# GLOBAL STRATEGY FOR THE CONSERVATION OF POTATO

With support from

CROP TRUST

The International Treaty
ON PLANT GENETIC RESOURCES
FOR FOOD AND AGRICULTURE

Federal Ministry
of Food
and Agriculture

## DISCLAIMER

This document aims to provide a framework for the efficient and effective conservation of potato genetic resources. The overall objective is to outline shared responsibilities and needs for the long-term conservation of these genetic resources and to facilitate their use for food security and sustainable agriculture. The Crop Trust considers this document to be an important framework for guiding the allocation of its resources. However, the Crop Trust does not take responsibility for the relevance, accuracy or completeness of the information in this document and does not commit to funding any of the priorities identified. This strategy document (12 November 2022) is expected to continue to evolve and be updated as and when circumstances change, or new information becomes available.


## ACKNOWLEDGMENTS

This 2022 edition of the 'Global Strategy for the Conservation of Potato' builds on the first strategy coordinated by van Soest (2006). It focuses on *ex situ* conservation of species of *Solanum* section *Petota* and includes priority actions to improve *ex situ* and *in situ* conservation and use of potato genetic resources. In addition, an overview of recent taxonomic studies, progress in breeding and sequencing and *in situ* conservation projects is provided, and new tools for *ex situ* conservation management, germplasm characterization & evaluation, including data management, are presented. The global strategy is the product of a collaborative effort, which could not have been accomplished without both individual and group contributions.

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Annex 2 of this document provides a summary of a recent report: "The plants that feed the world: baseline information to underpin strategies for their conservation and use". That study was produced as a collaboration led by the Secretariat of the Plant Treaty, and involving the Alliance of Bioversity, the International Center for Tropical Agriculture (CIAT and the Crop Trust, funded by the Norwegian Agency for Development Cooperation (NORAD, Government of Norway).



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## COVER

Created © Uli Westphal 2022. Uli Westphal is a visual artist who documents our declining crop diversity and the things that replace it. The 'Cultivar Series' portrays the existing diversity within individual crop species, one species at a time. www.uliwestphal.com/the-cultivar-series

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# EXECUTIVE SUMMARY

**Background.** Cultivated potato, *Solanum tuberosum* ssp. *tuberosum,* is the third most consumed crop globally and important not only for food but also for for the animal feed, pharmaceutical, textile and paper industries. To gain an overview on the current state of the conservation and use of potato genetic resources, the Global Crop Diversity Trust (Crop Trust), commissioned an update of *the 'Global conservation strategy for potato genetic resources'*. This updated strategy aims to support the efficiency and effectiveness of potato diversity conservation at national, regional and international levels, and to identify priorities for strengthening the conservation and use of potato genetic resources.

To provide an overview of the current status of the potato collections worldwide, a survey was sent out in 2020 and 2021, and responses were analyzed from 32 genebanks located in:

- Asia: India (**IND665**), China (**CHN116, CHN122**), Japan (**JPN183**)
- Europe: Belgium (**BEL023**), Bulgaria (**BGR001**), Czech Republic (**CZE027**), Estonia (**EST019**), France (**FRA010**), Germany (**DEU159**), Ireland (**IRL012, IRL036**), Netherlands (**NLD037**), Latvia (**LVA006**), Romania (**ROM007**), Russia (**RUS001**), Slovenia (**SVN019**), Spain (**ESP016**), Sweden (**SWE054**), United Kingdom (**GBR165, GBR251**)
- International Center: CIP (**PER001**)
- Latin America: Argentina (**ARG1347**), Brazil (**BRA020**), Chile (**CHL071**), Colombia (**COL017**), Cuba (**CUB005**), Ecuador (**ECU023**), Guatemala (**GTM001**), Peru (**PER860**),
- North America: Canada (**CAN064**), USA (**USA004**).

Data from WIEWS (2021), Genesys, EURISCO and current peer-reviewed literature was integrated and discussed at a 'Potato Strategy Meeting' held virtually between 10–12 November 2021. As a result, the strategy provides an up-to-date overview on the origin, domestication, taxonomy, gap analysis and breeding of potato and its economic importance. It summarizes recent *in situ* conservation projects, including threats and challenges for the preservation of potato landraces and wild species in the region of origin. Based on the survey, an overview is provided of *ex situ* collections, including storage, maintenance, regeneration, distribution, data management practices and information about the use of the material for research and breeding. A comprehensive analysis of the survey results, complemented by the major constraints and priorities identified by respondents and meeting participants, resulted in ten action points being identified as strategic priorities.

**Domestication and taxonomy.** Wild potatoes are native to the Americas, with highest number of species found in Peru, Mexico, Argentina, Bolivia, Ecuador and Colombia (Spooner et al., 2014). Cultivated potatoes were domesticated in the Andes about 8,000 to 10,000 years ago in a series of several domestication events (Ovchinnikova et al., 2011), and from there were spread around the world, most likely from 1562 onwards (Ugent, 1968; Hawkes and Francisco-Ortega, 1993). Nowadays, 370 million tonnes of potatoes are produced on 16.5 million ha globally (FAOSTAT, 2021b). Wild and cultivated potato belong to the genus *Solanum* L., subgenus *Potatoe* (G. Don) D'Arcy, section *Petota* Dumort. This is characterized by introgressions, interspecific hybridization, auto- and allopolyploidy and numerous evolutionary events, leading to many taxa. Hawkes (1990) divided this section into 21 taxonomic series, including 19 series for tuber-bearing species (subsection *Potatoe* G. Don) and two series of non-tuberous species (subsection *Estolonifera* Hawkes). Within the subsection *Potatoe* G. Don, Hawkes (1990) described 7 cultivated potato species and 228 wild potato species. The more recent taxonomic revision by Spooner et al. (2014) combines molecular studies and morphological data and groups wild potatoes into 107 species and the cultivated potatoes into four species: (1) *Solanum tuberosum*, with two cultivar groups; the 'Andigenum group' with diploids, triploids and tetraploid species, and the 'Chilotanum group' (tetraploid); (2) *Solanum ajanhuiri* Juz. & Bukasov (diploid); (3) *Solanum juzepczukii* Bukasov (triploid); and (4) *Solanum curtilobum* Juz. & Bukasov (pentaploid). Although most potato collections follow the taxonomic system defined by Hawkes (1990), some genebanks have already switched to Spooner et al. (2014) which hampers gap analysis and statistics. The use of different taxonomic treatments may limit stakeholders' ability to find and use material.

***In situ* conservation.** More than 3,000 different traditional landraces and 107 wild species according to the classification of Spooner et al. (2014) are native to the Americas and urgently require protection. Traditional landraces are threatened due to the migration of farmers, replacement by other crops and improved varieties, pests and diseases, and low accessibility of virus-free material. Among wild potatoes, 26 species are on the IUCN Red List and are threatened by urbanization, fire, and disturbance by humans and

livestock (Cadima et al., 2014). Therefore, projects in Peru, Bolivia, Ecuador, Argentina, Chile and Brazil have identified conservation sites and strategies to maintain potato genetic diversity in combination with knowledge, culture and traditions. One prominent concept is the support of "guardians" who cultivate and conserve native potato varieties and pass on traditional knowledge to the next generations (Naranjo, 2019). However, the role of *in situ* conservation is still underestimated in the countries of origin and inventories, biodiversity monitoring, staff training and protected sides are required to conserve potato diversity as well as biodiversity generally in their natural habitats.

***Ex situ* collections.** Worldwide, a collection of 82,293 potato accessions is maintained in 89 institutions and four international/regional centers located in 59 countries. Only five institutions (DEU159, FRA010, IND665, RUS001, USA004), together with the International Potato Center (PER001) conserve more than 50% of all potato accessions globally. Over the last 15 years, potato genebanks have increased the number of accessions by an average of + 42%, and now maintain collections composed of 20% wild species, 23% landraces, 25% improved varieties and 27% breeding lines. However, compared to the last survey (van Soest, 2006), the number of breeding lines has increased by +107%, while the number of accessions of wild species has decreased by 5.8%.

**The largest wild potato species** (applying Spooner et al. (2014)) collections are maintained by CIP (PER001; 95 species), USA (USA004; 79 species), Russia (RUS001; 70 species), Germany (DEU159; 66 species) and the Netherlands (NLD037; 60 species). The species with the largest number of accessions are *Solanum brevicaule* Bitter (1,896 accessions), *Solanum acaule* Bitter (1,491 accessions) and *Solanum stoloniferum* Schltdl. (1,255 accessions). Most accessions are preserved as orthodox seeds, but only a few of the genebanks are able to apply the ABS (active-base-security) sample system recommended by the Genebank Standards (FAO, 2014). Most seeds are sealed in aluminum bags and stored either at 4°C or at -10 to -20°C. Only seven genebanks have backed up their collection in the own country or at the Svalbard Global Seed Vault. Due to the urgent need to regenerate 30% of the Latin American wild species collections and 8% of the total collections, improvements in regeneration, duplication and conservation approaches are needed.

