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# Final publishable report on WP1



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<b>ABSTRACT (FOR DISSEMINATION)</b>	<p>The report summarises the general process of inventory collections of wheat, potato, soybean, buckwheat and multiplication of selected varieties by the project partners. It analyses in a synthetic way what are the problems in establishing working collections of plant genetic resources, what we have done in the ECOBREED project and what needs to be done to successfully implement their use in organic agriculture. An important part is the section on the results achieved in the making and use of working collections in the ECOBREED project. The last section presents the insights provided by the project partners and users.</p>
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### Executive summary

Genetic resources are integral to the success of organic agriculture. They provide the raw material for developing crop varieties that are well-suited to organic farming principles, promoting sustainability, resilience, and biodiversity in agricultural systems. Preserving and utilising genetic diversity is essential for ensuring the long-term viability of organic farming practices.

An inventory was created using accessible databases of plant genetic resources, research and testing institutions, and farmers for (*Triticum aestivum*), durum wheat (*Triticum durum*) potato (*Solanum tuberosum*), soybean (*Glycine max*), and buckwheat (*Fagopyrum esculentum* and *Fagopyrum tartaricum*). Varieties of each target species were multiplied at partner localities for use in the respective WPs.

Working collections within plant genetic resources are dynamic sub-sets actively used for breeding, research and addressing challenges in agriculture. They serve as valuable repositories of genetic diversity, fostering innovation and sustainable practices in plant science and agriculture. Overall, an inventory of plant genetic resources serves as a valuable tool for managing, preserving and utilising the genetic diversity of plants, contributing to global efforts in sustainable agriculture and biodiversity conservation. Effective identification of plant genetic resources involves a combination of these techniques, and the choice of methods depends on the goals of the identification process, available resources, and the specific characteristics of the plant species in question. Following these steps, we have created a comprehensive information portal for genotype and phenotype characterisation data that will facilitate efficient data management, collaboration and knowledge sharing within the scientific community. Overall, the management of collections of plant genetic resources contributes significantly to global efforts to conserve biodiversity, enhance food security, and promote sustainable agriculture. It also supports scientific research and innovation in the field of plant breeding and genetics.



### What are the issues with creating working collections?

Plant genetic resources play a crucial role in organic agriculture, contributing to the development of diverse and resilient crop varieties that are well-suited to organic farming practices. Plant genetic resources intersect with organic agriculture through crop diversity and adaptation and conservation of genetic diversity. Plant genetic resources encompass a wide range of plant varieties with diverse genetic traits. In organic agriculture, where synthetic inputs are not permitted, having a diverse pool of crop varieties is essential for adapting to different environmental conditions, pests and diseases.

Organic agriculture encourages the use of diverse crop rotations and multiple species in farming systems. Preserving and utilising a broad genetic diversity of crops help maintain resilient and adaptive agriculture systems. Some organic farming systems actively engage in participatory plant breeding programmes. These programmes involve collaboration between farmers, researchers and breeders to develop crop varieties that meet the specific needs and conditions of organic agriculture.

Genetic resources contribute to ongoing research in organic agriculture, aiding in the development of new varieties that are well-adapted to organic farming practices. This research often involves exploring the genetic basis of traits such as early vigour, disease resistance, drought tolerance and nutrient efficiency. Global seed banks store and maintain diverse collections of seeds, including traditional and heirloom varieties, contributing to the conservation of genetic diversity.

Assembling or organising groups of items, data, or resources that are relevant to a particular project, task, or purpose is commonly referred to as making working collections from the accessions of gGenebanks or other maintainers.

Several steps are needed for creating working collections:

- defining the purpose, e.g. the need for varieties with suitable traits for organic farming, i.e. competitiveness against weeds, pest and disease resistance/tolerance, increased nutrient utilisation efficiency, tolerance to abiotic stress, yield stability etc.
- in accordance with the defined purpose, identifying suitable germplasm,
- Select and multiply the working collection,
- update the working collection regularly to reflect changes, additions, or updates,
- put in place arrangements for backing up and securing the working collection.

A "working collection" in the context of plant genetic resources refers to a sub-set of a larger germplasm collection that is actively used and managed for specific purposes. Plant genetic resources encompass the genetic diversity within plant species and these collections are crucial for crop improvement, breeding programme, and research. The term "working collection" implies that it is not just a static repository but actively utilised for ongoing activities. This sub-set is actively managed and utilised for breeding programmes, research projects and other practical applications.



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Scientists and researchers use working collections to study the genetic basis of traits, investigate the interactions between genes and the environment, and conduct experiments to enhance our understanding of plant biology.

Plant breeders use working collections to introduce new genetic material into their breeding programs. This helps in developing improved crop varieties with desirable traits such as higher yield, resistance to diseases, or tolerance to environmental stress.

The main objectives of the ECOBREED project focused on working collections of wheat, potato, soybean, and buckwheat were to:

- Identify potential genetic diversity for each of the four species suited to organic production systems.
- Multiply seed material and creation of wheat, potato, soybean, and buckwheat working collections.
- Facilitating further use of the genetic material studied in ECOBREED by making available genotypic and phenotypic data gathered in the project through a user-friendly information portal.



**Fig 1** Field experiments using wheat genetic resources.



### What have we done?

In WP1, **Creation of working collections and seed multiplication**, we have used an integrated and multidisciplinary approach to increase the competitiveness of organic breeding and farming, focusing on:

- management and conservation of genetic resources to facilitate further use of genepool accessions,
- providing new knowledge of the current state of research on plant genetic resources for organic agriculture,
- ensuring effective exploitation of project results and innovations by relevant user/stakeholder groups.

