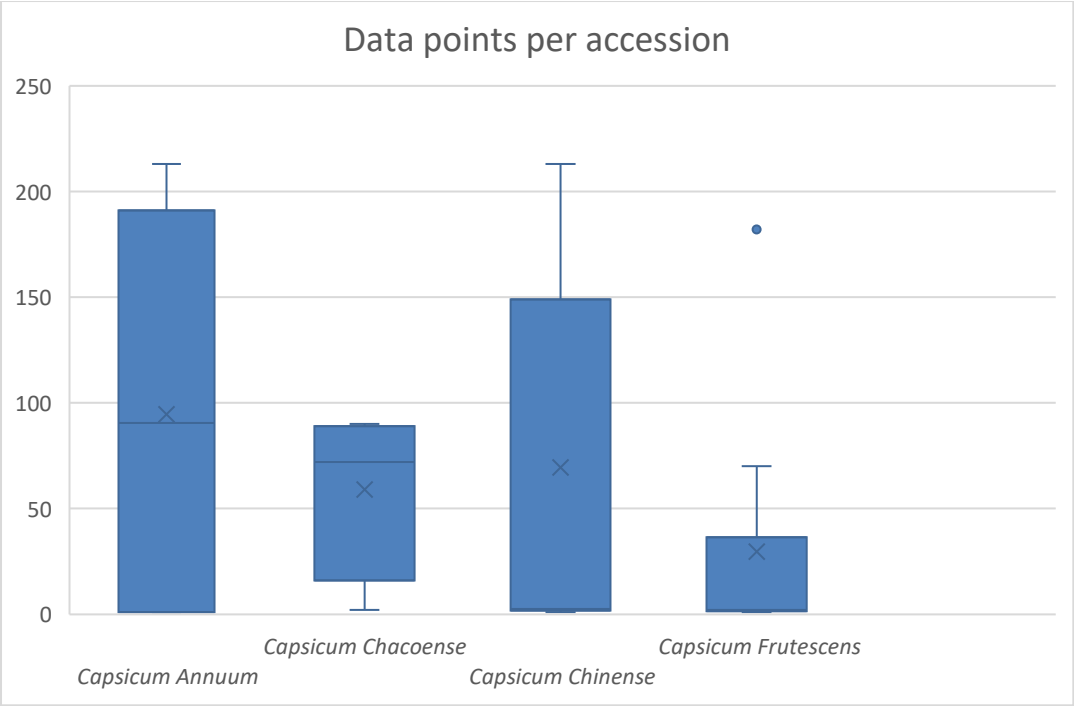

Figure 8. Distribution of individual data points collected for pepper accessions in 2021–2024.

Genotyping using 19k and 10k SNP arrays developed by SGS TraitGenetics was performed on 230 accessions, of which 160 are *Capsicum annuum* and thus available for GWAS analysis. One hundred and sixty-one (161) evaluated pepper accessions were also genotyped using specific markers linked to resistance and some morphological traits. Analysis of genotypic data showed that the collection used in the project reflects a diverse set of accessions, separating accessions by species and origin and highlighted Europe as a secondary centre of origin for pepper, with high diversity observed in European materials.

Detailed analysis of phenotypic data started in 2023 with data curation and quality checking, as well as definition of appropriate approaches and analysis pipelines. Preliminary GWAS of the abiotic stress trials identified several significant marker-trait associations; in some cases, the same SNP was significant for highly correlated traits.

The ECPGR Grant Scheme Activity EuroPepLand[18], led by the Solanaceae WG Chair Pasquale Tripodi, involves 16 WG members from 13 countries and will generate a European pepper landrace core collection with ~400 accessions from southern, eastern and central Europe. These should be regenerated, characterized and genotyped in the project and also incorporated into the AEGIS collection, where possible. The project will use EVA phenotyping protocols and templates and the same SNP array to ensure data compatibility and also intends to make the material available to the network for multilocation field evaluation, considering relevant phytosanitary requirements for regeneration and distribution. EuroPepLand partners have joined the EVA Pepper network for the next evaluation cycle.

