Genetic Resources

GENEBANK REPORT

Genetic Resources (2025), (S2), 91–105
DOI: 10.46265/genresj.GYDY5145
https://www.genresj.org
ISSN: 2708-3764

The German Federal Ex Situ Genebank for Agricultural and Horticultural Crops – Conservation, exploitation and steps towards a bio-digital resource centre

Stephan Weise[a], Frank R Blattner[a], Andreas Börner[a], Klaus J Dehmer[b], Marion Grübe[a], Dörte Harpke[a], Ulrike Lohwasser[a], Markus Oppermann[a], Nils Stein[a,c], Evelin Willner[d] and Manuela Nagel[*,a]

[a] *Genebank Department, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), OT Gatersleben, Corrensstr. 3, 06466 Seeland, Germany*
[b] *Genebank Department, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Parkweg 3a, 18190 Sanitz, Germany*
[c] *Martin-Luther-University Halle-Wittenberg, Universitätsplatz 10, 06108 Halle, Germany*
[d] *Genebank Department, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Inselstr. 9, 23999 Malchow/Poel, Germany*

Abstract: Over more than 80 years, the collections of the German Federal Ex Situ Genebank for Agricultural and Horticultural Crops have grown to around 152,000 accessions of 3,000 species preserved at three locations: Gatersleben, Groß Lüsewitz and Malchow/Poel. More than 96% of the material is stored as desiccation-tolerant orthodox seeds according to the active–base–safety (A-B-S) replicate approach at -18°C. Almost 70,000 freshly regenerated safety replicates are stored in the Svalbard Global Seed Vault. However, 4% of the material (2,000 field, 3,000 *in vitro* and 2,500 cryopreserved accessions) can only be maintained vegetatively, as no or few seeds or no true-breeding seeds are available.

Most of the accessions are provided via the standard material transfer agreement (SMTA) and more than 1.2 million samples have been distributed since the genebank was founded. To guarantee the identity of the living plant material, reference samples comprising about 450,000 voucher specimens, 110,000 seed and fruit samples and 57,000 cereal spikes are used for comparisons.

Genebank workflows are supported by the Genebank Information System (GBIS), which also manages workflow-independent data to describe the genebank accessions by passport, phenotypic and taxonomic data, thus allowing users to make targeted selections of material. The genebank-related processes, including acquisition, preservation, regeneration, documentation and material distribution, are certified for quality management in accordance with ISO 9001.

Nowadays, the genebank is undergoing a transformation process to become a bio-digital resource centre to improve utilization of the genetic resources in research and breeding to address future challenges.

Keywords: German crop genebank, plant genetic resources, conservation, *ex situ*, *in vitro*, cryo, documentation, exploitation

Citation: Weise, S., Blattner, F. R., Börner, A., Dehmer, K. J., Grübe, M., Harpke, D., Lohwasser, U., Oppermann, M., Stein, N., Willner, E., Nagel, M. (2025). The German Federal Ex Situ Genebank for Agricultural and Horticultural Crops – Conservation, exploitation and steps towards a bio-digital resource centre. *Genetic Resources* (S2), 91–105. doi: 10.46265/genresj.GYDY5145.

Received: 16.10.2024 | Accepted: 11.02.2025 | Published online: 10.03.2025

Introduction and historical background

The availability, accessibility and diversity of plant genetic resources (PGR) are the basis for the adaptation of our crops to environmental challenges and human needs. PGR are pivotal for breeding towards increased biotic and abiotic stress tolerance, optimizing human and animal nutrition and efficient use of renewable resources, including for the energy, chemical and pharmaceutical industries (Grusak and Dellapenna, 1999; Hoisington *et al*, 1999; Metzger and Bornscheuer, 2006; Tilman *et al*, 2006; Qian *et al*, 2018). However, since the beginning of industrialization and the introduction of the targeted selection of advantageous local plant varieties – so-called landraces – PGR have steadily disappeared (Tanksley and Mccouch, 1997). This effect was already recognized by various researchers at the turn of the 20^{th} century and led to the first collecting missions, e.g. those organized by Nikolai Ivanovich Vavilov and Frank Nicholas Meyer (Hammer and Diederichsen, 2009; Baranski, 2013). Against this background, the Seed and Plant Introduction Office (Beltsville, USA) and the Office for Agricultural Crops (St. Petersburg, Russia) were established in 1893 and 1894, respectively (Hammer, 2020), and are considered the two most important forerunners of today's genebanks. A first organized seedbank was established in the predecessor institution of today's N.I. Vavilov Institute of Plant Genetic Resources (VIR) in St. Petersburg (then Petrograd) and stimulated the worldwide movement to preserve the diversity of agricultural and horticultural plants as a basis for food security. Vavilov's postulation of geographical centres of origin, defining assumed regions where the domestication of cultivated plants began, played an important role in the guidance of early collecting trips (Vavilov, 1926). These narrowly defined geographical areas were characterized by a great diversity of cultivated and wild forms of domesticated species. Although only some of Vavilov's centres of origin turned out to be areas for crop domestication, the high genetic diversity in these regions is still present today.

In Germany, the latest findings on genetic mechanisms stimulated researchers such as Fritz von Wettstein and Erwin Baur to argue for the preservation and exploitation of the diversity of crops. At a seed breeding conference organized in Berlin in February 1914, Erwin Baur stated: "It is very urgent now to become active to save and maintain the quickly disappearing old and primitive varieties of our cultivated crops" (Baur, 1914). Since that time, efforts were initiated to establish an institute for research on crops which was finally founded in 1943 on the Tuttenhof estate near Vienna as Kaiser Wilhelm Institute for Crop Plant Research (Kaiser-Wilhelm-Institut für Kulturpflanzenforschung). The first collections included mainly materials from expeditions carried out before the institute was founded. After the Second World War, the first director, the geneticist Hans Stubbe, successfully re-established the institute in Gatersleben and initiated a period of systematically planned collecting trips all over the world (Müntz and Wobus, 2013). Larger collecting trips were made to southern Italy, Afghanistan, China and Mongolia, among others (Supplemental Table 1). From 1948 onwards, there was also an intensive exchange of seeds with botanical gardens, agricultural and horticultural institutes and breeders. While the collections comprised approximately 3,500 accessions at the time of the transfer to Gatersleben, by 1962 they had already grown to 23,000 (Lehmann, 1963).