### Inventory of genetic resources for each target species

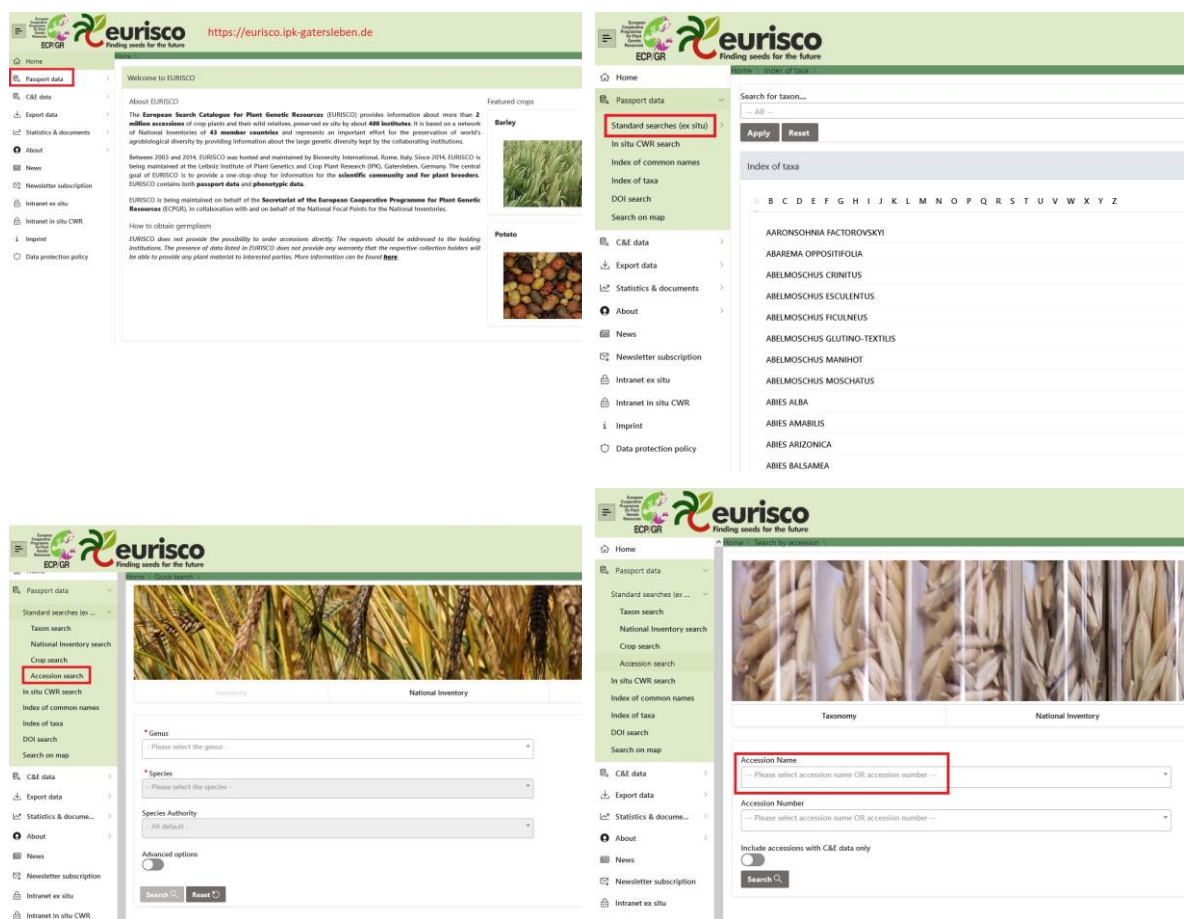
An inventory of plant genetic resources typically refers to a systematic and comprehensive record of the genetic materials of plants that are conserved for various purposes such as research, breeding and conservation. These inventories are often managed by genebanks, botanical gardens, research institutions, and organisations specialising in plant genetic resource conservation (Fig 2).

Key aspects associated with an inventory of plant genetic resources:

- Inventories aim to document the diversity within plant species, including cultivated crops, wild relatives and traditional varieties.
- The inventory includes information about germplasm collections, which may consist of seeds, tissues, or other reproductive materials.
- Each accession in the inventory is associated with detailed information such as its origin, morphological traits, genetic characteristics and any known uses or traits of interest.
- Inventories are managed through sophisticated databases that allow for efficient cataloguing, tracking and retrieval of information related to each plant genetic resource accession.
- Plant breeders use the inventory to identify and access genetic materials with traits of interest for crop improvement.
- Many inventories are part of international efforts to conserve and share plant genetic resources globally.
- Inventories often adhere to national and international policies and regulations related to the conservation and use of plant genetic resources. This includes considerations of benefit-sharing, access and benefit-sharing agreements, and adherence to the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA).
- Some inventories may have accessions aimed at raising public awareness about the importance of plant genetic resources for food security, biodiversity conservation, and sustainable agriculture.



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**Fig 2** Four steps illustrating the process of searching the EURISCO catalogue through taxon, genus and species up to the level of variety name.



### Identification of plant genetic resources

The identification of plant genetic resources involves various techniques and approaches to characterise and document the genetic diversity present within plant species. This process is crucial for conservation, breeding programme, and research in agriculture.