**The collection of landraces** has increased by +7% compared to the last survey (van Soest, 2006), and includes 18,491 accessions, most of which belong to the *Solanum tuberosum* 'Andigenum group'. However, the number of landraces has decreased in the Netherlands, UK, Argentina and Russia, which may indicate some challenges in their maintenance. In European, North American, Asian countries and at PER001, most, but not all, genebanks apply standardized protocols and use low-temperature tuber and *in vitro* storage facilities. PER001, DEU159 and JPN183 have major parts of their material cryopreserved. In Latin America, most landraces are maintained in fields and/or *in vitro* at 17 to 24°C. About 1,600 accessions, 53% of the Latin American landrace collection, require urgent regeneration and are affected by plant health issues, staff shortage and outdated infrastructure. Here, substantial support, in particular with staff training, cold storage facilities, *in vitro* back up systems and cryopreservation is needed to safely conserve the traditional landraces in the country of origin.

**Collections of improved varieties and breeding lines** have increased by 100% and 107% compared to the last survey and comprise 20,735 and 22,173 accessions, respectively. Most of these are working or breeding collections situated in Europe and Asia and focus on breeding and maintenance of national varieties. Most institutions keep the material in field collections, in *in vitro* facilities at 17 to 24°C and/or at 2 to 10°C. About 6% of the improved varieties and 3% of the breeding lines require urgent regeneration. In Latin America, however, the situation is comparable to that of landraces, and institutions require funding for training staff, as well as cold and *in vitro* storage facilities. In addition, support from the Global Plant Cryopreserva-

**Genebanks conserving 50% of potato germplasm.** Total number of accessions and percentage of wild species (W), landraces (L), improved varieties (V) and breeding lines (B) is provided for each collection.

| Institute Code | Country | Institute name and place | W-L-V-B | Number of accessions |
|---|---|---|---|---|
| FRA010 | France | INRAE, the Institute for Genetics, Environment and Plant Protection, Ploudaniel | 5-2-10-83% | 12,120 |
| RUS001 | Russia | VIR, N.I. Vavilov All-Russian Institute of Plant Genetic Resources, St. Petersburg | 24-40-29-7% | 8,150 |
| PER001 | Peru | CIP, International Potato Center, Lima | 35-60-5-0% | 7,467 |
| DEU159 | Germany | IPK, Leibniz Insitute of Plant Genetics and Crop Plant Research, Groß Lüsewitz | 22-37-31-10% | 6,247 |
| USA004 | USA | USDA, US Potato Genebank, Wisconsin | 69-20-5-6% | 5,900 |
| IND665 | India | ICAR, Central Potato Research Institute, Shimla | 8-3-69-2% | 4,257 |

tion Initiative is urgently needed for all clonally propagated potato accessions to enable secure long-term conservation.

**Data management.** Data related to registration, storage and regeneration methodologies, phytosanitary certificates, monitoring, characterization, evaluation and distribution generated in the management of potato collections need to be securely stored. Most genebanks use electronic information systems, such as GRIN-Global (e.g. BOL317, EST019, PER001, PRT102, SWE054, USA004), SIRGE (PER860), ALELO (BRA020), Germinate (GBR251), GBIS (DEU159), GENIS (NLD037) and/or Excel but paper records are still common. Overall, 65% of passport data, 35% of characterization data and 33% of evaluation data are available in electronic form. Twenty out of 32 collections provide this information at least partly via the internet or via international aggregator systems such as EURISCO or Genesys. To improve the usability of the collections, accessions should be linked to a Digital Object Identifiers (DOI) issued by FAO and trained staff should produce Findable-Accessible-Interoperable-Reusable (FAIR) phenotypic data and store all information on genebank information systems.

**Accessibility of the collections for breeding and conservation.** Globally, the access to potato genetic resources is limited and 37% of wild species, 43% of landraces, 64% of improved varieties and 82% of the breeding lines are not available for distribution. Among the reasons are insufficient number of seeds/tubers/*in vitro* plants, inadequate plant health status, packaging and shipping processes and difficulties in obtaining phytosanitary certificates. The terms and conditions of the International Treaty on Plant Genetic Resources for Food and Agriculture apply to most (21 genebanks) but not to all potato collections, i.e. ARG1347, CHL028, COL017, GTM001. Therefore, most material is provided with the standard material transfer agreement (SMTA) by larger collections such as USA004, PER001, DEU159 and is available at national (46%) and international level (37%). Nevertheless, in the last three years, only 2% was requested at the national and 16% at the international level by domestic users, academic researchers, farmers and breeders. The limited availability of data and material may restrict users' ability to search and request suitable material.

**Characterization and evaluation**. Sequenced, well-characterized and evaluated potato germplasm is a prerequisite for future breeding progress because potato productivity can only be maintained and increased by using new breeding tools such as molecular and hybrid breeding in combination with broadening genetic diversity. However, the complex genetic nature of the heterozygous tetraploid potato (AAAA, 2n = 4x = 48, estimated haploid genome size 844 Mb), the number of quality traits required, and the numerous pests and diseases which affect the crops have always been a challenge for potato breeding programs. So far, 27 respondents of the survey have partly screened their collections for late blight, the main biotic threat of potato production. About 50% of the collections are (partially) evaluated for nematodes and the potato viruses Y (PVY) and X (PVX). Screening for other insects, pests and diseases (i.e. common scab, potato wart, *Fusarium* dry rot, Colorado potato beetle) and abiotic stresses (i.e. drought, heat, cold) has been conducted only by a few genebanks. More characterization efforts are required in combination with the sequencing of all collections and accessibility of data on adequate platforms. In general, sequencing is of fundamental importance for taxonomy, conservation, genebank management and breeding and must be an overall goal for future genebank processes.

Overall, based on the survey, literature review and discussions with stakeholders, a number of key challenges for potato conservation and use were identified and recommendations were made to improve the status and use of potato collections. The implementation of the recommendations following strategic priorities would substantially support the conservation of potato germplasm and its use in breeding and *in situ* conservation programs.

Recommended strategic priorities:

- Comprehensive genotyping (sequencing) of *ex situ* and/or *in situ* collections
- Harmonization of potato taxonomy
- Documentation and monitoring of *in situ* populations and traditional landraces maintained on farm in American countries
- Capacity building for *in situ* conservation and improved strategic concepts for on farm conservation
- Collecting missions and linkage between *in situ*/on farm and *ex situ* conservation
- Capacity building to maintain high quality *ex situ* collections, in particular in Latin American countries
- Cryopreservation to ensure long-term survival of potato genetic resources
- Further digitalization, better linkage and visibility of publicly available data for *ex situ* and *in situ* conservation management
- Accessibility of collections for breeding and use
- Networking and training

Potatoes being sold at market in Huancayo, Peru.
Photo: Michael Major/Crop Trust

# 1 INTRODUCTION AND STRATEGY BACKGROUND

Cultivated potato, commonly *Solanum tuberosum* L.*,* is the third most important crop for human consumption and is grown on 16.5 million ha globally (FAOSTAT, 2021b). In the last 60 years, production volume has increased by 37% and further increases are expected, particularly in Asian and African countries, due to a higher harvest index and better water use efficiency compared to cereals (Monneveux et al., 2013; Haverkort and Struik, 2015). Due to the predominantly clonal propagation of cultivated potatoes, its production can be severely affected by pest and diseases. The European and Mediterranean Plant Protection Organization (EPPO) has identified 19 quarantine pests (EPPO, 2021) each of which can cause up to 100% loss in potato production. In addition, climate change scenarios predict changes in temperature and precipation patterns in some major potato production areas resulting in increased incidences of pests, diseases and abiotic stresses by the end of the century (Raymundo et al., 2018). Problematically, the introduction of stress resistances in new varieties remains a challenge and no major yield improvements have been achieved over the last 100 years (Douches et al., 1996). The heterozygosity of the tetraploid cultivated potato (AAAA, 2n = 4x = 48, haploid genome size 844 Mb), self-incompatibilites common in wild species, sterility barriers and inbreeding depression have been major hurdles for potato breeding. Nevertheless, new tools such as marker-assisted selection, molecular prediction, hybrid breeding, inbreeding and genomic engineering create new opportunities to adapt potato varieties to more stressful conditions and to achieve significant yield gains. Fundamental to all these approaches is the use of potato genetic resources. Therefore, these resources must be securely conserved *in situ* and *ex situ* and be made available and accessible to breeders and researchers.

Wild potato species of the *Solanum* section *Petota* are native to the Americas, with the highest diversity of species in Mexico and Peru (Hijmans et al., 2007). At high altitudes, under short-day conditions and moderate temperatures, Andean farmers used the great diversity of wild potato species for domestication and contributed substantially to the diversity of potato landraces that are still grown today. More than 3,000 traditional landraces are estimated to be cultivated in the Andes and the Chiloé islands (Spooner et al., 2014). Fortunately, in the last 20 years, awareness of this cultural heritage has increased and indigenous farmers and agrobiodiversity guardians support the cultivation, conservation and marketing of traditional potato landraces. However, due to economic and political challenges of these countries, *in situ* conservation is not substantially supported and more efforts are required to ensure the long-term maintenance of potato landraces, their wild relatives and associated biodiversity and habitats, i.e. establishment of protected areas and economic support to farmers.