The EVA Pepper network met twice in person, including the kick-off meeting of the EuroPepLand project in October 2024[19]. Multiple virtual meetings were held in between to coordinate activities and report on progress.

[18] https://www.ecpgr.org/working-groups/solanaceae/europepland
[19] https://www.ecpgr.org/eva/eva-networks/pepper/eva-pepper-project-meetings

EVA Legumes

Since 2024, the EVA Legumes Network[20] is being implemented, building on the ECPGR Grant Scheme Activity Fostering the need of implementation of the ECPGR European Evaluation Network (EVA) on Grain legumes (ForEVA), led by the ECPGR Grain Legumes WG and supported by the EVA project through an amendment in 2023, funding a workshop in Bucharest, Romania, in October 2023. The activity had 25 partners and identified 35+ additional stakeholders who signed letters of commitment to contribute to ForEVA and become part of the EVA Legumes Network, which now has 50 partners from 23 countries. Some of these stakeholders were already EVA partners for other crops or have also expressed interest in participating in other existing EVA Networks.

The EVA Legumes Network is implemented by seven overlapping crop groups working on common bean, chickpea, lentil, fava bean, lupines, pea and orphan legumes, with between 22 and 34 participating partners and a scientific lead identified in each group. In virtual meetings in early 2024, the crop groups discussed work planning including priority traits for evaluation, criteria for selection and size of accession sets, and partners' capacities for in-kind multiplications and evaluations. First accession sets for common bean (98; original accessions from genebank collections) and chickpea (200; SSD lines developed in INCREASE) were multiplied in kind by seed company partners of EVA Legumes during 2024. Implementation of the EVA Legumes network is implemented from 2024–2027 with financial support from BMLEH Germany within the EVA Boost project (GenR 2024-2)[21] and reported there.

INCLUSION OF ACCESSIONS AND DATA IN EURISCO AND AEGIS

An important objective of the EVA project was to enrich the existing data on EURISCO and to ensure that all accessions used in the evaluations are documented in EURISCO and included in the AEGIS European collection where possible.

The EURISCO-EVA intranet was designed to be able to synchronize with EURISCO, to import accession metadata from EURISCO and facilitate the upload of phenotypic data to the public system after the embargo period. The EURISCO-EVA intranet has also served as a template for project databases developed by IPK in the Horizon projects AGENT and INCREASE, which may feed back to the EURISCO-EVA intranet with relevant upgrades which could be implemented with available funding. After the end of the current project and data embargoes, we have now started developing the process to migrate data to EURISCO, which will require some additional discussion on data formats, data quality and associated metadata.

For example, data collected on derived materials (SSD lines or crosses), which are not included in EURISCO cannot be directly associated with the original accession in EURISCO. A process for handling these data has been proposed at the last EURISCO Advisory Committee meeting[22] and its implementation will enable integration of EVA data.

Secondly, the datasets created by the Networks are complex and include many datapoints for each accession (see Table 2 and description of the networks above). Not all trials produced useful data, some qualitative traits produced homogeneous data over multiple trials and some trait scoring should be considered in relation to the included check varieties. Phenotypic data that would be included in EURISCO should therefore undergo additional curation steps to ensure data quality and final upload will require the approval of National Focal Points of the holding institutes' national collections.

[20] https://www.ecpgr.org/eva/eva-networks/legumes
[21] https://www.ecpgr.org/fileadmin/templates/ecpgr.org/upload/EVA/ECPGR_EVA_Boost_proposal.pdf
[22] https://www.ecpgr.org/about/eurisco-advisory-committee/4th-meeting-of-the-eurisco-advisory-committee

Table 9. Summary of coverage of EVA accessions in EURISCO, within the AEGIS European collection and with C&E data available in EURISCO. France, Spain and Israel are not member countries of AEGIS at this time. PRT053, ROM002 and SRB056 are not yet associate members of AEGIS, although their country is an AEGIS member. EVA accessions here refers only to original accessions, not derived materials (i.e. SSD or crosses).