Some key methods and strategies used for the identification of plant genetic resources:

- Morphological characteristics, such as plant height, leaf shape, flower colour, and seed size, are often used for the initial identification of plant genetic resources. These traits can provide valuable information about the diversity within a species.
- Molecular markers, such as DNA-based markers (e.g., SSRs, SNPs), are widely used for precise identification of plant genetic resources.
- Profiling the protein content of seeds can help in the identification of plant genetic resources.
- Advanced statistical analyses of morphological and molecular data can be employed to identify patterns of variation and relationships among different plant accessions.

### Making collection of each target species identified

Making collection of identified target species involved a systematic and organised effort to collect, document, and evaluate samples representing the genetic diversity of these species.

Procedures for creating a collection for each target species:

- We have defined the collection objectives in the ECOBREED project focused on research and breeding for organic agriculture.
- We identified the target species wheat, potato, soybean and buckwheat of the ECOBREED project.
- F
- We developed a sampling strategy based on the objectives and distribution of the ECOBREED target species.
- We conducted laboratory and field experiments to evaluate accessions, obtain results, develop new hybrids, and use them for users.
- We have made a database containing information about each accession/variety evaluated and used in the ECOBREED project.
- We collaborated with other institutions, researchers, farmers, breeders, and other stakeholders to exchange knowledge, resources and genetic materials.

To develop a comprehensive collection of each target species is a meticulous process that requires collaboration, attention to detail and adherence to ethical and legal considerations. It contributes significantly to biodiversity conservation, scientific research and the sustainable management of plant genetic resources.



### **Multiplication and distribution of genetic resources for further evaluation**

Multiplication of genetic resources for further evaluation was the process of increasing the amount of genetic material to use it for extensive testing, research and investigation of their characteristics in the ECOBREED project.

- We have multiplied genetic material of wheat, potato, soybean, and buckwheat in a conventional way to generate a larger number of selected genetic resources in the ECOBREED project.
- We shared the multiplied genetic resources of wheat, potato, soybean and buckwheat with ECOBREED partners and stakeholders.

### **Establish an information portal for genotypic and phenotypic characterisation data of the working collections.**

The making of an information portal for genotypic and phenotypic characterisation data of working collections involved several steps:

- defined the scope of the working collections of genetic resources to include the collection of accessions of all target crops in the ECOBREED project
- outlined the objectives of the information portal and the range of genetic resources we have included in the working collections
- selected a platform to host our information portal
- made a structured database to organise genotype and phenotype data
- established standards for data format, ensuring consistency and interoperability
- designed an intuitive and user-friendly interface for easy navigation, especially because of the need for researchers, breeders and other stakeholders to interact with the portal
- introduced a mechanism for entering new data and updating existing records.



## What are the results achieved in the ECOBREED project to increase the efficiency and competitiveness of organic crop breeding?

In step 1 we used the European Plant Genetic Resources Search Catalogue (EURISCO) providing information on more than 2 million accessions of cultivated plants and their wild relatives that have been conserved *ex-situ* by about 400 institutes [Home \(ipk-gatersleben.de\)](http://ipk-gatersleben.de).