For the first years, the seeds of genebank accessions could only be stored at ambient conditions and thus had to be regenerated every 3–5 years (Lehmann and Mansfeld, 1957). The construction of a seed cold-storage facility, completed in 1976 (Anon, 1978), led to a drastic change in conservation management. The increased storage capacity and storage temperatures of -15 to -18°C extended the storage periods of the seeds, resulting in fewer regeneration cycles and lower costs (Figure 1). However, systematic large-scale screening on various crops for raw protein content and the essential amino acid lysine began in the late 1960s, see e.g. Lehmann *et al* (1978) and Grebenščikov (1985), and led to a sharp increase in seed regeneration in some years.

The Gatersleben genebank collections had grown to more than 65,000 accessions by the end of the 1980s. However, with the German reunification in 1990 and the desire to consolidate the PGR for agriculture and horticulture in one institute, the collections in Pillnitz (fruit genetic resources), Gülzow (rye and triticale), Malchow (oil and forage crops) and Groß Lüsewitz (potato) were integrated. The total collection size thus increased to almost 96,000 accessions by 1992. The institute was now renamed the Institute of Plant Genetics and Crop Plant Research (IPK). Between 2001 and 2003, around 50,000 accessions from the former West German genebank were transferred to the IPK genebank. Originally, the West German genebank was established at the Research Centre for Agriculture (Forschungsanstalt für Landwirtschaft, FAL) in Braunschweig in 1970 (Hammer, 1998). It was later assigned to the Federal Centre for Breeding Research (Bundesanstalt für Züchtungsforschung, BAZ) now part of the Julius Kühn Institute (JKI). In this context, the collection of fruit genetic resources in Pillnitz was transferred to the BAZ by the end of 2002 and the IPK genebank was renamed the 'German Federal Ex Situ Genebank for Agricultural and Horticultural Crops'.

The composition and conservation of the genebank collections

Composition

The IPK genebank collections today comprise almost 152,000 accessions of 3,000 species from 750 genera (Table 1). They are actively managed by eight curator

*Corresponding author: Manuela Nagel (nagel@ipk-gatersleben.de)

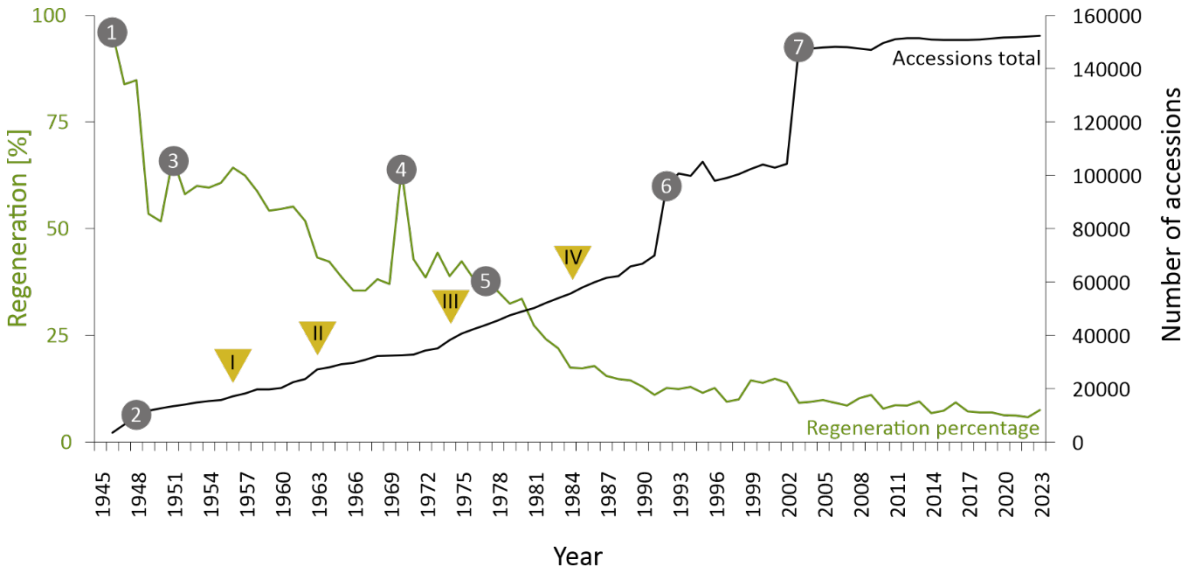

Figure 1. Development of the number of accessions and the regeneration percentage of the IPK genebank collections since the relocation to Gatersleben in 1945/1946. Selected events that can be seen from the curves are: 1) the regeneration rate of almost 100% due to the transfer of 3,500 accessions to Gatersleben, 2) the increase in the number of accessions due to the establishment of a lively exchange of seeds between botanical gardens, research institutes and breeders from 1948, 3) the renewed increase in the regeneration rate due to the incorporation of material from the first major collecting trips, 4) the start of large-scale screening of the raw protein content and the essential amino acid lysine in various cultivated plants, 5) the introduction of seed cold storage, which led to longer storage times and thus to a reduction in regeneration cycles, 6) the integration of the collections from Pillnitz, Gülzow, Malchow and Groß Lüsewitz, 7) the integration of the West German genebank collections and transfer of the fruit genetic resources in Pillnitz to BAZ. Supplemental Table 1 provides an overview of collecting missions of genetic resources worldwide that have been at least partially incorporated into the IPK genebank and have contributed to the continuous increase in the number of accessions. Four of these are mentioned here as examples: I) integration of material from the FAO collecting missions to Iran under H. Kuckuck (1952–1954) from 1956, II) integration of E. Mayr's alpine landrace collection (1922–1932) from 1964, III) start of various landrace collections in Slovakia and Moravia and integration into the genebank from 1974, IV) various collecting missions to Italy and continuous integration into the genebank (1980–1992).

groups – cereals, vegetables, tomatoes and beans, legumes, medicinal plants, potatoes, oil and forage crops, and *in vitro* and cryopreservation – organized in three research groups at three different locations. All groups collaborate intensively and contribute to the reference collection (Figures 2 and 3). About 86% of the material is maintained at the main site in Gatersleben (DEU146), the remainder at two satellite stations in Groß Lüsewitz (DEU159, 4%) and Malchow/Poel (DEU271, 10%).