As a complementary approach, more than 80,000 potato accessions have been conserved in about 89 *ex situ* genebanks (WIEWS, 2021). To conserve the great diversity of potato resources, a combination of seed storage, field genebanks, *in vitro* storage and cryopreservation is used. Although genebank operations have been optimized in recent decades (FAO, 2014), the management of a potato collection is particularly challenging because seed production from wild species can be problematic due to self-incompatibilities, and cultivated potato accessions require clonal propagation in the field or *in vitro,* which is time consuming and vulnerable to environmental stresses. In addition, for optimal use of potato diversity, comprehensive information on accessions needs to be publicly available, which requires a substantial investment in staff training and infrastructure.

To support the efficient and effective conservation and use of potato diversity, the Crop Trust initiated and facilitated the assessment of the conservation status of potato and the identification of strategic priorities. A survey was sent out in 2020 and 2021 and the current literature was carefully reviewed and summarized. Based on the response of 32 genebanks located in Asia, Europe, Latin America and North America, data obtained from (WIEWS, 2021), FAOStat, peer-reviewed publications, personal communications and a virtual meeting (10–12 November 2021) attended by key stakeholders, the present '*Global Strategy for the Conservation of Potato*' provides a comprehensive overview covering the current status and needs of potato collections. To ensure long-term conservation of potato genetic resources and their use for breeding, 10 strategic action priorities have been identified. Their implementation would significantly benefit the active conservation and use potato genetic resources and contribute to global food security.

Farmer with potatoes for planting, Colmar, Peru.
Photo: Michael Major/Crop Trust

# 2 ORIGIN, DOMESTICATION AND CENTERS OF DIVERSITY

Potato was domesticated in the South American Andes about 8,000 to 10,000 years ago (Ovchinnikova et al., 2011) and distributed around globe during post-Columbian times. According to Hawkes (1990), *Solanum tuberosum* L. is used for the tetraploid indigenous cultivated populations, also termed landraces, grown in lowland Chile and the high Andes. The last taxonomic classification (Spooner et al., 2007; Ovchinnikova et al., 2011) includes di-, tri- and tetraploid landraces grown in the high Andes ('Andigenum group') as well as the Chilean tetraploid landraces ('Chilotanum group'). Nowadays, *S. tuberosum* is the name applied to advanced potato varieties that have undergone intensive plant breeding during the last 200 years.

## 2.1 Definition of wild species, landraces, improved varieties

**Wild species.** Di-, tri-, tetra-, penta-, hexaploid wild species from the *Solanum* section *Petota,* native to the Americas, are considered. These comprise 228 species according to the taxonomy of Hawkes (1990) and 107 species following the classification system proposed by Spooner et al. (2014). In nature, wild potatoes reproduce by both sexual and clonal propagation. In genebanks, due to various crossing barriers, diploids and most polyploids are usually preserved as seeds reproduced in heterozygous populations. However, some collections, i.e. triploid and pentaploid wild potato species, require the conservation of clonal propagules.

**Landrace.** The term 'landrace' was first mentioned at the International Congress of Agriculture and Forestry in Vienna in 1890 (Zeven, 1998). It is defined as a cultivated, heterogeneous variety selected in a specific ecogeographical area and well adapted to edaphic and climatic conditions and to traditional management and use there. However, due to continuous evolution and further natural and artificial selection, the definition of 'landraces' has been reconsidered several times since then. Casañas et al. (2017) suggest that the term 'landrace' should be used for cultivated varieties that have evolved through conventional but also modern breeding technologies in a traditional or modern agricultural environment within a specific ecogeographical area. With regard to potato germplasm, we consider as landraces the cultivated varieties evolved in South America, namely the landraces of the 'Andigenum group', 'Chilotanum

group' and those belonging to the highland bitter potato species. Furthermore, non-commercial heterogenous varieties adapted to farming systems which may have been introgressed from genetically improved varieties (Figure 2.1.1) or other landraces in a particular ecogeographical area in Africa, America, Asian, Europe and Oceania are also considered as landraces. In addition, 'heirloom varieties' that have undergone conservative selection and may have remained free from introgression are also considered as landraces. In order to maintain the specific genotype, this germplasm is often maintained as clonal plants, but can also be preserved as seed.

**Improved varieties** including modern and commercial varieties, are generally very homogenous and widely available without reference to specific ecogeographical areas, and are managed by breeding companies and cooperatives (Casañas et al., 2017). Regarding potato germplasm, all modern varieties that are very homogenous and have been distributed widely by commercial companies are considered as improved varieties maintained as clonal plants.

**Breeding lines.** Potato breeding lines can be understood as more or less homogenous, di- or polyploid potato plants, which are the result of crossing activities between different varieties, landraces, and introgression of wild species by using modern breeding technologies. These are maintained as clonal plants, usually highly selected and only available for a short time.

## 2.2 Domestication process

***Solanum tuberosum* 'Andigenum group'**. The domestication of cultivated potato has been considered as a series of events (Figure 2.2.1) which began around Lake Titicaca at 3,000 to 4,000 m altitude with high light intensity and temperatures between 10 and 20°C (Grun, 1990). Andean landraces are considered to be descended from members of the *Solanum brevicaule*

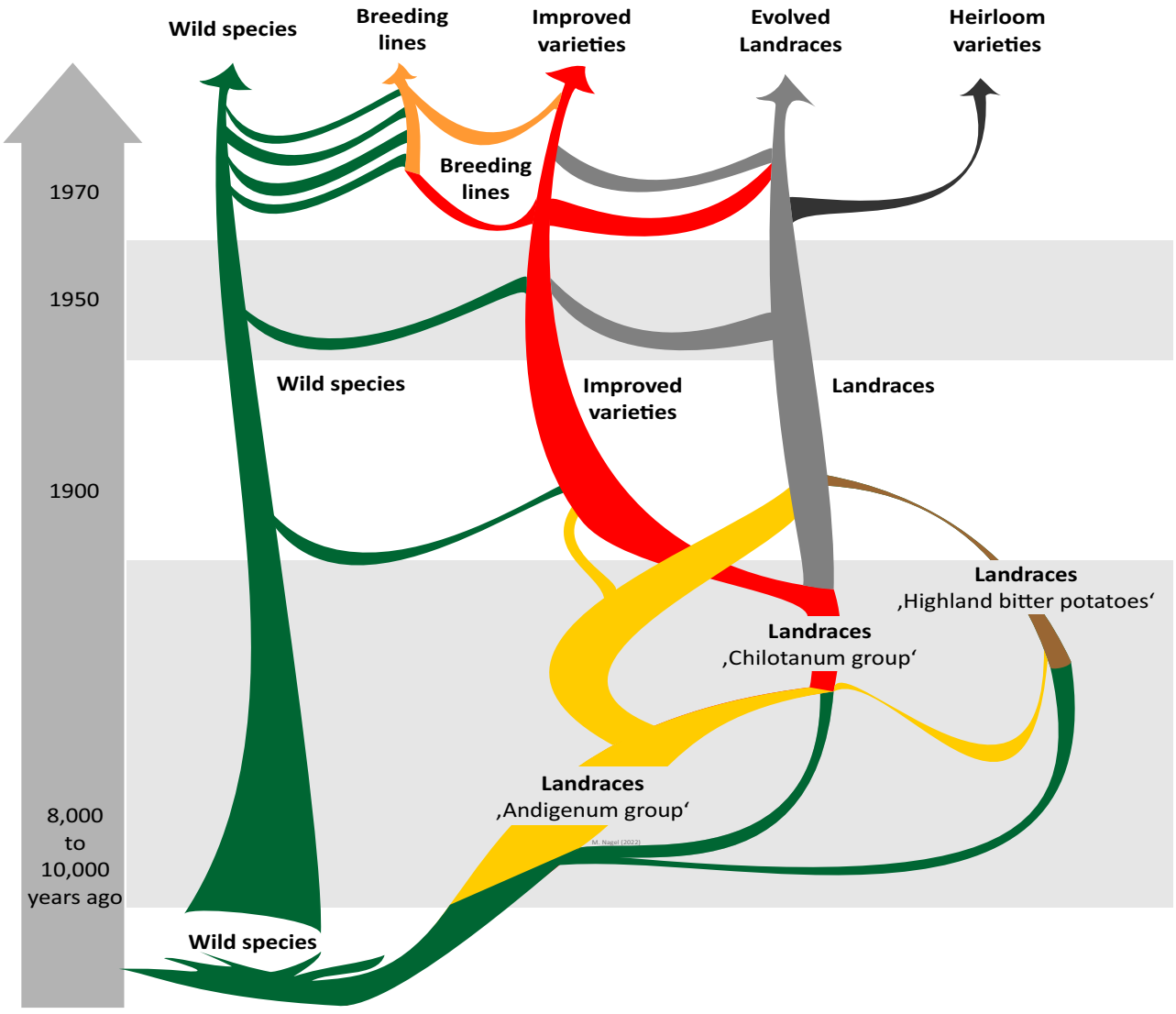



Figure 2.1.1. Historic relationship between wild potato species, landraces, improved varieties, breeding lines and heirloom varieties. Color code is based on Figure 2.2.1 and refers to the most prominent haplotype frequency present in the different landraces. Figure adapted for potato is based on Casañas et al. (2017).