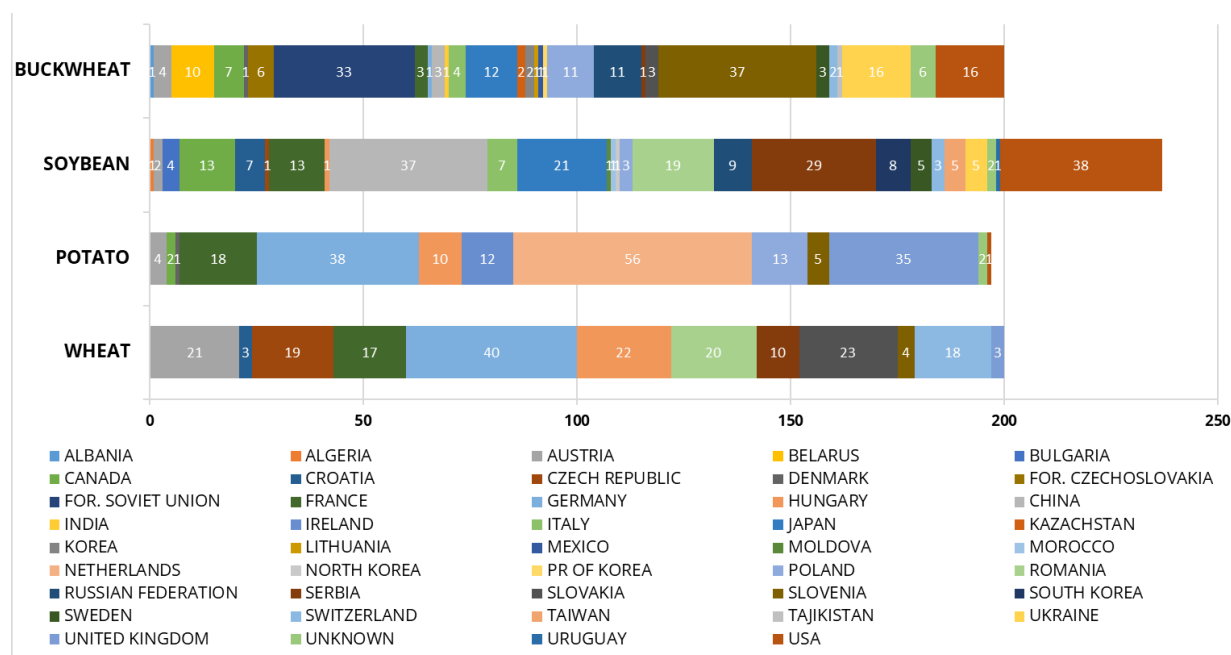
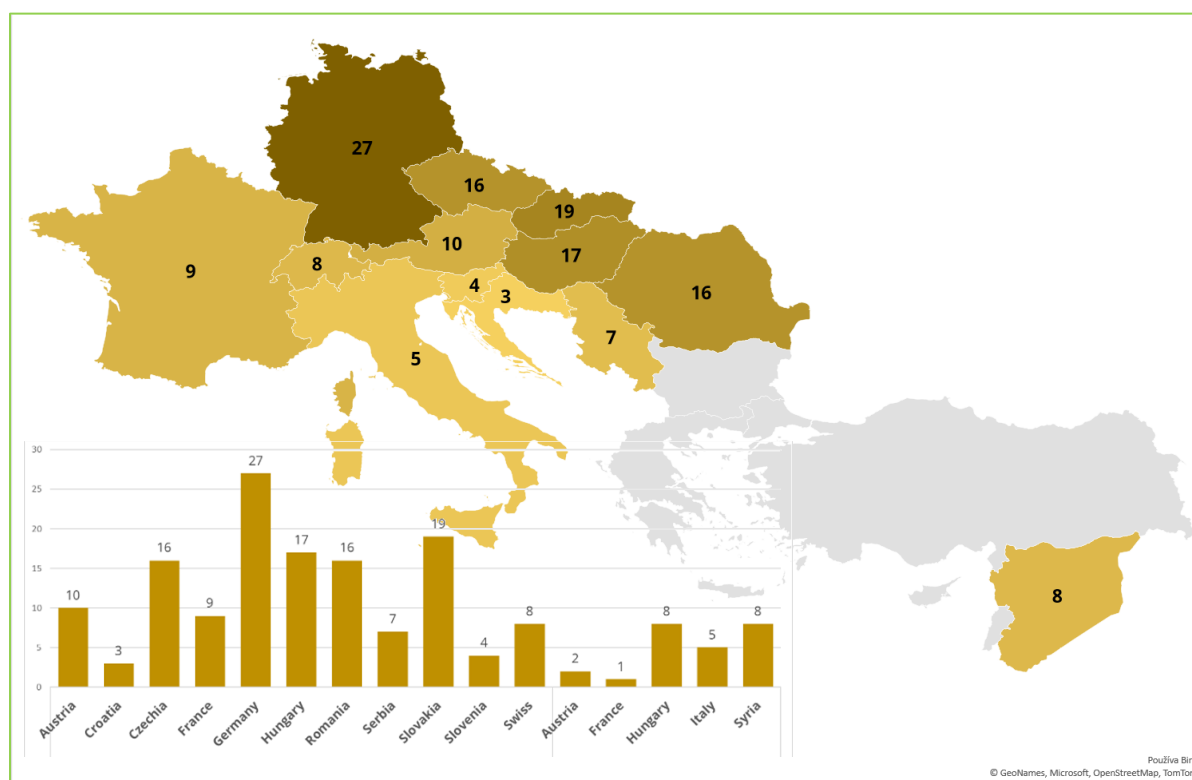


Fig 3 Number of accessions in collections by the project partners.

### Inventory and identification of wheat accessions

Inventory and identification and selection of wheat accessions/varieties was based on information which was gained from previous European research projects such as COBRA (Core Organic II), SUSVAR (COST 860), national projects and national testing carried out either by breeders or within national organic VCU trials. The selected wheat genotypes originate from 12 different European countries; most of the material has its origin in Germany and represents cultivars which were released in the last two decades and are still included in either the European list or national lists. The rest of the material include both, landraces and old varieties, as well as modern breeding lines which are at the moment subject to national organic VCU tests and/or internal organic trials. It is worth mentioning that several genotypes are from bio-dynamic breeding programmes in Germany and Switzerland, i.e. Getreidezüchtungsforschung Darzau, Dottenfelderhof and Getreidezüchtung Peter Kunz. Moreover, the collection includes several cultivars which were developed within so-called BFOA (breeding for organic agriculture) programmes (Wolfe et al. 2008, Löschenberger et al. 2008), e.g. at Saat-zucht Donau, Austria, Secobra in Germany and INRA Le Rheu in France, and passed organic VCU trials in the respective countries.