Overall, the largest collections comprise accessions of wheat (18%), barley (15%), *Phaseolus* bean (6%) and potato (4%), which are among the largest global genebank collections. For example, IPK holds 6% of the total accessions of barley, 5% of *Phaseolus* bean and 11% of the potato held in the global genebanks (Wiews, 2025). About 37% of the accessions are classified as traditional cultivars/landraces, 28% as advanced or improved cultivars, 15% are wild or weedy and 10% are breeding/research material. The remainder is not specified. The country of provenance is known for almost 125,000 accessions in the collections. Most accessions originated in Europe (66,400 accessions), followed by Asia (32,200), the Americas (13,800), Africa (12,000) and Oceania (500) (Figure 4).

Seedbank

About 96% of the material is preserved as orthodox, desiccation-tolerant seed and maintained according to the genebank standards for plant genetic resources for food and agriculture (FAO, 2014). Every year, about 8,000 to 10,000 accessions are regenerated or multiplied in the fields, following best agricultural practices concerning fertilizer supply, pest/weed control and crop rotation. Self-pollinating species are grown side by side on areas of 10–15 hectares. Most accessions are separated by a different crop, e.g. wheat accessions by barley or forage grasses by rye. Cross-pollinators such as rye are grown in separation strips with larger distances or in more than 170 isolation greenhouses of 5–10m^2. The latter are mainly used for insect-pollinated accessions and are equipped with solitary bees, bumblebees or flies. Biennial accessions are often grown in the open field and transferred to isolation greenhouses or cages after evaluation in the second year. During the growing season, crop-specific descriptors based on IPGRI/Bioversity descriptor lists (Bioversity, 2024) are used for characterization. Extended morphological and physiological information about adaptation and resistances towards environmental stresses and diseases are often obtained during targeted projects, e.g. on

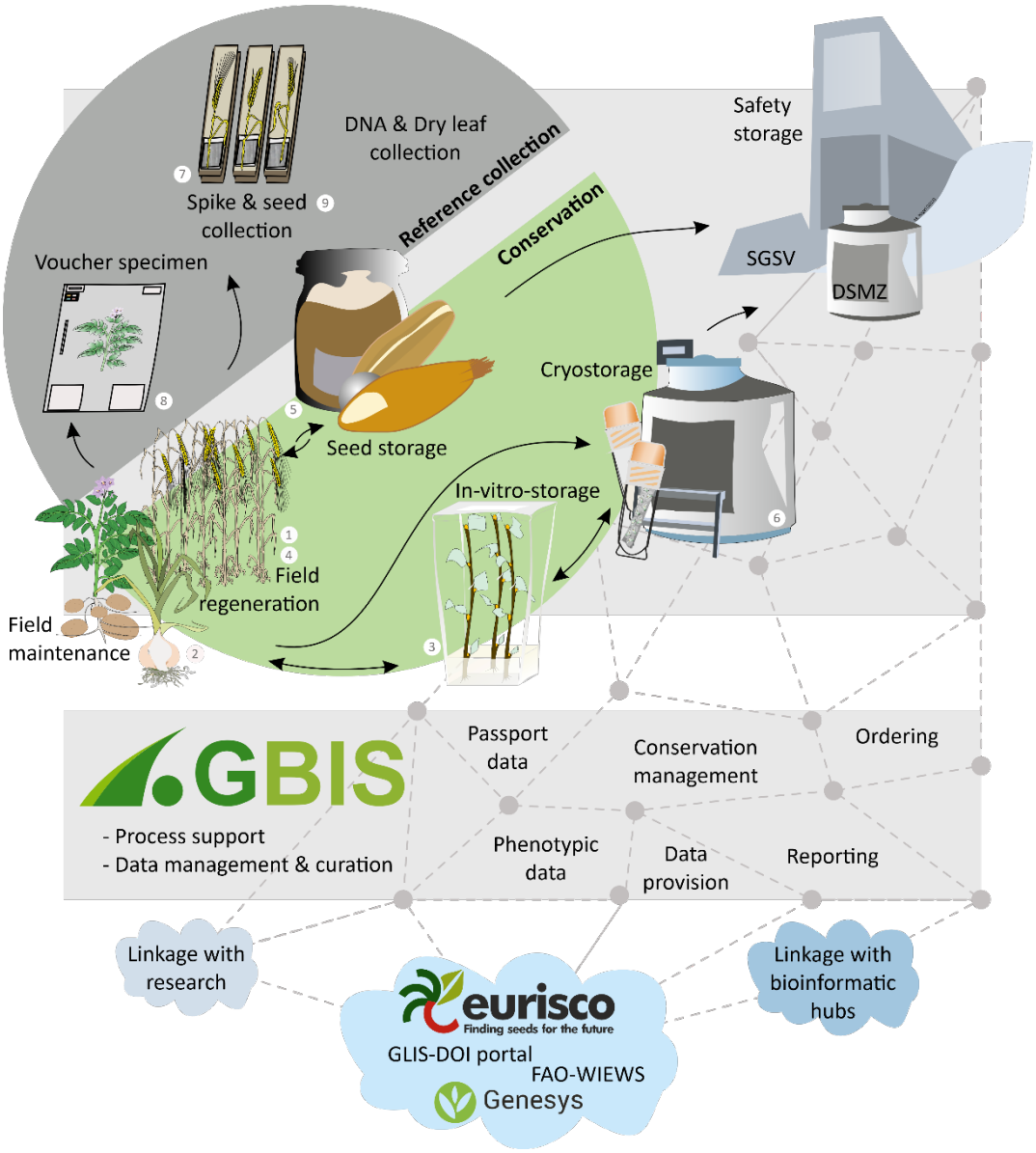

Figure 2. Overview of genebank management for conservation of seed and clonal accessions including safety storage of seeds at the Svalbard Global Seed Vault (SGSV) and of cryosamples at the German Collection of Microorganisms and Cell Cultures (DSMZ). Arrows indicate the direction of the main workflows. The Genebank Information System (GBIS) provides process support including management and curation of data, allowing users to specifically select and order material, and is linked to international information systems, bioinformatics hubs and research projects. 1-9, Numbers in circles indicate steps visualized in Figure 3.

legumes, forage grasses (Supplemental Table 2) and support data complementation and breeders to select and utilize PGR.