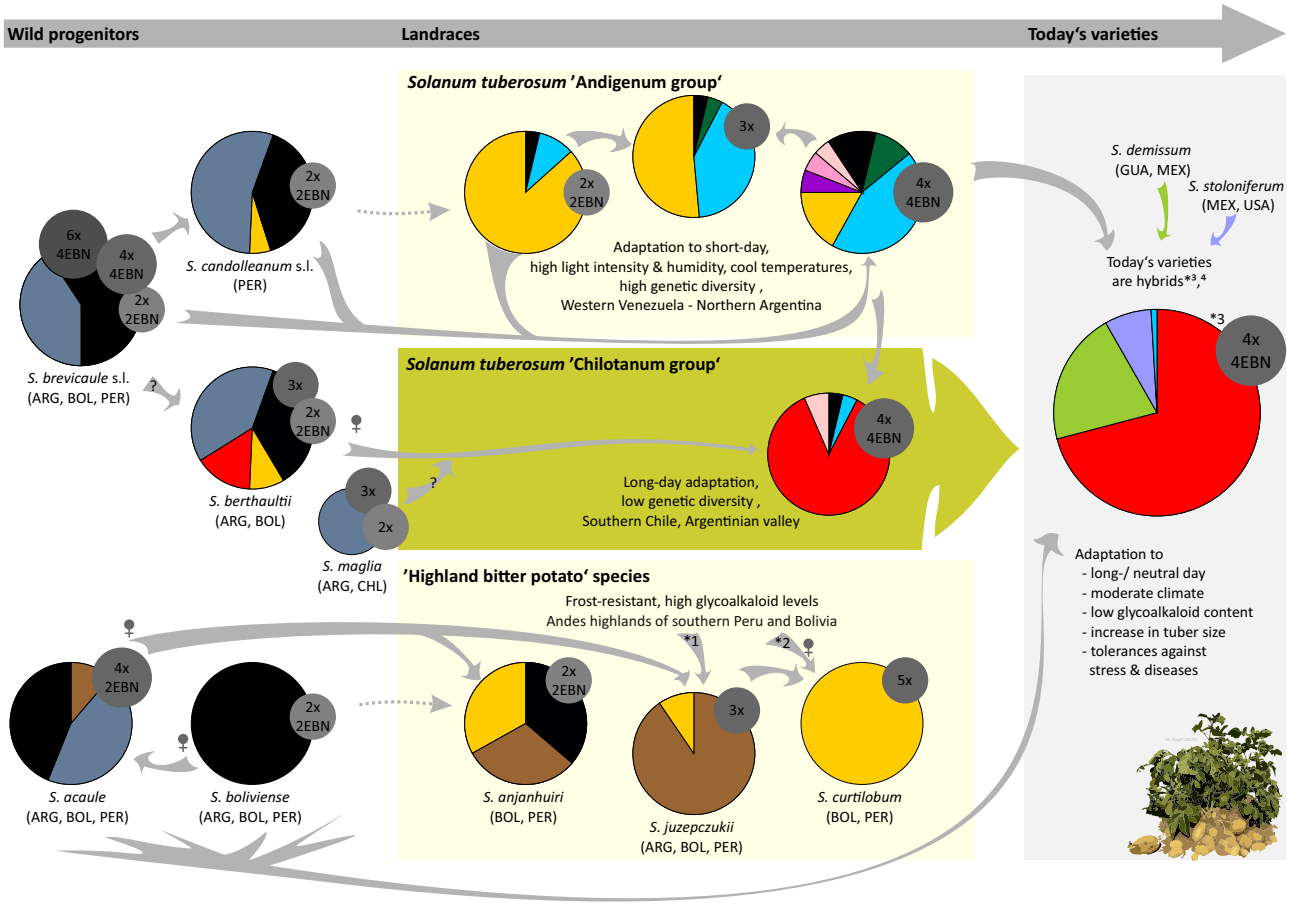



**Figure 2.2.1.** Origin of modern potatoes including potential hybridization and domestication events. Solid arrows show putative hybridization events, broken lines indicate natural variation and anthropogenic selection. Figure and data are adapted from Gavrilenko et al. (2013) and Spooner et al. (2014). *1 Hybridization with diploid members and a *2 tetraploid members of the 'Andigenum group'. Colors represent different plastid SSR haplotypes: **Black**, unique haplotypes; **Grey**, Rare haplotypes VII, IX to XXIII found in various combinations in the wild species-progenitors (Gavrilenko et al., 2013); **Yellow**, plastid SSR haplotype I; **Red**, plastid SSR haplotype III of the *Solanum berthaultii* (=S. tarijense); Blue, plastid SSR haplotype II; **Brown**, plastid SSR haplotype IV; **Pink**, plastid SSR haplotype V; **Purple**, plastid SSR haplotype VIII; **Light Purple**, haplotype W/gamma introduced from *Solanum stoloniferum* Schltdl. according to Hosaka and Sanetomo (2012) and Sanetomo and Gebhardt (2015) (*3); **Green**, plastid SSR haplotype VI; **Light green**, haplotype D introduced from *Solanum demissum* Lindl. according to Hosaka and Sanetomo (2012) and Sanetomo and Gebhardt (2015). ***Solanum candolleanum* Berthault s.l.**, northern members of the *S. brevicaule* complex; ***S. brevicaule* s.l.**, southern members of the *S. brevicaule* complex. *s.l., sensu lato*; *4 Gavrilenko et al. (2019b).

Bitter complex, specifically from those with the plastid SSR haplotype I [yellow, (=P cytoplasm type according to Hosaka and Sanetomo (2012), Figure 2.2.1], that is common in diploids of the 'Andigenum group' and endemic to central Peru, Bolivia, and northern Argentina (Ugent, 1970; Spooner et al., 2005; Hosaka and Sanetomo, 2012; Gavrilenko et al., 2013). Members of the *S. brevicaule* complex are diploid, tetraploid or hexaploid (Ochoa, 1990; Spooner et al., 2014) and according to Hawkes (1990) have been described by 19 taxonomic names. Based on the morphological and genetic similarity, Spooner et al. (2014) and Spooner et al. (2016) lumped 18 names into in *S. brevicaule* (Table 3.2.1), which increased to 35 synonyms in the monographic treatment of wild potatoes of the Southern America (Spooner et al., 2016; Spooner et al., 2019). Although genetic marker analysis did not clearly distinguish groups, two geographical subsets, the Bolivian/Argentinian populations and the Peruvian populations, were recognized as *S. brevicaule s.l.* (southern members of the *S. brevicaule* complex) and *Solanum candolleanum* Berthault *s.l.* (northern members of the *S. brevicaule* complex), respectively. In the latter group, Spooner et al. (2014) merged 32 taxa accepted by Hawkes (1990). AFLP analysis (Spooner et al., 2005) supported a monophyletic origin of the Andean landraces from the northern members of the *S. brevicaule* complex. Further hybridization, polyploidization, natural variation and selection led to the great morphological and genetic diversity of the Andean landraces, termed *Solanum phureja* Juz. & Bukasov, *Solanum stenotomum* Juz. & Bukasov, *Solanum chaucha* Juz. & Bukasov, *S. tuberosum* subsp. *andigena* following the classification system of Hawkes (1990) or *S. tuberosum* 'Andigenum group' following Spooner et al. (2014). The di-, tri-, tetraploid landraces are widespread and can be found from western Venezuela to northern Argentina (Ovchinnikova et al., 2011).

***Solanum tuberosum* 'Chilotanum group'.** Further domestication events were studied based on two hypotheses: (1) the multiple origin hypothesis and (2) the restricted origin hypothesis. Under the multiple origin theory, Juzepczuk and Bukasov (1929) hypothesized that *S. tuberosum sensu stricto* according to these authors [= *Solanum tuberosum* subsp. *tuberosum* according to the nomenclature of Hawkes (1990), or *Solanum tuberosum* 'Chilotanum group' using the system of Spooner et al. (2007)] evolved from wild tetraploid species, i.e. *Solanum fonckii Phil.* ex *Reiche (a nomen nudum), Solanum leptostigma* Juz. and *Solanum molinae* Juz. native to Chiloé Island. Hawkes (1990) considered *S. leptostigma* and *S. molinae* as synonyms for *S. tuberosum,* whereas Ovchinnikova et al. (2011) suggested that they are plants of the 'Chilotanum group' and not wild species' progenitors, supporting the 'restricted origin hypothesis' of Hawkes (1990) and Grun (1990). According to this, the 'Chilotanum group' evolved from the 'Andigenum group'. Using AFLP data, Spooner et al. (2005) confirmed that all potato landrace populations descended from the northern component of the *S. brevicaule* complex, arguing for an origin from a single species or its progenitor. However, unlike the 'Andigenum group', landraces of the 'Chilotanum group' have T-type cytoplasm (Hosaka, 2002; 2003) or cpSSR haplotype III (Gavrilenko et al., 2013). Therefore, putative wild maternal ancestors of the 'Chilotanum group' are populations of *S. berthaultii* having this plastid cytoplasm type. Plants of a potential maternal ancestor (*S. berthaultii*) and plants of the tetraploid 'Andigenum group' might have reached together the Chilean coast and the Argentinian valley of Mendoza Province, where they found ideal growing conditions (Spooner et al., 1991). Further reproduction might have been entirely via tubers, which explains the low genetic diversity. However, microsatellite studies of Spooner et al. (2012) and Gavrilenko et al. (2013) revealed discrepancies in the further position of *Solanum maglia* Schltdl. as a wild progenitor and hence, the full background of the 'Chilotanum group' remains to be elucidated.