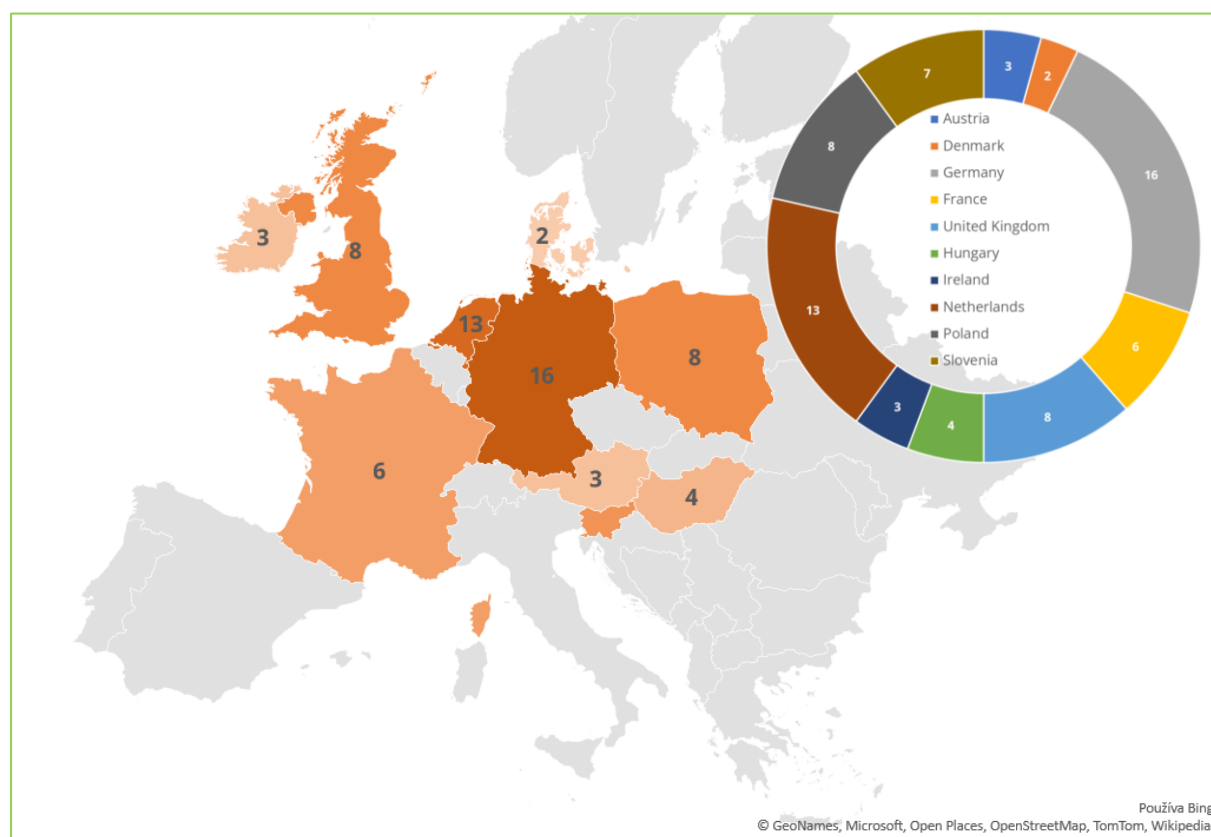


**Fig 4** Geographic distribution and number of winter wheat and durum wheat accessions in ECOBREED.

### Inventory and identification of potato accessions

Accessions of potato were identified by all four partners in the project (KIS, IHAR, UP, UNEW) based on their data on potato varieties available from databases such as The European Cultivated Potato Database, World Catalogue of Potato Varieties, ADHB Potato Variety Database, ARVALIS database on potato varieties, SASA database on organic seed lots in Scotland produced in 2017, Data on organic seed produced in 2017 in Austria, data on organic potato varieties tested in FiBL, Switzerland (data for the last 10 years), data on organic potato varieties from Bioland, Germany, Descriptive List for Potato Bundessortenamt BSA for Potato for 2017, Breeders variety catalogue (Netherlands: Agrico, HZPC, Meijer, Den Hartigh, Stet Holland, Agroplant; Germany: Europlant, Norika, Solana; France: Germicopa, Grocep, Bretagne Plants, Comite Nord, Austria: NOES, UK: Sarpo Potatoes Ltd, James Hutton Institute) and personal contacts .





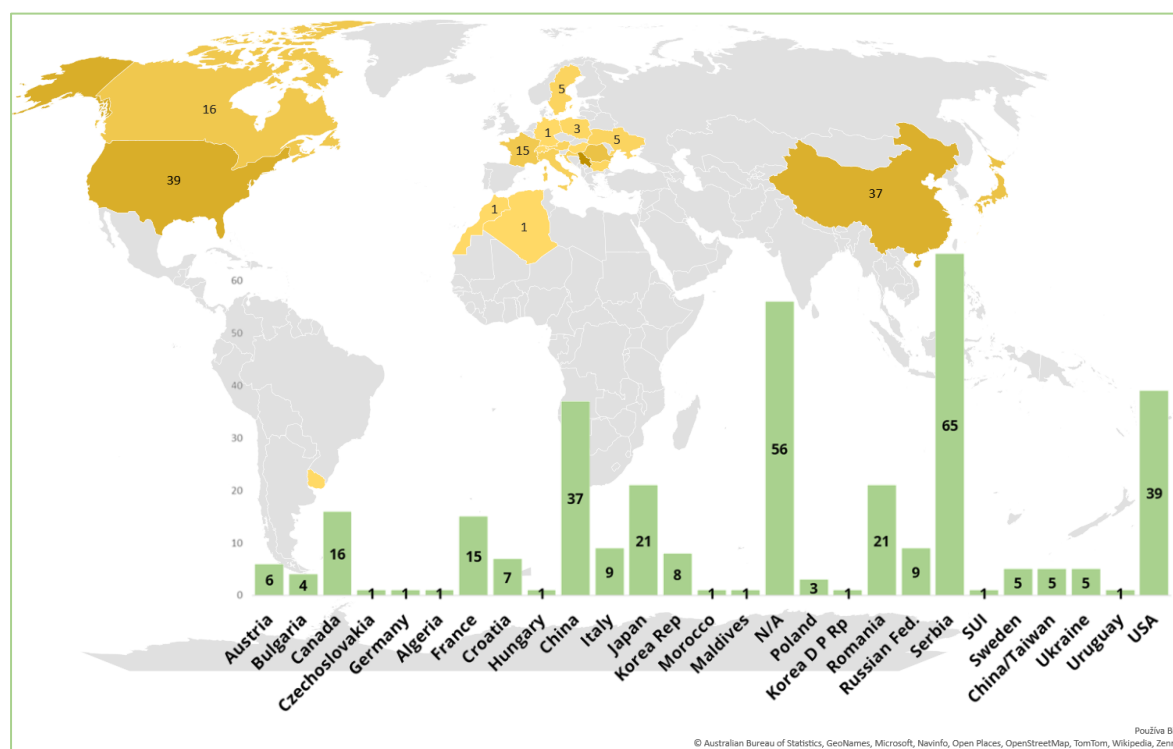
**Fig 5** Geographic distribution and number of potato accessions in ECOBREED.