Maturity of seeds is crucial for the development of optimal desiccation tolerance and seed longevity (Leprince *et al*, 2017). When full seed maturity is reached, the plants are cut manually. Most of the material is placed in drying cabinets at 20% relative humidity (RH) and a temperature of 20°C. Depending on the workload, the material is further threshed and cleaned. Clean seeds or separately harvested spikes are compared with reference material and then transferred to drying cabinets at 15% RH and 20°C to reach a final seed moisture content of 5–7% depending on the species. In parallel, the initial germination capacity and moisture content of the seeds are tested. If germination of cultivated species reaches more than 80%, the material is further processed and separated into active–base–safety replicates. Active replicates are mainly kept in sealed glass jars with silica gel tops and stored at -18°C, in some cases also at -8°C or 4°C. Base and safety replicates are vacuum sealed and stored at -18°C. Once per year, safety replicates are transferred to the Svalbard Global Seed Vault, Spitsber-gen. Within the last 16 years, freshly reproduced seeds of almost 70,000 IPK accessions have been deposited at the global backup storage, providing an important level of security against the loss of seeds due to human-caused or natural disasters.

Highly vigorous seed material is the basis for the long-term availability of genetic resources (Ellis and Roberts,

Figure 3. Various steps during conservation of seed and clonal genebank accessions. 1, Regeneration of cereal accessions in the Gatersleben fields (Photo: Michael Grau, 2008); 2, *Allium* field genebank in Gatersleben (Photo: Manuela Nagel, 2020); 3, *In vitro* slow-growth storage of potato (*Solanum tuberosum* L.) in Groß Lüsewitz (Photo: Manuela Nagel, 2019); 4, Regeneration of red clover (*Trifolium pratense* L.) accessions in Malchow/Poel (Photo: Daniela Impe, 2019); 5, Active storage of runner beans (*Phaseolus coccineus* L.) in Gatersleben (Photo: Heike Müller, 2014); 6, Long-term cryostorage of clonal accessions (Photo: Lynne Main, 2016); 7, Spike reference collection (Photo: Sam Rey, 2012); 8, Voucher specimen (IPK Herbarium); 9, Seed reference collection in Gatersleben (Photo: Sam Rey, 2012).

Table 1. Composition of the IPK genebank collections shown by species groups by June 2024.

Species groups	Accessions	Species groups	Accessions
Cereals and grasses	**66,434**	**Vegetables**	**17,861**
Wheat	28,307	Tomatoes	3,910
Barley	23,839	Pepper	1,533
Oat	4,863	Eggplants	113
Rye	2,582	Beta beets	2,376
Triticale	1,619	*Raphanus*	766
Aegilops	1,513	Carrots	505
Millets	841	Chicory	673
Maize	1,532	*Allium*	1,974
Others	1,338	*Brassica*	2,178
		Lettuce	1,145
Legumes	**27,862**	Spinach	215
Phaseolus	9,013	Celery	254
Field beans	3,038	Quinoa	953
Soybeans	1,491	Others	1,296
Other beans	615		
Pea	5,392	**Medicinal and spice plants**	**8,244**
Chickpea	527	Poppy	1,135
Vetchling	514	Tobacco	590
Vetches	1,845	Others	6,519
Lupines	2,712		
Lentils	473	**Mutants**	**1,684**
Clover	1,970	Tomato mutants	743
Others	272	Soybean mutants	527
		Antirrhinum mutants	414
Cucurbitaceae	**2,668**		
Pumpkins	1,054	**Potatoes**	**6,357**
Melons	728		
Cucumbers	738	**Small-grained oil and forage crops**	**15,157**
Others	148	Oilseed rape and forage kale	2,645
		Grasses	11,157
Larger-grain oil, fibre and dye plants	**5,470**	Red clover and alfalfa	1,344
Flax	2,324		
Sunflower	677		
Dye plants	458		
Fibre plants	191		
Oil plants	548		
Others	1,272	**Total**	**151,737**

1980). A lower number of regeneration cycles increases the cost-efficiency of the genebank and lowers the risk of loss of genetic integrity. Therefore, all accessions stored at -18°C are regularly checked for seed germination after 8–20 years and are considered for regeneration when seed germination has dropped to less than 70% of the initial germination. Regeneration is also considered when the number of actively stored seeds is reduced due to the distribution of seed samples. Depending on the species, most seeds have been regenerated after 20 to 40 years. However, seed storability depends on the genetic background, the environmental conditions during growth and the storage conditions (Nagel *et al*, 2015). In future, advances in sensor technology may allow the individual control of e.g. seed moisture content and temperature in storage to optimize survival periods.

Field genebank

Maintaining clonal plants in the field is the most traditional conservation method. It allows characterization and evaluation on site and immediate distribution of material (Engels and Visser, 2003; Panis *et al*, 2020). At IPK, about 4% of the accessions are preserved vegetatively, because no or little seeds or no true breeding seeds are available. Of these, about 2,000 accessions