Holding Institute Code	AEGIS member	Flagged EVA accessions	# EVA Accessions	# EVA Accessions in EURISCO	# EVA Accessions in AEGIS	C&E data in EURISCO
AUT001	Yes		58	58		
BGR001	Yes	Yes	152	152	14	
CHE001	Yes	Yes	363	360	224	
CZE122	Yes	Yes	268	268	159	216
DEU146	Yes	Yes	724	724	474	327
ESP004	No		275	271		
ESP007	No		6	1		
ESP009	No		139	72		
ESP016	No		1			
ESP027	No		13	13		
ESP119	No		4	4		4
EST019	Yes	Yes	21	21	20	21
FRA011	No		103	41		
FRA015	No		80	80		16
FRA250	No		15	15		14
GBR006	Yes	Yes	25	25	6	
GBR247	Yes		235			
HRV041	Yes		50	50		
HUN003	Yes		4	4		
ISR003	No		3	3		
ITA382	Yes		271	220		62
ITA383	Yes	Yes	74	74	30	
ITA386	Yes	Yes	54	54	54	27
ITA391	Yes		5			
ITA393	Yes		1	1		
ITA436	Yes	Yes	124	124	118	79
LBN002	No		12			
LTU001	Yes	Yes	10	10	5	
LVA009	Yes	Yes	13	13	13	5
MKD001	No		1	1		
NLD037	Yes	Yes	237	236	44	235
POL003	Yes	Yes	91	91	2	
PRT001	Yes		136	136		42
PRT053			5			
ROM002			230	228		
ROM007	Yes	Yes	58	58	58	7
SRB001	Yes		91	88		
SRB056			20	20		
SVK001	yes	Yes	256	256	242	
SWE054	Yes	Yes	568	568	280	208
Total	**25**	**16**	**4,796**	**4,340**	**1,743**	**1,264**

Therefore, no phenotypic data from the EVA networks have been included in EURISCO as of now, although some have been published in peer-reviewed journals. In order to preserve the context of the trials and enable users to search for suitable accessions, an open version of the EURISCO-EVA information system should be developed to provide open and free access to the generated data, while the transfer of data to EURISCO is not completed.

As neither the EURISCO-EVA intranet nor the public EURISCO catalogue can handle the generated genotyping data, the different networks have discussed and developed appropriate methods and repositories to store and exchange the genotyping datasets and analysis results and to ultimately make them publicly available. Genotyping datasets that were small enough (e.g. data from SNP arrays) have been made available to the networks via the EURISCO-EVA intranet, although inclusion in the database is not foreseen. A SNP-viewer for the EVA datasets based on DivBrowse, developed by IPK Gatersleben, has been implemented for EVA Lettuce as a tool to access and visualize genotyping data. The maize genotyping data have been integrated with other data generated by INRAE in the frame of other projects and have been made available to EVA Maize partners via ThaliaDB.

The AEGIS European Collection includes unique PGR accessions that are conserved by associated institutes according to defined quality standards and accessible to users via SMTA. Among the 40 EVA partner genebanks, 25 institutes are AEGIS associate members, and 16 of these have flagged 1,743 EVA accessions as part of AEGIS (Table 9; for details, see information on the individual crop networks). Almost all EVA accessions are documented in EURISCO (accessions from LBN002-ICARDA are documented in Genesys, the accessions from GBR247-John Innes Centre are individual lines from the Watkins×Paragon populations and not included in EURISCO). One thousand, two hundred and sixty (1,260) accessions also have C&E data already associated in EURISCO, most of which have been collected and curated in the frame of this project (for wheat, barley and maize).

COMMUNICATION AND DISSEMINATION ACTIVITIES

The EVA project contributed to general communication and dissemination activities for ECPGR and especially the EVA Networks through various activities.