### Inventory and identification of soybean accessions

Identification of soybean accessions suitable for organic and low-input production and breeding were sought through several databases, as well as germplasm collection of project participants. Accession list contains 236 which originated from all around the world.

The accessions were selected according to the value for further breeding purposes using several criteria: diverse germplasm, popular organic variety, conventional variety and landraces, special traits germplasm and biotic and abiotic resistance and tolerance. Disease resistance is crucial for successful organic production due to limitations in crop protection. Several diseases (stem canker, Pythium root rot, SMV) were identified as future potential problems and source of resistance were included. An important trait, with benefit for farmers and the processing industry is grain quality. High protein, large/small seed, coloured test, low Kunitz inhibitor, allergen free accessions represent a genetic base for developing a special type of variety that can satisfy diverse demands of the processing industry while farmers can achieve economic benefits growing that type of variety.





**Fig 6** Geographic distribution and number of soybean accessions in ECOBREED.

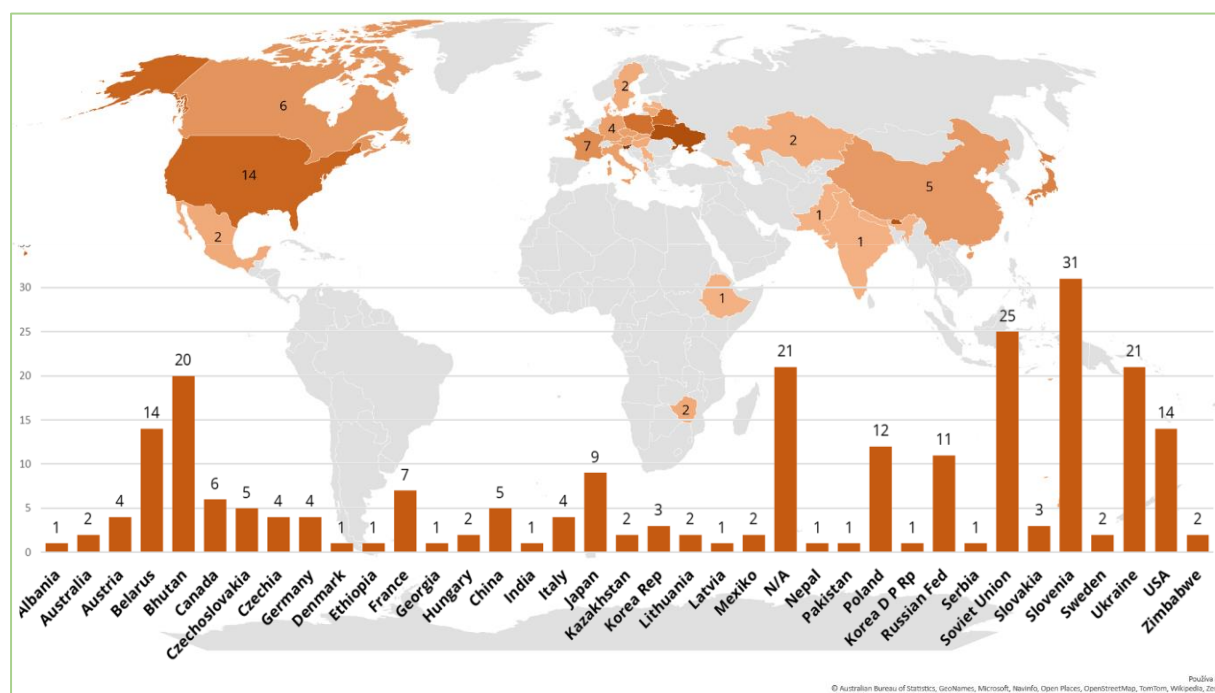
### Inventory and identification of buckwheat accessions

Worldwide, thousands of buckwheat accessions are stored in collections. To facilitate better handling of these accessions, a working collection has been created by partners SZG, KIS and RGA for further breeding and evaluation of selected traits.

Accessions of common and Tartary buckwheat were sought through the databases of EURISCO, GRIN Global, GRIN Czech and through personal contacts with other curators of buckwheat or/and partners involved in the project. The biggest buckwheat collections are in China and Russia, however, the possibility to obtain any of these accessions is very limited even when partner countries have a memorandum of understanding (exchange of seed samples between genebanks). Interesting traits were discussed with farmers, manufacturers and producers. Unfortunately, no data was available on quality of the grain and on processability as the main characteristics demanded by processors and producers of buckwheat are known. Nor are there any data available on lodging and the determination of flowering time required by farmers.