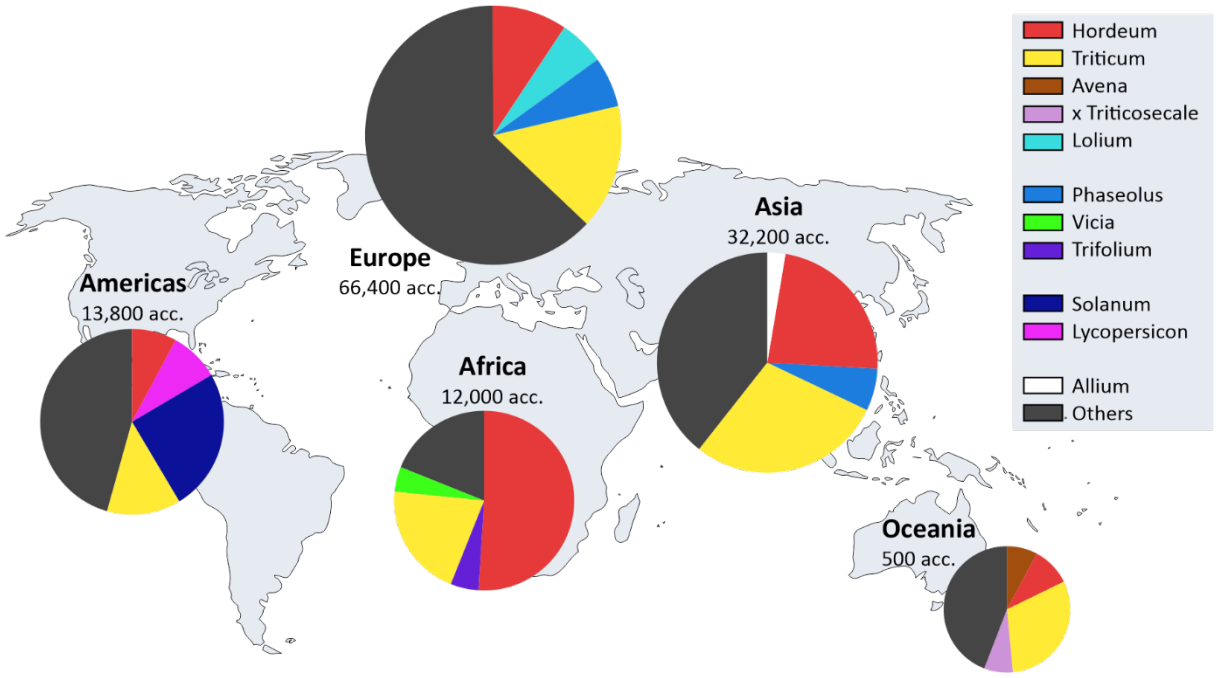

Figure 4. Overview of main genera presented by continent. Approximately 750 genera have been summarized as 'Others'.

of various *Allium* species, changing accessions of potato landraces, as well as mint and other species are grown in a field genebank.

The management of the field genebank varies in terms of growth requirements, propagation cycle and field design depending on the species. For example, the present *Allium* collection, merged from the Taxonomic Reference Collection and the *Allium* Crop Collection (Keller and Kik, 2018), comprises 1,080 accessions of 189 species and has been located at the main site for 5–6 years. Although best field management practices are applied, *Allium* accessions lose vigour over time due to soil exhaustion and need to be transplanted to another site to minimize the risk of infections and diseases. In the case of 392 garlic (*Allium sativum* L.) accessions, for example, cloves and bulbils are harvested in July after full senescence of leaves and stems. The material is then cleaned, prepared for planting and kept at 7°C. In autumn, the cloves are planted in plots of 1.5×1.5m and develop adventitious roots and flat leaves before winter. Some accessions bolt and develop inflorescences with flower buds and bulbils in May. Other materials, i.e. 82 shallot accessions and approximately 200 potato accessions are grown annually. At the IPK site in Groß Lüsewitz, the potato collections (GLKS) comprise 2,800 accessions from Europe and North America and approx. 650 native landraces from the Andes that are maintained clonally, most of them *in vitro*. For field reproduction and characterization, 10 tubers are pre-germinated and planted in the field between March and April. Over the vegetation period, various phenotypic traits are recorded following Huaman *et al* (1977), and tubers are harvested after 4–5 months before or at maturity. On average, about 400 field accessions have been distributed annually to 122 users, mainly private individuals, since 2017. The accessions are available for distribution but require phytosanitary certificates for shipment abroad and systematic evaluation of quarantinable diseases. Recent projects, i.e. 'ECPGR Garli-CCS' and 'ObiVonKnobi' (see Supplemental Table 2) intensively evaluate the morphology, composition and genetic architecture to provide more comprehensive data to breeders and support identification of unique and duplicate genotypes for further decision-making processes.

Major challenges for field collections depend on the year's climate and are the potential exposure of accessions to unfavourable conditions or threats such as pests and diseases. The *Allium* collection, for example, was exposed to an infestation of larval stage click beetles (Elateridae family, known as wireworms) in 2013. As a consequence, 52 *Allium* accessions were lost while 73 could be rescued by replanting (Panis *et al*, 2020). In addition, material that is maintained permanently in the field accumulates viruses, bacteria, fungi and mutations (McKey *et al*, 2010). This increases the necessity for careful evaluation and selection, besides frequent weeding, and seed or propagule harvest to avoid mixing of different accessions. Due to this high workload in field collections, *in vitro* slow-growth storage and cryopreservation were established at the Gatersleben genebank in the 1980s and 1990s, respectively.

In vitro slow-growth storage

In vitro slow-growth storage is an essential tool for the conservation of accessions that are permanently propagated clonally, as they fail to produce seeds due to sub-optimal field/greenhouse conditions. The

storage of *in vitro* cultures allows the preservation of disinfected, pathogen-free material under precisely controlled environmental conditions, which is available for distribution. If plant physiology permits, lower temperatures and light intensities are used to reduce the metabolic activity, which extends the storage period and reduces the workload (Panis *et al*, 2020). At IPK, 2,900 potato, 150 mint, 30 *Dioscorea* and 50 accessions from other species are preserved in *in vitro* slow-growth storage. Here, 967 samples of *in vitro* potato accessions have been distributed to breeders and researchers since 2017.

Similar to the field genebank, the conservation practices vary between species, specifically regarding media composition and growth conditions. In the case of potato, apices from sprouting potato tubers are excised, surface-sterilized and grown on a Murashige and Skoog (1962) medium (MS). Accessions are tested for the common virus strains, such as Potato Virus A (PVA), Potato Leaf Roll Virus (PLRV), Potato Viruses M, S, X, Y (PVM, PVS, PVX, PVY), and quarantine pests, e.g. bacterial ring rot (BRR), among others (Nagel *et al*, 2022). If plants test positive for six common potato viruses, they are subjected to chemo- or thermotherapy (depending on the virus) followed by meristem isolation. The procedure is repeated until the viruses are eliminated. The meristems are then grown on MS media supplemented with 6% sucrose and exposed to a combination of warm (20°C for 1–2 months) and cold phases (10°C for 2–4 months, low light intensity). Under cold conditions, *in vitro* potato plants develop microtubers, which can be kept in a dormant state at 4°C and low light intensity for 12–15 months. When microtubers begin to sprout, either these or the nodal segments are transferred to fresh media and the cycle is initiated again. For other *in vitro* cultures, nodal segments of young plants grown in the field or greenhouse are surface-sterilized and grown on MS media supplemented with 3% sucrose and species-specific phytohormone compositions (Senula and Nagel, 2021). Most mint accessions, but also 18 *Antirrhinum* and 17 *Brassica* accessions, are kept for 12–20 months under two different cold regimes at 2°C and 6°C, and 16h light before they need to be sub-cultured. Warm-adapted mint, *Dioscorea*, but also eight *Artemisia*, three *Salvia*, three *Sechium*, three *Orthosiphon* and two *Plectranthus* accessions are kept at 25/20°C and 16/8h light/dark and need to be sub-cultured after 2–5 months.