The Jubilee Video for ECPGR's 40th anniversary was released in early 2021 and is available on the ECPGR website and YouTube channel[23]. The video based on the narration of a charismatic National Coordinator in his fields at the Centre Wallon de Recherches Agronomique in Belgium has been viewed more than 1,600 times and received positive feedback from stakeholders across ECPGR. It was also shown on screen at the launch of the Genetic Resources Strategy for Europe in Brussels, November 2021 (final event of the Horizon 2020 project GenRes Bridge).

The promotional video for EVA was produced under the leadership of the ECPGR communications officer and released in early 2024[24]. The video incorporates animations and video footage from EVA partners and aims to inform the general public and potential stakeholders about the project, as well as attracting new partners or new networks. It has been promoted through various channels and so far received 600+ views.

The EVA Networks were also promoted through ECPGR news items and LinkedIn[25] posts that highlighted recent developments and achievements, increasing the visibility of EVA activities, including published papers, events and the promotional video.

Various dissemination and communication activities have generated wide interest in the project and its approaches, creating visibility for the EVA project and ECPGR, attracting new partners

[23] https://www.youtube.com/watch?v=6JsTUZ-fOFM
[24] https://www.youtube.com/watch?v=AZ1NB6hC_ZU
[25] https://www.linkedin.com/company/ecpgr

and resulting, inter alia, in the establishment of a new EVA Legumes network as part of an ECPGR Grant Scheme Activity. Significantly, the ECPGR Steering Committee, in its 17th meeting in Oeiras, Portugal (30 May–1 June 2023), has agreed to include the EVA Networks as a priority activity in the ECPGR work plan for Phase XI, guaranteeing funding for the EVA coordinator after the end of the current project.

Table 10. List of peer-reviewed scientific publications of the EVA Networks published by the project's end.

Network	Title	Reference
Lettuce	Development and application of Single Primer Enrichment Technology (SPET) SNP assay for population genomics analysis and candidate gene discovery in lettuce	Tripodi P, Beretta M, Peltier D, Kalfas I, Vasilikiotis C, Laidet A, Briand G, Aichholz C, Zollinger T, Treuren Rv, Scaglione D and Goritschnig S (2023) *Front. Plant Sci.* 14:1252777. doi: 10.3389/fpls.2023.1252777
Carrot	Exploring European carrot diversity through public-private partnerships in EVA Carrot	Goritschnig, S., Pagan, P., Mallor, C., Thabuis, A., Chevalier, J., Hägnefelt, A., Bertolin, N., Salgon, S., Groenewegen, M., Ingremeau, A., Santillan Martinez, M., Lehnert, H., Keilwagen, J., Burges, T., Budahn, H., Nothnagel, T., Lopes, V., Allender, C., Huet, S. and Geoffriau, E. (2023). *Acta Hortic*. 1384, 63-70. https://doi.org/10.17660/ActaHortic.2023.1384.8
Maize	Genetic and Phenotypic Evaluation of European Maize Landraces as a Tool for Conservation and Valorization of Agrobiodiversity	Balconi C, Galaretto A, Malvar RA, Nicolas SD, Redaelli R, Andjelkovic V, Revilla P, Bauland C, Gouesnard B, Butron A, et al. *Biology*. 2024; 13(6):454. https://doi.org/10.3390/biology13060454
All	The EURISCO-EVA Information System, an innovative approach to the data management of multi-site crop evaluation data	Kumar, S., Guzzon, F., Goritschnig, S. and Weise, S. (2024), *Genetic Resources*, 5(10), pp. 117–125, doi: https://doi.org/10.46265/genresj.IHXU5248
All	Strengthening European research cooperation on plant genetic resources conservation and use	Goritschnig, S., Weise, S., Guzzon, F., Maggioni, L., van Hintum, T., Steffensen, L. L., Stein, N. and Giuliano, G. (2025) *Genetic Resources*, (S2), pp. 119–134. https://doi.org/10.46265/genresj.LUZJ7324
Maize	Maize landraces as useful donors of genetic diversity for resilience to drought	Santiago R, R.A. Malvar, P. Revilla, A. Butrón (2025), *Journal of Agriculture and Food Research*, Volume 23, https://doi.org/10.1016/j.jafr.2025.102297

Dissemination of EVA networks' results through conference presentations and publications has been active and, so far, yielded six peer-reviewed publications (Table 10), one of which in a high-impact open-access journal (*Frontiers in Plant Science*), sparking wide interest. Additional manuscripts are in preparation to exploit EVA results in publications, which will be complementary to their exploitation in breeding programmes by private sector partners.