**Highland bitter potato species.** *Solanum curtilobum* Juz. & Bukasov (2n = 5x = 60) and *Solanum juzepczukii* Bukasov (2n = 3x = 36) contain high glycoalkaloid levels and are commonly used for freeze-drying (Hawkes, 1962). In total, three frost-resistant species of cultivated potato (*Solanum ajanhuiri* Juz. & Bukasov, *S. curtilobum* and *S. juzepczukii*) evolved from the 'Andigenum group' and are involved in introgression with the wild species series *Solanum acaule* Bitter and *Solanum boliviense* Dunal in DC. (Bukasov, 1933; Hawkes, 1962; Schmiediche et al., 1982; Ovchinnikova et al., 2011; Spooner et al., 2014). Nuclear DNA sequence data (Rodriguez et al., 2010) and plastid SSRs (Gavrilenko et al., 2013) supported that these wild species are the maternal ancestors of *S. ajanhuiri* (2n = 2x = 24) and *S. juzepczukii*. Plastid SSR data also indicated the multiple maternal origin from reciprocal crosses for these two highland bitter cultivated species. By contrast, the pentaploid *S. curtilobum* might have a monophyletic maternal origin because the plastid SSR haplotype I was present in all studied accessions of *S. curtilobum* (Gavrilenko et al., 2013). Furthermore, *S. curtilobum* might have arisen by hybridization of 'Andigenum group' diploids x *S. juzepczukii,* by 'Andigenum group' triploids x *S. acaule,* or by 'Andigenum group' tetraploids x *S. juzepczukii,* as in all such crosses unreduced gametes can arise (Gavrilenko et al., 2013).

## 2.3 Domestication traits

Natural selection and domestication had an enormous impact on the genome arrangement of today's potato. Meyer and Purugganan (2013) have identified 15 traits of root and tubers crops relevant for domestication and diversification. Key traits for domestication include flavor, resource allocation, starch content, ability to thrive in modified landscapes, and reduced branching, all of which are relevant to potato. Sequencing of a potato diversity panel of 67 genotypes/accessions including modern varieties, South American landraces and wild diploid species, revealed that more than 2,600 genes were under strong selection pressure (Hardigan et al., 2017). One of the most important adaptations was the transition from short-day conditions in the equatorial region to tuber formation under temperate southern Chilean and later European long-day conditions. Kloosterman et al. (2013) identified the *StCDF1* gene (*Solanum tuberosum CYCLING DOF FACTOR1)* located on chromosome 5 as a candidate for controlling plant maturity and the onset of tuberization. Natural allelic variants of *StCDF1* alleles indicated that StCDF1 protein structure has been disrupted by TE-induced (*StCDF1.2*) and non-TE-induced mutations (Hardigan et al., 2017) leading to tuberization outside equatorial short-day conditions.

Other important gene signatures have been identified for tuber enlargement specifically affecting cell cycle, circadian rhythm and sucrose transport and mobilization, including effects on sucrose-phosphate synthase, sugar transporters, fructokinase, inorganic pyrophosphatase proteins and shifts to sucrose synthase (Susy) activities (Hardigan et al., 2017). Furthermore, in potato, glycoalkaloids are an important component of the plant defense mechanism and comprise mainly $\alpha$-solanine and $\alpha$-chaconine in commercial varieties (Kuhn and Low, 1954). The presence of glycoalkaloids can cause acute toxic effects and the lowest observed adverse effect level is considered to be 1 mg total potato glycoalkaloids $kg^{-1}$ body weight per day.

Although the content can be reduced by up to 90% (EFSA et al., 2020) by peeling, boiling, frying in oil, selection was made for lower glycoalkaloid levels. Nowadays, most potato varieties contain less than 5% of total glycoalkaloid contents in tubers (Milner et al., 2011).

## 2.4 Geographic distribution and centers of diversity

Potatoes can generally be grown in climates where temperature during tuber formation and bulking ranges between 4 and 18°C and temperatures for optimal plant development are below 30°C (Hammes and De Jager, 1990; Griffin et al., 1993; Raymundo et al., 2018). Therefore, potato is grown at latitudes between 69° N to 50° S and up to 4,000 m altitude (Hijmans, 2003), covering 17.3 million ha during the frost-free period of the temperate zones, in the highlands of the tropics i.e. in the Andes, Eastern Brazilian highlands, the African highlands and the volcanic mountains of Southeast Asia, and during the heat-free period of the subtropics i.e. the Mediterranean, southern China and northern India (Devaux et al., 2020). The wild species are native to the Americas and are found only between the southwestern United States and the southern end of South America (Hawkes and Hjerting, 1969). South American landraces are found on farms between western Venezuela and northern Argentina, on Chiloé Island and the adjacent Chonos Archipelago of south-central Chile.

### Wild species

Wild species are widespread from the southwest of the USA (Arizona, Colorado, New Mexico, Texas, Utah), through the tropical highland of Mexico, Central America and the Andes down to Argentina, Chile and Uruguay. They occur in a range of environments between 38° N and 41° S but are usually found in cool climates, in the tropical lowlands at average temperatures above 20°C and at altitudes between 2,000 and 4,000 m (Hijmans and Spooner, 2001). In these areas, rainfall is usually less than 800 mm. Except for *Solanum morelliforme* Bitter & Muench, which is endemic in oak and pine forests, and *Solanum clarum* Correll, which can be epiphytic and grows among mosses, all potato species are terrestrial and morphological discrimination can be very difficult (Hijmans et al., 2002). Many of them have a similar appearance and show dissected leaves, corollas in different shades of white, blue, purple and pink, and pentagonal or rotate in shape, and spherical to ovoid berries (Hijmans and Spooner, 2001). Due to the difficulties in identification and complex taxonomy, the delineation of distribution areas is problematic. Hijmans et al. (2007) estimated ranges based on ploidy levels. The species of the *Petota* section have a basic number of chromosomes of x = 12 and ranges are shown for diploid (2n = 2x = 24), triploid (2n = 3x = 36), tetraploid (2n = 4x = 48), pentaploid (2n = 5x = 60) and hexaploid (2n = 6x = 72) species (Figure 2.4.1.1, Table 4.2.1).

For 187 wild potato species, Hijmans et al. (2007) analyzed 5,447 reports of ploidy determination and found that 123 species were diploid (green, Figure 2.4.1.1). These species covered the largest geographical range and were predominantly present at the extreme northern (southwestern USA) and/or southern (Argentina, Chile, Uruguay) latitudes of the wild potato distribution range. Forty-three species were exclusively polyploid. Of both groups, 30, 20, 14 and two species contain tetraploid, triploid and hexaploidy and pentaploid populations, respectively. Triploids and pentaploids cover a smaller area than tetraploids and hexaploids. Tetraploids (yellow, Figure 2.4.1.1) are dominant in northern Mexico, Ecuador and Peru down to northern Argentina. *S. acaule* is especially common in the latter two areas in South America and *Solanum stoloniferum* Schltdl. in North and Central America. In contrast, triploids appear more in the extreme dry and warm areas, especially at the south-eastern end of wild potato distribution but records are relatively rare. Some species were observed to have even three cytotypes, i.e. *Solanum verrucosum* Schltdl. was predominantly diploid, but triploids and tetraploids were also observed (Hijmans et al., 2007). However, data produced by Hawkes (1990) and Spooner et al. (2014) suggest that diploid wild potatoes evolved in Mexico and spread to South America. The many polyploids in northern Peru also suggests that species diversified a long time ago (Hijmans et al., 2007).

Hijmans and Spooner (2001) determined the number of wild species per country by analysing 6,073 georeferenced observations. These data were complemented by Spooner et al. (2014), who analyzed 11,485 georeferenced data and confirmed that Peru is the country with most (51 wild species) but also highest number of rare species (13) with fewer than five observations (Figure 2.4.1.2). Mexico, Argentina and Bolivia have 27, 17 and 16 wild species, respectively, with 13 species rare in Mexico. Dependent on the type of study and time of publication, these numbers can vary, overall species richness is highest between central to northern Peru, identifying this country as the primary center for species richness and diversity (Figure 2.4.1.1, 2.4.1.2) and Mexico as secondary center of diversity.