Although *in vitro* slow-growth storage has been established for a number of species, some plant species fail to grow and develop (Benson, 2000). This phenomenon, also called *in vitro* recalcitrance, was observed in *Allium* species. In 1995, IPK maintained 645 *Allium* accessions *in vitro*. After some sub-cultures, the plants failed to grow and were contaminated indicating that growth conditions were not optimal and favoured growth of endophytic microorganisms. Unfortunately, efforts to adapt the media and conditions failed, and hence, plants rejuvenated in the greenhouse were used for immediate cryopreservation. For the remaining accessions, field material, i.e. bulbs, cloves and bulbils, was collected and used to introduce *Allium* species directly into cryopreservation. For potato and mint, *in vitro* propagation is an essential step to achieve year-round cryopreservation and long-term preservation of clonal plants with minimal workload and costs.

Cryobank

Cryopreservation is the storage of biological material at ultralow temperatures, usually below -130°C. This is realized in liquid nitrogen (LN, -196°C), in its vapour phase (between -165°C and -190°C) or in electric freezers (-150°C). Under these conditions, molecular movements cease, which increases the possibility of storing biological material indefinitely. However, the cryopreservation of plants was only established in the 1980s, when particular challenges, such as uncontrolled ice crystallization due to the presence of stiff plant cell walls and vacuoles, had to be overcome (Panis *et al*, 2020; Nagel *et al*, 2024). At IPK, international progress in cryopreservation triggered the start of safety duplication of the clonal potato collection stored in Groß Lüsewitz and led to the cryopreservation of the first potato accessions in 1997. Later, as a part of the restructuring of the German Federal Ex Situ Genebank, 578 accessions were transferred from BAZ Braunschweig to Gatersleben, resulting in a collection of 900 potato accessions in 2002 (Keller and Dreiling, 2003). Over the next two decades, a range of methods, i.e. DMSO droplet freezing, PVS2 and PVS3 vitrification, were tested and adapted (Keller *et al*, 2014) and form the basis for about 2,100 potato, 250 *Allium* and 160 *Mentha* accessions cryopreserved by 2024 (Nagel *et al*, 2024).

Nowadays, IPK routine cryopreservation of potato, *Allium* and *Mentha* is based on a vitrification approach using the cryoprotectant PVS3. This method has been applied to a range of clonal species preserved at the IPK genebank and proven the most convenient, successful, rapid and reproducible for these accessions. In brief, 1–2mm shoot tips are excised, precultured on MS media with 3% sucrose and exposed first to a loading solution with 13.7% sucrose and 18.4% glycerol and then to PVS3 solution containing 50% sucrose and 50% glycerol (Senula and Nagel, 2021). The increased sucrose concentrations facilitate osmotic dehydration and stabilize proteins and membranes (Lerbret *et al*, 2011). Glycerol permeates quickly into cells, replaces hydrogen bonds and prevents ice formation by separating water molecules (Towey *et al*, 2012). Shoot tips treated with a combined solution are transferred to vials or aluminium foil strips containing fresh PVS3 droplets and submerged to LN. The rapid temperature drop of ~130 K/s results in vitrification of the cytoplasm which reduces the potential to develop lethal intracellular ice. Based on statistics of Dussert *et al* (2003) and availability of propagules, 300 shoot tips for potato and *Mentha*, and 150 for *Allium* species are cryopreserved, of which 90 and 50,

respectively, are thawed to evaluate the cryopreservation success. If more than 30 shoot tips regrow, they are considered safely cryopreserved. On average, however, potato, *Allium* and *Mentha* regrew at higher percentages of 47%, 38%, 64%, respectively, which is a promising basis to increase the threshold to 35%, as suggested by an international team of cryoexperts (Volk *et al*, 2017). After successful cryopreservation, the number of shoot tips is divided into triplicates; two replicates are stored in separate tanks at IPK and one in tanks at a backup storage facility at the German Collection of Microorganisms and Cell Cultures (DSMZ) in Braunschweig, Germany.

The cryopreserved material is occasionally requested for activation, comparisons and distribution, which provides information about their status of viability. However, activating the material is time-consuming and costly. Therefore, permanent conservation in cryo is only considered at IPK if the accessions are not actively used, such as duplicates or non-requested accessions, or material which does not survive in the field or *in vitro*. For the *Allium* collection, 60 accessions exist only in cryo due to unfavourable field conditions.

Reference collection

The IPK genebank has been operating reference collections of preserved plants and plant parts since 1946 (Anon, 1953). Some reference materials even date back to the early 19^{th} century (e.g. *Allium angulosum*, GAT0011009, from 1809). Today, the reference collections comprise more than 450,000 herbarium voucher specimens, 110,000 reference seed and fruit samples and 57,000 cereal spikes, which serve as important sources to guarantee the identity of the reproduced genebank material. Besides the genebank reference collection, the herbarium contains a representative specimen collection of cultivated plants and their wild relatives which provided the basis for Mansfeld's Encyclopedia of Agricultural and Horticultural Crops (Hanelt, 2001). Moreover, the herbarium stores important types, i.e. the specimens of organisms to which newly described taxonomical units such as species or subspecies refer, and also functions as a repository for physical references of plants used in molecular systematics studies.

To prepare herbarium vouchers, entire plants or plant parts important for determination and differentiation are collected during the vegetation period, pressed, dried and mounted as voucher herbarium specimens. A label including taxonomic and collection information is attached to the voucher, which is then stored in the IPK herbarium. Plant parts that cannot be prepared such as tubers or fruit clusters were preserved dry or wet (in alcohol) (Anon, 1953). However, due to the high workload, the latter activity had not been continued and only the available reference material is refreshed occasionally. To ensure long-term preservation of the reference collections, they are protected by separate quarantine areas where the vouchers are prepared and frozen at -20 °C for one week to kill parasites before they are introduced into the collection. Insects are prevented by mosquito meshing at the windows and annual fumigations with phosphine (PH_3) help to keep museum beetles (*Anthrenus museorum* L.) in particular out of the collections.