In another communication activity, a podcast/audiobook was produced, and is targeted at a general audience to further promote our work. The podcast was produced by SciPod and describes the results in the publication of the EVA Lettuce Network (Tripodi et al, 2023)[26]. It is available on the EVA website[27] and through various podcast distribution sites.

[26] 10.3389/fpls.2023.1252777
[27] https://www.ecpgr.org/eva/documents-and-links/multimedia

4. Project progress towards expected outcomes and challenges

The project has reached and even exceeded most of the expected outcomes. It has not only facilitated the implementation of first evaluation cycles of two field crops (EVA Wheat and Barley, Maize) and three vegetable networks (EVA Carrot, Lettuce, Pepper) but also created sufficient interest to support the initiation of another network on grain legumes. Thus, by the end of the project, six EVA Networks have been established with Letters of Commitment and Consortium agreements signed by 125 partners, some of whom engage in more than one network (Table 1).

Although the COVID-19 pandemic has affected the work of multiple networks, delaying or necessitating cancellation of activities such as multiplication or evaluation trials, postponement of in-person project meetings and delaying some administrative activities, an extension of the project to March 2025 compensated for the experienced delay and allowed finalization of project activities and exploitation of results.

Evaluations of accessions in the field crop networks (EVA Maize and EVA Wheat and Barley) have far exceeded the planned amounts, and the vegetables networks have also reached the planned amounts of accessions. More than 4,700 accessions of 15 crops have been phenotyped and genotyped, and several hundred derived materials (SSD lines and crosses) have also been phenotyped. Data have been collected on diverse traits of interest to participating breeders, including agronomic and morphology traits as well as biotic and abiotic stress traits, which are of particular importance in the light of climate change. The EVA Carrot Network has generated a record 1,500+ data points per accession, with data for 139 different traits. Data have been recorded from 456 trials in field, greenhouse and lab, creating a wealth of phenotypic data (Table 2).

Genotyping data have been made available to project partners via the EURISCO-EVA intranet, when datasets were small enough, as well as through graphic interfaces and SNP viewers to facilitate analysis and visualization.

Data curation, management and analysis have emerged as major challenges for the project, considering the large and diverse datasets created in the genotyping and phenotyping experiments of the different networks. Data were generated by many different contributors and despite providing standard protocols and data collection templates that were simplified as much as possible and providing guidance and training in the use of these templates, extensive data curation and communication with the evaluators were often required. Management of corresponding metadata and maintenance of the EURISCO-EVA intranet to ensure the high quality of the datasets, also in view of publication in EURISCO, required special attention. These data management tasks remained centralized with the EVA coordination.

With the end of the embargo period for project data, the transfer of phenotypic data from EURISCO-EVA to the public database was a relevant topic at the end of the project. Some partners questioned the usefulness of uploading raw data to EURISCO and suggested that it would be more appropriate to include only statistically validated data of a minimum quality (e.g. BLUEs) in the public database, to ensure the data are reliable. For example, some disease trials of field crops yielded useful data only for some of the scored pathogens, and thus only these data should ultimately be made available for public reuse. Furthermore, much of the data was generated on SSD lines, subpopulations of the original accessions recorded in EURISCO. A mechanism for incorporating data on these materials and associating it with the original parent accession in EURISCO was developed by the EURISCO Advisory Committee, as well as a pipeline for approval and upload of phenotypic data.

Nevertheless, while phenotypic data generated in EVA have not yet been included in EURISCO, owing to some technical and procedural concerns which emerged during the project, the project has resulted in a significant increase in available C&E data in EURISCO, sourced from previous projects (primarily on wheat, barley and maize accessions). Furthermore, 40% of EVA accessions documented in EURISCO have been included in AEGIS. A further 1,848 accessions would be available for AEGIS flagging if they are considered by

their holding institutes as unique. Three institutes in Portugal, Romania and Serbia could become AEGIS Associate Members, while institutes in France and Spain require that their country join the AEGIS initiative before being able to flag AEGIS accessions.