**Peru**. North-central Peru, especially the departments of Amazonas, Cajamarca, La Libertad and San Martín, is recognized as a diversity hotspots of Solanaceae (Stern et al., 2008). For example, in the Cajamarca department, nine species comprising *Solanum cajamarquense* Ochoa, *Solanum contumazaense* Ochoa, *Solanum guzmanguense* Whalen & Sagást., *Solanum*

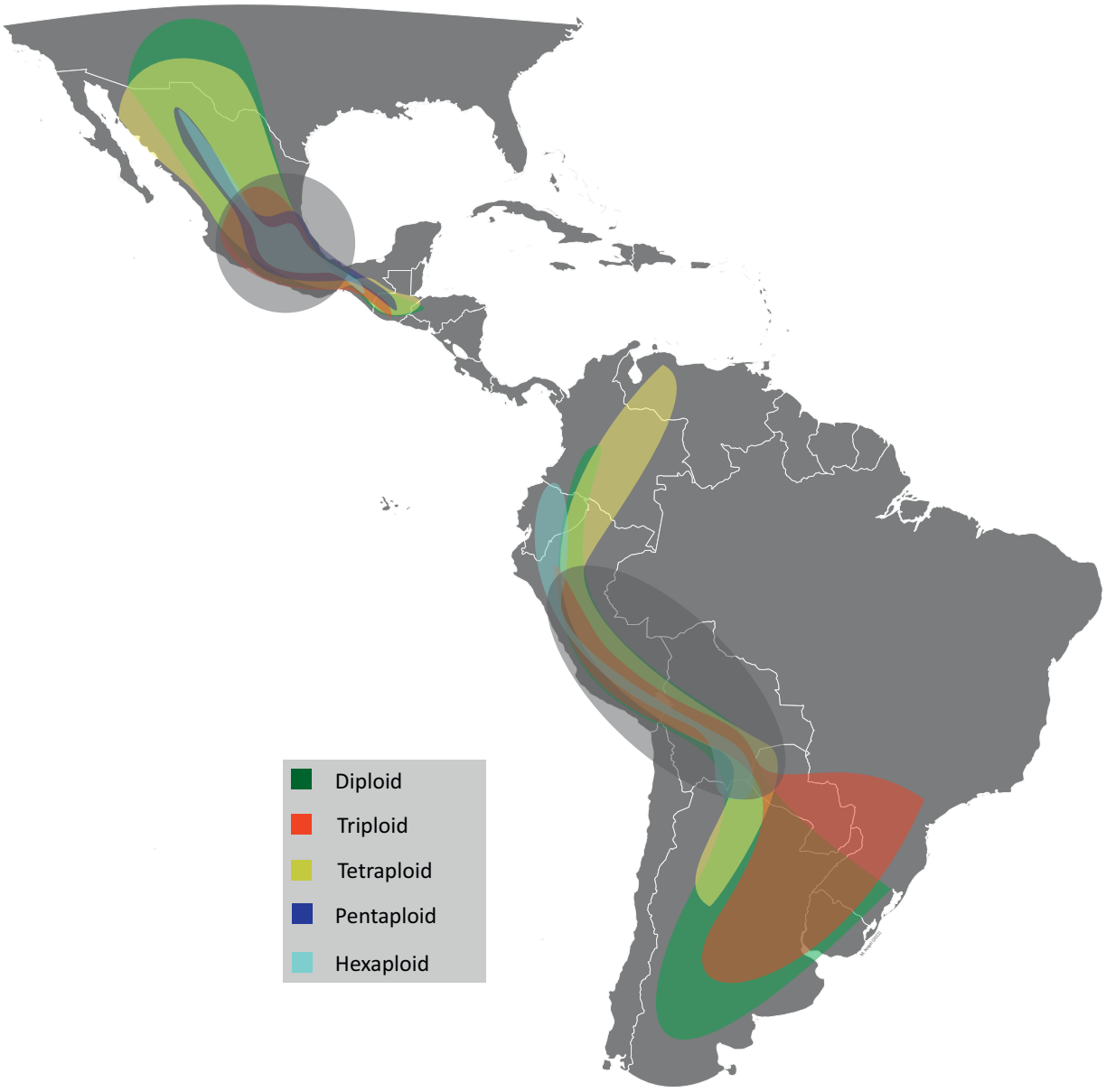



Figure 2.4.1.1. Geographical distribution of wild species with different levels of ploidy. The colored areas represent distribution of 2x, 3x, 4x, 5x and 6x species and are based on data of Hijmans et al. (2007). Shaded areas indicate centers of diversity in Peru and Mexico.

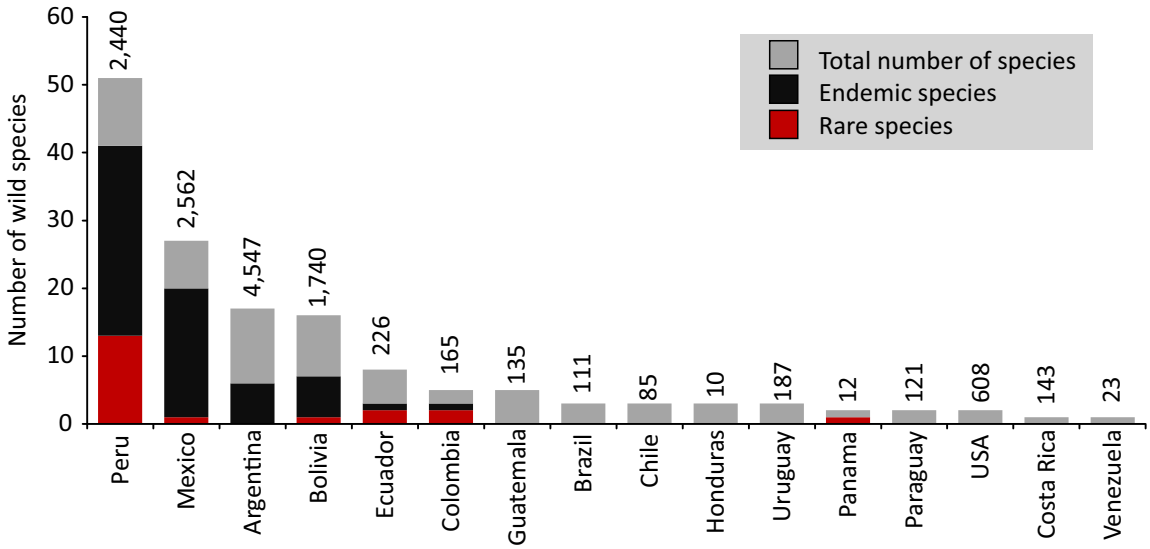



Figure 2.4.1.2. Distribution of wild potato species in America. The total number of species observed (grey), the number of endemic (black) and rare species (red) with fewer than five reports and the number of observations (above the column) are presented. A few overlaps between endemic and rare species were ignored. The figure is based on data of Spooner et al. (2014).

*hypacrarthrum* Bitter and *Solanum lopezcamareane* as well as *Solanum jalcae* Ochoa (endemic to La Libertad), *Solanum raquialatum* Ochoa (endemic to the entire Amotape-Huancabamba Zone) and *Solanum chomatophilum* Bitter and *S. tuberosum* were reported.

**Mexico**. A national inventory of the priority crop wild relatives was conducted for Mexico (Contreras-Toledo et al., 2018), including 20 of the 27 *Solanum* species endemic to the country. In particular, two wild potato species (*Solanum cardiophyllum* Lindl. and *Solanum ehrenbergii* (Bitter) Rydb.) are being conserved *in situ* (Contreras-Toledo et al., 2019). Thereby, Contreras-Toledo et al. (2019) recommended potential priority areas where plants of *S. cardiophyllum* should be collected first. These include the states of Aguascalientes, Hidalgo, Jalisco, State of Mexico, Michoacan, Morelos, Oaxaca, Puebla, Queretaro, Sinaloa, Zacatecas, and Mexico City. Plants of *S. ehrenbergii* are recommended to be collected in Aguascalientes, Guanajuato, Hidalgo, Jalisco, State of Mexico, Michoacan, Nayarit, Puebla, Queretaro, San Luis Potosi, Zacatecas, and Mexico City.

**Argentina.** Seventeen wild potato relatives are found in Argentina (Spooner et al., 2016; Palchetti et al., 2020), of which seven are considered endemic (*Solanum* x*aemulans* Bitter & Wittm., *Solanum* x*brucheri* Correll, *Solanum kurtzianum* Bitter & Wittm., *Solanum neorossii* Hawkes & Hjert., *Solanum* x*rechei* Hawkes & Hjert., *Solanum venturii* Hawkes & Hjert., and *Solanum vernei* Bitter & Wittm.) and ten as native (*S. acaule*, *S. berthaultii*, *S: boliviense*, *S. brevicaule*, *Solanum chacoense* Bitter, *Solanum commersonii* Dunal, *Solanum infundibuliforme* Phil., *S. maglia*, *Solanum malmeanum* Bitter and *Solanum microdontum* Bitter). Wild potato populations were identified in different protected areas by Clausen et al. (2018) and Kozub et al. (2019).