The herbarium collection is continuously processed and digitized in high resolution and currently provides about 53,000 digital images of the vouchers that can be accessed online in the joint herbarium management system JACQ (https://www.jacq.org/, herbarium code: GAT) and, hence, via the Global Biodiversity Information Facility (GBIF). Further scans are currently being processed. This reduces shipping of the valuable specimens among herbaria, thus minimizing the danger of losing materials. Moreover, researchers who work on taxonomic revisions of specific plant groups have fast access to digital collections, which very much speeds up taxonomic procedures, as high-resolution scans provide the most important details. The availability of digitized vouchers will support emerging machine learning approaches for species determination, help in understanding the geographic distribution and ecological settings of certain species, and allow easier search for and compilation of datasets of developmental and anatomical features of the taxa.

Documentation

Documentation plays an important role in both conservation and exploitation, and thus, utilization of PGR. The more information is available about a resource, the more precise statements can be made about its value for breeding and research. Furthermore, a genebank collection can only be developed further in a meaningful way if its composition is well documented. This makes it possible, for example, to identify species or geographic regions that are underrepresented in the collection via gap analysis. Moreover, the management of information is essential both for the physical management of the collection and for the fulfilment of legal obligations (Weise *et al*, 2020).

There are three categories of data: 1) pure management data, 2) data of legal significance and 3) data that allows the assessment of PGR value. The first category includes data like germination percentage, age of samples, storage quantities and locations, results of health tests and responsibilities for conservation. This data needs to be stored in a structured way. The second category comprises the documentation of collecting permits, correspondence with other institutions or documentation of receipt. The third category can be further subdivided into different kinds of data. Passport data comprise the basic information on PGR, in particular they facilitate the identification of the material. Stable and unique identifiers, such as Digital Object Identifiers (DOIs), are of great importance in this context (Garrity *et al*, 2009; Alercia *et al*, 2018). In addition, passport data contains, among others, the scientific name, information on origin and acquisition as well as the type of material and

is based on the Multi-Crop Passport Descriptors (MCPD) data standard (Alercia *et al*, 2001, 2015). Other important data that help to assess the potential value of an accession for research and breeding are phenotypic characterizations, including morphological and agronomic traits. At IPK, this information is initially collected during the first cultivation of each accession and checked during each subsequent regeneration.

The first system for the management of the IPK genebank data was established in the 1980s and has been continuously developed thereafter. As part of the fusion of the former Eastern and Western German genebank collections (see above), resources were also made available to develop an integrated information and management system, the Genebank Information System (GBIS) (Oppermann *et al*, 2015). In 2006, GBIS started to operate and has been managing the above-mentioned data. In parallel, GBIS supports the processes for maintaining genebank accessions. For this purpose, it is made up of three components. The GBIS/M management module is primarily used to support the daily work processes in the genebank and enables the management and curation of data on the preserved material. The GBIS/B evaluation module is used for the electronic recording of phenotypic data with mobile devices during the regeneration, and the GBIS/I internet module provides potential users of genebank material with relevant information via a public web interface, thus allowing them to specifically select and order material (Figure 5). GBIS also documents genebank-related processes including acquisition, preservation, regeneration, documentation and material provision under the regulations of the standard material transfer agreement (SMTA) for quality management. Furthermore, it supports the fulfilment of reporting obligations at national and international levels, e.g. with regard to the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA). As a result, all of the genebanks' accessions are also listed in international aggregator systems such as EURISCO, Genesys and FAO-WIEWS.

The active curation of data on PGR is becoming increasingly important (Shaw *et al*, 2023). The genebank's information pool is therefore continuously updated. This includes comparing and supplementing existing data sets with those from external sources, e.g. from information systems of other collections. This significantly increases the quality and quantity of information on genebank accessions. Furthermore, historical data has also been explored and stepwise added. Even unbalanced data, i.e. phenotypic data recorded during reproduction in different years, can provide added value, for example by being used to predict the phenotypic performance of genebank accessions (Philipp *et al*, 2018; Berkner *et al*, 2024).

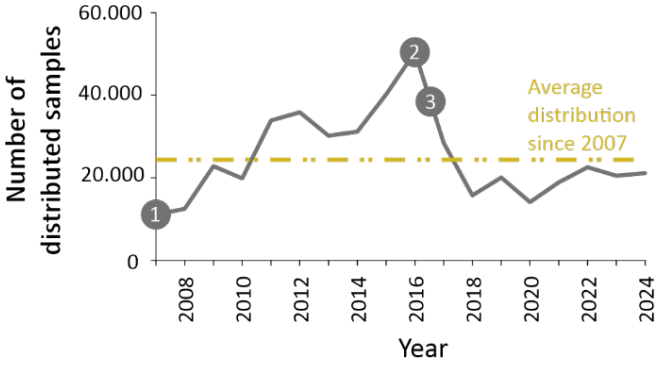

Figure 5. Development of the number of samples distributed. In 2007, the Genebank Information System (1, GBIS) was introduced allowing scientists, breeders and private persons to order accessions free of charge. This led to a continuous increase in the number of samples reaching over 50,000 samples in 2016 (2). Due to the financial burden and workload, a processing fee was introduced in mid-2016 (3), which has limited the annual distributions to a manageable level of 25.000 samples on average (yellow line). Overall, the IPK genebank has distributed more than 1.2 million samples over the last 80 years.

Quality management

The IPK genebank aims to efficiently use the available economic, human and technical resources to ensure the permanent availability of collection material and to offer the users a high-quality service. Therefore, the IPK genebank introduced a quality management (QM) system according to ISO 9001 in 2007. Quality management is a tool for monitoring all activities, tasks and processes required to maintain a desired level of quality in products and/or services. An effective QM system involves clear organizational strategies and goals, efficient and transparent processes, measurable results and continuous process improvements. The establishment of a QM system and certification according to ISO 9001 is a measure to increase the satisfaction of the stakeholders (service quality) and to improve the internal genebank management. Moreover, the documentation of the individual processes is a key issue to perpetuate the long-standing experience of the employees and their knowledge for a sustainable continuation of PGR conservation. Finally, the transparency of the genebank processes ensures that they are aligned with agreed genebank quality standards.