The first step was identification of 263 accessions from more than 30 countries (including the Former Soviet Union, Czechia etc.) – (sources - Czech Gene Bank, US Gene Bank, Ukrainian Gene Bank, Austrian Gene Bank, Slovenian Gene Bank and Arche Noah). The accessions were selected according to the value for further breeding purposes (tetraploids, red and/or green corolla, different colours of achenes etc.) and according to the country of origin; it was not possible to receive any accessions from China where buckwheat originated (Fig. 8).





**Fig 7** Geographic distribution and number of buckwheat accessions in ECOBREED.

The biggest number of accessions originated from the Former Soviet Union, Ukraine, and Russia where most breeding programmes have been launched during the past 60 years; also, Polish breeding is represented.

### Making collection of each target species identified

For winter wheat, the varieties used in the ECOBREED project were from 12 different European countries (Austria, Switzerland, Czechia, Germany, France, United Kingdom, Hungary, Romania, Serbia, Slovenia and Slovakia). This group included a total of 160 varieties of winter wheat and 24 varieties of durum wheat.

For the ECOBREED project, commercial potato varieties that already exist in Europe and have sufficient seed, were selected. A working collection of potato was established. It turned out that seed availability had a big impact on the list of varieties in the working collection. All 65 varieties were grown for seed multiplication in the ECOBREED project by partners.

The soybean working collection has been largely derived from Serbia (132), Romania (50) and Germany (26). The selection of germplasm for the ECOBREED soybean working collection was carried out considering cold tolerance during the flowering period, early maturity and low requirements in terms of accumulated temperature, drought tolerance, high grain weight, stable yield performance and high resistance to different diseases.

The collection of buckwheat accessions was dynamic, and the number of accessions increased during the project and varied according to the tasks. The working collection was composed of 54 common genotypes and several additional genotypes were added at individual sites depending on availability.



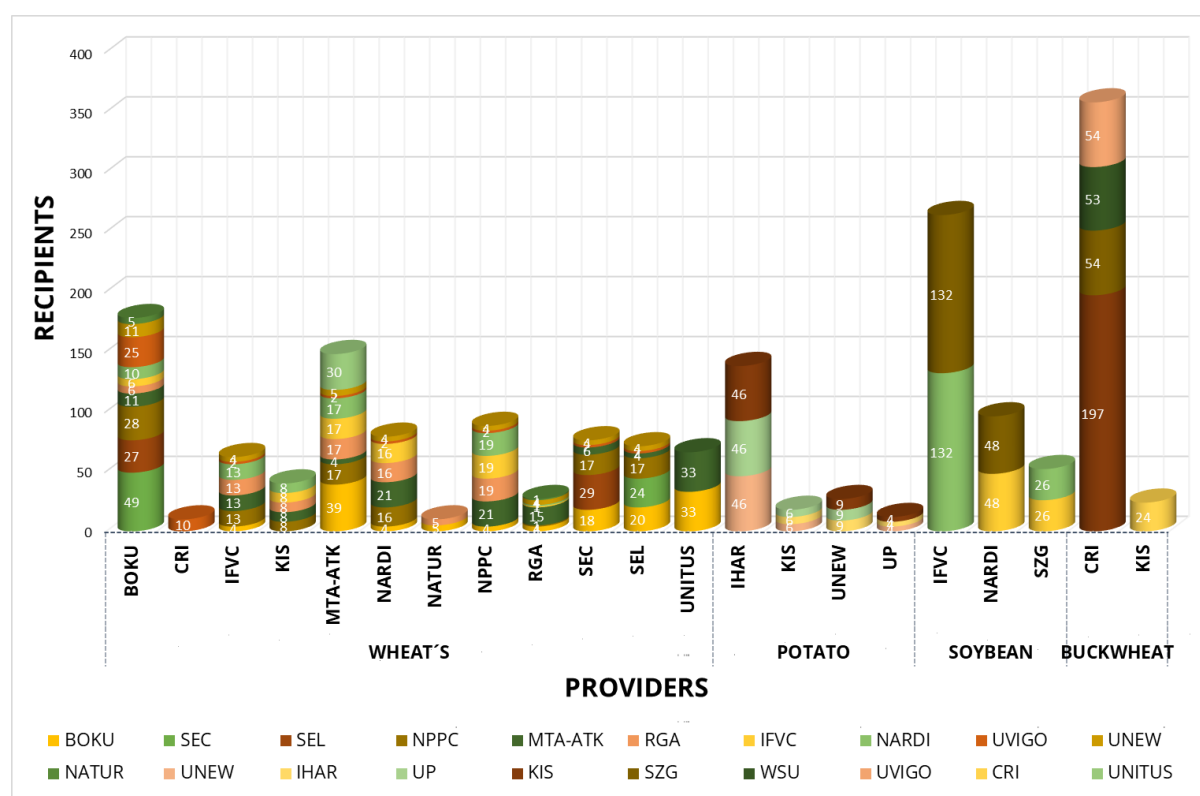
## Multiplication and distribution of genetic resources for further evaluation

From the accessions of the preliminary collection, samples were multiplied for further evaluation and based on the results of the multiplication, working collections of individual crops were made and sent to partners. The partners multiplied the varieties of wheat, potatoes, soybeans, and buckwheat for several tasks in WP2-WP6. Multiplication of the wheat genotypes was done in Piešťany, Raasdorf, Martonvasar, Novi Sad, Jablje, Murska Sobota, Fundulea, Feldkirchen, Stupice/Uhřineves, Viterbo and South Crete by ECOBREED partners.