Data analysis activities were not initially budgeted in the project, creating the need to identify capacities and funds to ensure effective analyses could be conducted within the project time frame. A project amendment and extension approved in November 2022 created a new budget line for data analysis, securing the funds needed for data analysis in all networks. Results from data analyses have provided the basis for four scientific publications already published and several studies that are in preparation.

Relevant preliminary results from several networks highlight the advantages of participating in collaborative public–private partnerships and jointly creating valuable tools and resources. EVA Lettuce has identified several wild lettuce accessions with resistance to multiple *Bremia* strains; these are available for partners to incorporate in their breeding programmes and have been genotyped to allow GWAS analyses. EVA Lettuce has also developed a novel SPET genotyping panel (jointly with IGA Tech), which will be useful for lettuce breeders and researchers, as there are no low-cost genotyping tools available for this crop. The EVA Carrot Network has used three different genotyping approaches (GBS, WGS and a SNP array) and comparing the generated data will allow the development of low-cost genotyping methods for maintenance and conservation of carrot landraces. The EVA Maize Network identified new maize genetic diversity based on genotyping data and was able to show the pathways of maize introduction into Europe based on the EVA Maize collection. Preliminary results from biotic stress trials indicate potentially useful germplasm for maize breeding programmes. Preliminary results from disease trials in the EVA Pepper Network suggest the presence of material resistant to ToBRFV, an emerging pathogen across Europe; this germplasm will be useful in breeding ToBRFV-resistant pepper varieties. The wealth of data generated by the EVA Wheat and Barley Network was used to identify QTLs for resistance traits as well as material with multiple resistances against known and emerging diseases, both of which will be invaluable in breeding efforts to generate climate-adapted crops.

Communication activities and products developed during the project (two promotional videos, a brochure, a roll-up on EVA and a podcast) have been effective outreach mechanisms for ECPGR. They have also attracted possible new partners who may join the EVA crop-specific networks for the next project cycles.

5. Outlook

While the field crops and vegetables networks finalized their first project cycles, the EVA Legumes Network has initiated work in seven crop groups (common bean, chickpea, fava bean, lentil, lupins, orphan legumes and pea), which is now supported by another project funded by Germany, EVA Boost (GenR 2024-2). Overall, both the public and private sector partners generally view the collaboration and generated output of the EVA Networks very positively, and the majority are willing to continue this collaborative work. In practical terms, discussions in the various networks revolved around the sustainability of the EVA Networks going forward and on how to coordinate follow-up activities and projects.

While the coordination of the networks is supported by the ECPGR Secretariat with a dedicated budget line and many of the evaluation activities will continue to be provided in-kind by project partners, primarily from the private sector, several important aspects will require centralized and financial support to ensure smooth operations of future evaluation cycles. For example, regenerating sufficient material for multilocation trials was considered to best be done centrally by one provider with the relevant expertise and phytosanitary capacity, where necessary, and may not be easy to provide in kind to the network, based on the number of accessions and associated workload. This has been noted in the EVA Pepper and Legumes Networks as well as the EVA Wheat and Barley Network. Timely seed distribution is also essential and requires reliable and responsive partners. For some crops, field evaluations alone are not sufficient to provide the knowledge needed for breeders to select useful materials; additional tests under

controlled conditions or using specific equipment to assess quality traits should be included in the evaluations, but require additional funding. Furthermore, some breeders view an extension of EVA activities to include also pre-breeding as beneficial, e.g. by generating populations incorporating interesting material into elite lines. As discussed above, the EURISCO-EVA intranet is a useful tool for managing the phenotypic data generated in EVA and has served as a template for other projects' data management platforms. Further upgrades could make this platform more useful by creating a public interface to display data, potentially integrating some data analysis applications that have been developed in AGENT or INCREASE and enhancing the website interface. One suggestion from breeders was to enable easy search mechanisms to find the best-performing accessions for different traits and in different regions in a sort of breeder's toolbox or catalogue. However, the above-described activities will require additional funding towards the implementation of regular, future evaluation cycles of EVA networks.