Since 2007, all relevant key processes have been visualized in 51 procedure instructions and described in detail in 72 working instructions. A quality management handbook and an operational genebank manual, available on the ECPGR website (https://www.ecpgr.org/aegis/aquas/genebank-manuals/), describe the QM system. Internal and external quality audits are planned and carried out annually, and a certification company recertifies the genebank every three years. The continuous improvement is pursued through the development and implementation of state-of-the-art knowledge and research conducted at IPK. These collaborative activities guarantee high-quality services and progress in the field of preservation, propagation, conservation, taxonomic classification as well as information technologies.

Development of a bio-digital resource centre

Progress in life sciences is increasingly centred around data availability, quality and management. In line with this, the genebank is undergoing a transformation process to become a bio-digital resource centre (Mascher *et al*, 2019). This means describing PGR on an ever-better scale in order to optimize their use for research and breeding. The aims are to successively raise existing data to a higher level through curation and complementation, and to obtain additional data. The latter pursues two goals: on the one hand, additional data from domains that are already being used will be tapped. This includes, among other things, further phenotypic data integrated from additional sources, e.g. from high-throughput phenotyping. On the other hand, data from domains that have not yet been used in the past will be harnessed, in particular genetic characterizations. Genomic data can help to decipher genetic diversity and provide insights into geographical origin, row type, growth habit or domestication status, for example. It can also help with the identification of duplicates and enables applications such as genome-wide association studies. Entire sub-collections are increasingly being genotyped, for example barley (Milner *et al*, 2019) and wheat (Schulthess *et al*, 2022), and their data are made available via crop portals.

The above-mentioned processing of historical data from the last 80 years, particularly from seed regenerations, also plays an important role for the bio-digital resource centre as it helps to assess the value of PGR accessions for breeding and research purposes. This data is extensively curated and published in accordance with the Findability-Accessibility-Interoperability-Reusability principles (FAIR; (Wilkinson *et al*, 2016)). In addition, this data is also analyzed together with genotyping data.

A cooperation with the DSMZ in Braunschweig has been established with regard to a safety backup for cryomaterial (see above). To store valuable resources together with their most important data, a pilot project together with the Norwegian company GenEver was initiated and special cryoboxes developed. The boxes combine cryovials with data on a roll of film (piql film). This technology is extremely robust and promises to last for centuries. Until the end of 2024, all cryo backup samples stored at the DSMZ will be supplemented with data on film strips.

In recent years, a great deal of energy has been invested in establishing efficient data management at IPK, and previously isolated information systems have been and are being successively interlinked. In addition, IPK is also involved in the establishment and further development of data standards such as 'Minimum Information About a Plant Phenotyping Experiment' (MIAPPE; Krajewski *et al* (2015); Papoutsoglou *et al* (2020)) and is embedded in national and international networks for PGR. For example, the European Search Catalogue for Plant Genetic Resources (EURISCO) has been operated and further developed by an IPK genebank working group on behalf of the European Cooperative Programme for Plant Genetic Resources (ECPGR) since 2014 (Weise *et al*, 2017; Kotni *et al*, 2023).

Challenges and future plans

As in any genebank, there are a number of challenges associated with the various activities; maintenance and regeneration in particular are labour-intensive and costly. In order to utilize the available resources as efficiently as possible, one of the options currently being discussed is to rely on a higher degree of automation and digitization. Furthermore, cryopreservation of heterozygous, short-lived and hybrid seeds might also be a backup solution for material which cannot be maintained adequately by conventional long-term storage.

The identification of duplicates also plays an important role in the more efficient use of resources. In large collections comprising hundreds or even thousands of accessions of a species (such as wheat and barley in the German genebank), duplicates within the collection are unavoidable. In addition, there is a large percentage of duplicates between genebanks (van Hintum and Visser, 1995). Unfortunately, the identification of duplicates is not a trivial task; reliable statements can only be made by jointly analyzing passport data, phenotypic data and genotyping data in combination with comparative cultivations. In addition, the definition of threshold values is useful here. Such approaches have been tested as examples, but have not yet been carried out on a larger scale. However, duplicates, both within and between collections, open up possibilities for normalizing data, especially historical phenotypic data. This is an approach that is currently being pursued in the AGENT project (https://www.agent-project.eu/).

Despite progress, at least in the large sub-collections (see e.g. González *et al* (2018); Philipp *et al* (2018)), there is still a great need for the digitization and curation of historical data. However, consistent recording, storage and curation of data also require continuous maintenance and further development of the Genebank Information System. This includes the regular porting of both data and software components. To facilitate the recording of phenotypic data, a new client for mobile devices was recently finalized. It is based on the PhenoApp (Röckel *et al*, 2022) and has been specially extended to meet the needs of the genebank. A particular challenge is the integration of phenotypic data that was not collected as part of the regeneration of material by the genebank staff themselves, but in the context of research projects. There are still no widely accepted standards regarding the collection of phenotypic data using standardized traits and methods (Krajewski *et al*, 2015). However, approaches such as MIAPPE facilitate description and reproducibility, at least for future data.

Not all biodiversity is secured in the world's genebanks. Especially against the backdrop of the

climate crisis, this represents a race against time. It is therefore necessary to specifically analyze existing sub-collections and to identify priority species and regions for collecting. Such an analysis has already been carried out using oilseed rape as an example (Weise *et al*, 2023). This allows the targeted acquisition of material from other collections and, if possible, the organization of collecting trips.

The IPK genebank is involved in various infrastructure projects and research programmes, and has genotyped entire sub-collections. However, the participation in the exploitation and utilization of (neglected) crops and crop wild relatives (e.g. Legume Generation (https://www.legumegeneration.eu/) and COUSIN (https://cousinproject.eu/) projects) as well as the participation in the establishment of a European research infrastructure for PGR (PRO-GRACE project, https://www.grace-ri.eu/) will continue to conserve and utilize our European PGR as efficiently as possible.

Supplemental data

Supplemental Table 1: Collecting trips by German-speaking researchers
Supplemental Table 2: Recent third party-funded projects under participation of the IPK genebank

Author contributions

SW and MN drafted the manuscript. All authors revised and edited the manuscript, and approved the final version.

Conflict of interest statement

The authors declare that they have no competing interests.

Acknowledgements

We would like to thank the past and present genebank employees for their passionate work and commitment in establishing the collections and best-practice procedures to maintain them. This work was supported by the European Union's Horizon projects AGENT (Activated GEnebank NeTwork, Grant agreement No. 862613).

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