65 potato varieties from the working collection were supplied to partners for phenotyping trials, propagation of tubers for the next season and breeding work. Potato seed was multiplied by all four partners: KIS, IHAR-PIB, UNEW and AKT.

IFVC, NARDI and SZG e multiplied seeds of 217 soybean varieties. Based on the results of the seed multiplication, the partners compiled the final list of the working collection, which consists of 208 accessions.

46 accessions of Tartary buckwheat and 10 of common buckwheat were multiplied for reproduction using isolation cages and pollination by bees by CRI in Czechia. Also, buckwheat accessions and commercial varieties for field trials were selected for evaluation due to high demand and availability of seed.



**Fig 8** Distribution of accessions from working collections of wheat, potato, soybean, and buckwheat varieties among partners.





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### Establishing an information portal for genotypic and phenotypic characterisation data of the working collections.

In Task 1.3, project partners have prepared a publicly accessible database for accessions/varieties of all four crops that are being evaluated and used in the project. A link to the European Search Catalogue for the Plant Genetic Resources (EURISCO) database is added to the Excel file for EURISCO accessions. The database is a user-friendly information portal containing all genotypic and phenotypic data for the working collections used in ECOBREED and published in scientific and technical papers. The database is accessible through the project website, hosted by KIS (<https://ecobreed.eu/outcomes/database/>). The database is created in MS Excel with one file and one sheet for each of the four ECOBREED crops including following species: *Triticum aestivum* L. (winter wheat and spring wheat), *Triticum turgidum* subsp. *durum* (Desf.) Husn. (durum wheat), *Solanum tuberosum* L. (potato), *Glycine max* (L.) Merrill (soybean), *Fagopyrum esculentum* Moench (common buckwheat) and *Fagopyrum tataricum* (L.) Gaertner (tartary buckwheat).

The structure of the table contains several attributes about the accessions: botanical taxon name; cultivar name with active link to institution or society; accession number (with direct link to EURISCO); country of origin, status (information on where each cultivar is listed with added filters for breeding lines, cultivated variety, genetic strain, heterogeneous material); country; original breeder (link to institution or society); year of release; details (with direct link to Zenodo repository); source (with link to society or EURISCO).

160 wheat genotypes were included in the information portal, including 136 winter wheat genotypes and 24 durum wheat genotypes, which contained genetic and phenotypic characterisation data.

The ECOBREED project gathered all available information and established a working collection of 65 selected potato varieties. An overview of the status of the potato collection is given in Figure 1.4. More detailed information on the diversity of potato varieties that have been genotyped and phenotypically characterised in the ECOBREED project is available on the information portal.

In the soybean collection the largest representation of accessions came from Serbia, USA, China, Japan, Romania, Canada and France. Fewer accessions were evaluated for phenotypic and genotypic characteristics in WP4 with other European countries, but partners had accessions from Africa and some countries from which data are less available. Information on the diversity of soybean varieties that have been genotyped and phenotypically characterised in the ECOBREED project is available on the information portal and ZENODO repository.

The ECOBREED buckwheat collection is represented by accessions from Slovenia, Russian Federation, Ukraine, Bhutan, Belarus, USA, Poland and Japan. The ECOBREED project partners evaluated phenotypic and genotypic characteristics. The results of the evaluation with buckwheat varieties in the ECOBREED project have been the subject of several scientific papers and are available on the information portal and in the ZENODO repository.



### What knowledge do working collections provide to users?

The management of collections of plant genetic resources (PGRs) involves the preservation, documentation, and utilisation of genetic material from plants. These collections, often stored in genebanks or seed banks, play a crucial role in preserving biodiversity and ensuring the availability of genetic diversity for breeding programs, research, and sustainable agriculture. The goal of ECOBREED is to enhance collaboration researchers and stakeholders to improve crops using advanced breeding techniques, with a focus on organic and low-input agriculture.

Knowledge provided to ECOBREED users on plant genetic resources collections:

- Collections of plant genetic resources contain a diverse range of genetic material, including different varieties, landraces and wild relatives of cultivated plants. This diversity is a valuable resource for breeding programmes to develop new crop varieties with improved traits, such as resistance to diseases, pests, and environmental stresses.
- ECOBREED project provide users with access to diverse plant genetic resources, including traditional varieties, landraces and wild relatives. This includes details about the origin, characteristics and properties of the plant material.
- The results of the ERCOBREED project provide insights into the characterisation of genetic resources, including information on the origin, traits and agronomic characteristics of different accessions.
- Given the focus on organic and low-input agriculture, ECOBREED may provide knowledge on sustainable farming practices, organic crop management, and strategies for developing crop varieties that perform well under low-input conditions.
- The results of the ERCOBREED project provide insights into the characterisation of genetic resources, including information on the origin, traits and agronomic characteristics of different accessions.
- Knowledge is provided on effective strategies for the conservation of plant genetic resources. Management of plant genetic resources involves understanding and complying with international agreements, treaties, and national laws related to the exchange, use, and conservation of genetic resources.
- Plant genetic resources are essential for breeding programs aimed at developing crops with desirable traits such as improved yield, nutritional content, and resilience to environmental challenges.

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