Considering the above conditions, all networks are in principle continuing their collaboration, although in the absence of dedicated funding, the extent of further work and activities depends on the capacity of partners. Field trial capacities of private sector partners in all networks could be sourced for future evaluations (these were typically provided in kind), however, in kind contributions of public sector partners (towards regenerations or evaluations) are limited by budget constraints and genotyping or other technically intensive activities, such as lab assays, biochemical tests, and in depth data analyses will require funding.

Two ECPGR Grant Scheme Activities, EuroPepLand and MALANIRS, started in late 2024 and allowed an extension of the EVA Pepper and Maize Networks, respectively, to new genebank partners as well as selection and genotyping of new accession sets for evaluation. The EVA Carrot Network has already selected and distributed a new set of carrot landraces, which will be evaluated in kind by company partners, but genotyping of these will require additional funds. The EVA Lettuce Network is seeking to involve the ECPGR Leafy Vegetables WG to engage new partners and plan new activities, potentially exploring abiotic stress traits through a grant scheme application or other external projects. The Wheat and Barley Network partners are interested in continued screening of landraces (from AGENT and other sources), but some also consider that EVA could contribute to moving interesting accessions with novel alleles to the first pre-breeding steps, making them more accessible for further breeding. This development of introgression populations could be funded through external projects or the ECPGR Grant Scheme, and provide a new focus for the network. This could mean that the EVA Wheat and Barley Network could be consolidated around different priorities, potentially reducing the complexity of the current collaboration. Also here, not all partners will be able to continue providing in-kind contributions, and further public investment will be needed.

During the implementation of the EVA project over the past five years, several general issues have emerged in discussions across the different networks and should be followed up involving the larger ECPGR community in order to ensure that the project's outputs are made widely available. These include: (1) representation of EVA accessions within the AEGIS European collection – invite EVA genebank partners to become AEGIS Associate Members, incorporating their value-added collections into AEGIS where possible, (2) genebank management of diverse material types and maintenance of derived materials (e.g. SSDs) for which large datasets have been created – inclusion in EURISCO and in genebanks' catalogues to ensure conservation of and access to these valuable resources, and (3) incorporation of phenotypic data into the EURISCO public database after the embargo – considerations of relevant quality criteria and filtering of datasets to ensure the shared data provides a real value for the end user. Discussions on these issues have been initiated involving the EVA Networks and relevant ECPGR WGs and other bodies.

6. Conclusion

The above report shows that the public–private partnership (PPP) system applied in the EVA Networks has gained wide recognition, not only as part of ECPGR Phase XI. In fact, the EVA approach has been included as part of the *Plant Genetic Resources Strategy for Europe*[28] and is increasingly quoted as a positive example in various stakeholder fora where it has been presented (e.g. Euroseeds, SIGA, ISTA, EUCARPIA). Transnational PPP cooperation is considered an important aspect to advance the European plant breeding sector, especially for niche crops, and where SMEs are involved, as it provides a critical mass necessary for efficient plant breeding research and knowledge sharing. Several Horizon projects have engaged with the EVA Networks (e.g. AGENT, BRESOV, INCREASE, BreedingValue, Pro-GRACE) and our approach has been embedded in various funding proposals. The desire to adopt this approach has become visible during the project, with the creation of new EVA Networks, even applying EVA principles to perennial crops.

Taken together, this project has provided an important impetus to kickstart the ECPGR EVA network, with results above expectations, although some challenges remain to be addressed. Going forward, specific funding mechanisms should be developed to facilitate follow-up activities of the networks and ensure their sustainable continuation, building on the successful model of combining in-kind contributions with regular and activity-based budgets.

[28] www.ecpgr.org/pgrstrategy21