**Bolivia.** Although Spooner et al. (2016) identified 16 wild potato species in Bolivia (Table 3.2.1), Cadima et al. (2014) listed 21 endemic potato wild relatives, including *Solanum achacachense* Cárdenas, *Solanum alandiae Cárdenas, Solanum arnezii* Cárdenas, *Solanum avilesii* Hawkes & Hjert., *S. berthaultii, S: boliviense, Solanum bombycinum* Ochoa, *S. brevicaule, Solanum circaeifolium* Bitter, *Solanum* x*doddsii* Correll, *Solanum flavoviridens* Ochoa, *Solanum gandarillasii* Cárdenas, *Solanum hoopesii* Hawkes & K.A. Okada, *Solanum* x*litusinum* Ochoa, *Solanum neocardenasii* Hawkes & Hjert., *Solanum neovavilovii* Ochoa, *Solanum soestii* Hawkes & Hjert., *Solanum sucrense* Hawkes, *Solanum ugentii* Hawkes & K.A. Okada, *Solanum violaceimarmoratum* Bitter and *Solanum virgultorum* (Bitter) Cárdenas & Hawkes.

The difference in numbers may be due to different taxonomic classifications. These wild species occupy mainly the Andean valleys and the subtropical Andean rainforest (Yungas), where they normally occur at altitudes between 700 and 4,500 m (Ochoa, 1990). They do not grow in the tropical lowland forests (Spooner and Bamberg, 1994). *S. circaeifolium* and *S. soestii* are considered to be rare (Coca, 2020). The more abundant *S. circaeifolium* is considered as endemic in the North of the department of La Paz, and is threatened by deforestation and urbanization. *S. soestii* also has limited distribution in the Department of La Paz and is threatened with extinction due to drastic changes in native vegetation due to eucalyptus plantations (Coca, 2020).

## Landraces

More than 3,000 landraces are maintained by indigenous farmers in the Andes and the Chiloé island (Spooner et al., 2014). Compared to the wild potato species, no specific habitats for different ploidy variants could be identified for the traditional landraces, although the distribution of the *S. tuberosum* 'Chilotanum group' in Chile and extreme northern and southern range extensions of the 'Andigenum group' are well-known (Spooner et al., 2010). In Mexico and Central America, landraces were introduced during colonialization (Ugent, 1968).

Landraces can be grouped according to their market presence and tuber characteristics (De Haan and Rodriguez, 2016). So-called commercial or cosmopolitan landraces cover large areas of cultivation and are well-known among consumers. In Peru and Colombia, the diploid 'Peruanita' and the 'Criollo Amarilla' are important landraces (Table 2.4.2.1). In Argentina, the tetraploid 'Tuni' is offered in specialty restaurants (De Haan and Rodriguez, 2016). Another category comprises thousands non-commercial and floury, non-bitter landraces. These landraces are diverse and show great differences in shape, and skin and tuber color (Ovchinnikova et al., 2011). De Haan and Rodriguez (2016) identified hotspots of diversity in Huancavelica (Peru), Paucartambo (Peru), northern La Paz (Bolivia), and northern Potosí (Bolivia). A third category of native bitter landraces belong to *S. juzepczukii* and *S. curtilobum* and are grown in central and southern Peru and Bolivia. They are bitter, often frost resistant and the frozen tubers are used for chuño, moraya or tunta. The degree of bitterness can vary and can be also present in genotypes of *S. ajanhuiri* and varieties of the 'Andigenum group'. In this case, the products are used for freeze-drying. Further details on landraces and *in situ* conservation are provided in Chapter 5.

## 2.5 Geographical spread and the rise of modern varieties

Spanish explorers were most likely the first Europeans to discover the potato in the tropical lowlands of Colombia when they arrived in the Magdalena River Valley in 1536, as reported by Juan de Castellanos (Spooner et al., 2014). The first tubers were likely brought from the Andes to the Canary Islands in approximately 1562 (Figure 2.5.1, No 1), where they were cultivated and propagated for onward transport to Europe. As the Spanish name for potato (patata) is very similar to sweet potato (batata), the interpretation of historical records can be difficult. However, the Spanish word 'patata' and the English term 'potato' were likely derived from the Quechua-Inca word 'papa' which was adopted and transformed by the Spanish into their Castilian language. In Chile, the word for potato is 'poni' (Ugent, 1968; Hawkes and Francisco-Ortega, 1993). After its arrival in Europe, different words were used to the crops in different languages. The word 'tartouffli' (truffle) in Italy was further developed into 'Kartoffel' in Germany. The Czech word 'brambor' and the Croatian word 'krumpir' come from the Southern German dialect 'Gromberen' or 'Grundbirne' (ground pear) and the French and Dutch terms 'pomme de terre' and 'aardapple' refer to apples from the soil.

The arrival of potatoes in continental Europe represents a milestone in the geographical spread of the crop (Hawkes and Francisco-Ortega, 1993). Among the early records is a shipment from the Canary Islands to Rouen, France, in 1574 (Figure 2.5.1, No 3). Salaman

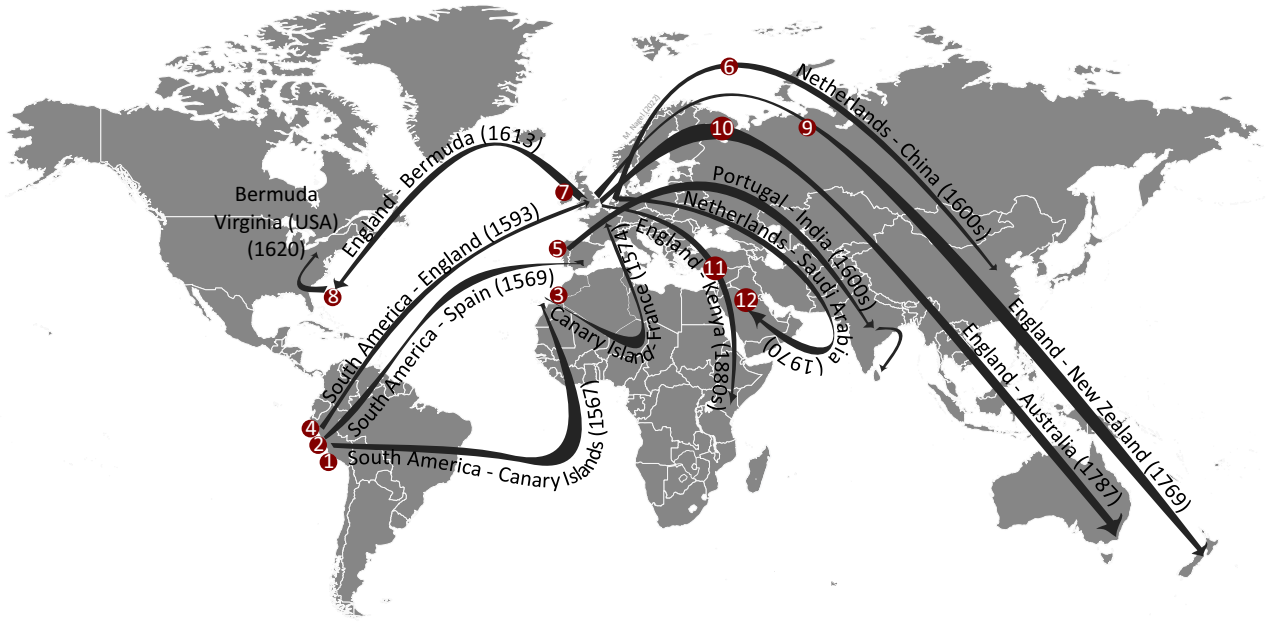



**Figure 2.5.1.** Important events for the global potato distribution.

**Table 2.4.2.1.** Diversity of potato landraces from centers of origin. Modified from De Haan and Rodriguez (2016)

| Country | Approximate total *in situ* diversity of landraces | Well-known commercial or cosmopolitan landraces | Well-known bitter landraces |
|---|---|---|---|
| Argentina | 50–70 | Chacarera, Tuni, Perija, Negrita, Collareja, Churqueña, Waicha | |
| Bolivia | 1000–1500 | Alqa Imilla, Yana Imilla, Yuraq Imilla, Imilla Rosada, Waycha Paceña | Azul Luki, Wila Luki, Laran Luki, Qanqu Chuqipitu |
| Chile | 300–400 | Michuñe Roja, Michuñe Negra, Michuñe Blanca, Cabra, Murta, Clavela | |
| Colombia | 180–240 | Criolla Amarilla, Tuquerreña, Carriza, Argentina, Salentuna, Colombina, Bandera, Mambera, Ratona, Tornilla | |
| Ecuador | 350–450 | Yema de huevo, Uvilla, Leona Blanca, Leona Negra, Coneja Negra, Coneja Blanca, Puña, Bolona, Jubaleña, Chaucha Amarilla | |
| Peru | 2800–3300 | Peruanita, Camotillo, Muru Huayro, Huayro, Macho, Huamantanga, Amarilla Tumbay, Amarilla del Centro, Ccompis | Yuraq Siri, Yana Siri, Piñaza, Qanchillu, Locka |
| Venezuela | 30–40 | Arbolona Negra, Cucuba, Tocana, Concha Gruesa, Tiniruca, Guadalupe | |

(1946) found evidence that cultivated potato left a northern port in South America and reached Spain in 1569 (Figure 2.5.1, No 2) and was introduced to England (Figure 2.5.1, No 4) by Sir Francis Drake in 1593 (Salaman et al., 1949). The first 'European' tetraploid potatoes originated in the Andes (Ames and Spooner, 2008; Gutaker et al., 2019). Due to adaptation to short-day conditions, the cultivation of these plants in continental Europe must have been a challenge as tuber formation only started just before the onset of the cold season. To overcome the short-day dependence on the continent, farmers most likely selected plants that adapted to local conditions. Gutaker et al. (2019) used historical herbarium samples to show that plants with Chilean-related chlorotypes were also introduced from the 17th century onwards. However, from 1600 onwards, potatoes spread globally. The Portuguese shipped potatoes to India (Figure 2.5.1, No 5) and the British to Sri Lanka (Graves et al., 2001). Dutch settlers introduced potatoes to Penghu Islands, China (Figure 2.5.1, No 6) (De Haan and Rodriguez, 2016). In 1613, potatoes arrived in Bermuda (Figure 2.5.1, No 7) and reached Virginia in 1621 (Figure 2.5.1, No 8) (Graves et al., 2001). In the 18th century, Captain James Cook and Marion du Fresne, introduced potatoes to New Zealand (Figure 2.5.1, No 9) and Australia (Figure 2.5.1, No 10) (De Haan and Rodriguez, 2016), and in the 19th, German and English settlers and missionaries brought the crop to Africa (Figure 2.5.1, No 11) (Kiple and Ornelas, 2000).

Until the end of the 17th century, the potato was hardly accepted as staple food in Europe. However, as potatoes were hard to plunder during wars, the Prussian King Frederick the Great promoted potato cultivation to farmers, who began to grow potatoes in small gardens. Besides, potatoes were very advantageous because they were hardly visible to the tax collectors. Further, political promotion and field trials in various countries supported potato cultivation so that by the beginning of 19th century, 120 potato varieties had been documented in Europe (Stuart 1937; Zuckerman, 1998; Ames and Spooner, 2008). Examinations of the chlorotype frequencies of 88 individuals comprising landraces and modern varieties (Gutaker et al., 2019) showed that varieties carrying the Andean-related chlorotypes were reduced by half compared to the late 18th century. The Irish potato famine between 1845 and 1847, caused by the late blight fungus (*Phytophthora infestans*) largely eradicated the predominant cultivated varieties, requiring farmers to reintroduce older stocks which had a higher Andean background and were more tolerant to the disease. However, only crosses between females plants of Chilean potatoes and pollen of Andean potatoes have been successful and are responsible for most of today's modern varieties combining nuclear genes of *andigenum* and subsp. *tuberosum* with the cytoplasmic factors of Chilean landraces (Grun, 1979). Later, in the 20th century, intensive breeding programs introduced diversity from wild species, i.e. *S. vernei, Solanum demissum* Lindl. and *S. stoloniferum* and northern-adapted strains of the 'Andigenum group', to improve tolerance to the pathogen, rather than using material descended from plants of the 19th century (Ross, 1966; Grun, 1990; Hawkes, 1990; Spooner et al., 2014).

Further information on the worldwide distribution and production of potato is provided in Chapter 4.

**In summary**, molecular data have revealed, confirmed and supplemented earlier assumptions about the progenitors, distribution and global spread of our modern potato. It could be shown that the progenitor of the 'Andigenum group' derived from the northern members of the *S. brevicaule* complex. Except for maternal ancestors of *S. berthaultii*, the wild ancestors of the 'Chilotanum group' are not yet fully elucidated, although there is a strong proposal on the monophyletic origin of this group, also tracing back to the *S. brevicaule* complex. The great diversity of di-, tri-, tetra-, penta- and hexaploid wild species forms the basis for a large number of landraces with different tuber characteristics that evolved in the Andes and the Chiloé Islands. In particular, the decline of glycoalkaloids and the adaptation of plants of the 'Chilotanum group' to long/neutral day conditions enabled the further rise of the crop, which was shipped to continental Europe and cultivated there in the 16th century. Political promotion and worldwide spread supported the acceptance of the plant as a crop, which became the third most important starchy staple in modern times.


*Solanum tuberosum* in Lehrbuch der Botanik, 1911

# 3 TAXONOMY

Taxonomic classifications and descriptions are essential guides for genebanks and their users and are particularly important for characterization, regeneration/multiplication, distribution, gap analysis and collecting, and further breeding efforts. The organization of biological diversity is shaped by the ongoing development and discussion of species concepts (Rapini, 2004; de Queiroz, 2005). So far, a large range of different species concepts have been proposed with little agreement among them (Hausdorf, 2011). The Biological Species Concept, also called the Isolation Concept (Mayr, 1942), is the most influential and refers to the geographic model of speciation and also includes breeding relationships. Rapini (2004) suggest that the integration of genetic results may lead to semantic problems. The reason for this is that species are regarded as units of identification whereas geneticists regard populations as evolutionary units (Ehrlich and Raven, 1969). In order to avoid further challenges and to provide clarity, it is important that these concepts are further developed by incorporating available molecular results.

## 3.1 Historic background of potato taxonomy

Wild and cultivated potato belong to the Solanaceae family, which includes 90 genera and 3,000 to 4,000 species that vary widely in growth habit, morphology and ecology. About 1,000 to 2,000 species are members of the genus *Solanum*, in the subfamily Solanoideae, which have a basic chromosome number of x = 12 (Olmstead and Palmer, 1992; Olmstead et al., 1999). The wild and cultivated potato belong to the *Solanum* section *Petota.* This section has been shaped by various introgressions, interspecific hybridization events, and auto- and allopolyploidy. Because of sexual compatibility among many species, a combination of sexual and asexual reproduction, and phenotypic plasticity, the *Petota* section shows a high degree of morphological similarity among species (Spooner, 2009). As a consequence, the biological concept of a species proposed by Mayr (1942) is difficult to apply and led to many taxa being described and used synonymously, leading to major inconsistencies between

descriptions and authors. Therefore, while in the past 494 epithets have been used for wild and 626 for cultivated potato species, in the most recent classification only 107 wild and 4 cultivated potato species are accepted (Ovchinnikova et al., 2011; Spooner et al., 2014).

A first description of potato diversity was documented by Alefeld (1866). However, a more detailed taxonomic classification was attempted by Russian taxonomists, who used ecogeography as the main characteristic in combination with ploidy and analysis of morphological and physiological traits (Ovchinnikova et al., 2011). The first taxonomic treatment of cultivated potatoes dates back to 1929. Based on studies of the first germplasm collection of cultivated potatoes, the Russian taxonomists Juzepczuk and Bukasov (1929) named and described 13 cultivated species. Later, based on the complex intraspecific systems, dating back to Vavilov (1922), Vladimir Lekhnovich recognized hundreds of subspecies, 'convarieties', varieties and forms (Lekhnovich, 1972). In 1978, Bukasov re-classified the 13 species recognized by Juzepczuk and Bukasov (1929) into 17 cultivated species (Bukasov, 1978). John (Jack) Hawkes learned about this system during his visits to the All-Union Institute of Plant Industry in Leningrad (now St. Petersburg) (Ovchinnikova et al., 2011) and at first recognized 18 cultivated species (Hawkes, 1944). Later, he reduced them to 7 cultivated species and 228 wild potato species, divided in 19 taxonomic series (Hawkes, 1990). Although the Hawkes (1990) treatment was not universally accepted (Huamán and Spooner, 2002), potatoes were classified as distinct species under the International Code of Botanical Nomenclature (ICBN). However, under the International Code of Nomenclature of Cultivated Plants (ICNCP), cultivated potatoes were also treated as cultivar groups (Dodds, 1962; Huamán and Spooner, 2002; Spooner et al., 2007; Ovchinnikova et al., 2011). As the classification and nomenclature of cultivated plants are supposed to follow the strict rules of ICNCP or ICBN, potato taxonomy has been controversially represented by different assumptions about the evolutionary dynamics of potato species (Huamán and Spooner, 2002). Moreover, the application of the biological concept of species is very challenging to potato species (Knapp, 2008). Nevertheless, a taxonomic treatment was elaborated, simplified and proposed extensively by Hawkes (1990) and is still used for classifications in most genebanks.

Since the beginning of 21st century, high-throughput sequencing approaches have shed more light on the complex taxonomy of potato. In 2002, the phenetic analysis of potato landrace populations supported the recognition of *S. ajanhuiri*, *S. chaucha*, *S. curtilobum*, *S. juzepczukii* and *S. tuberosum* subsp. *tuberosum* but not other taxa, as they may have multiple origins involving common species and continuing hybridization events. Huamán and Spooner (2002) recognized all landrace populations as the botanical species *S. tuberosum*. This included eight cultivar groups: *Ajanhuiri*, *Andigena*, *Chaucha*, *Chilotanum*, *Curtilobum*, *Juzepczukii*, *Phureja* and *Stenotomum*. However, the further investigation of 742 landraces using SSR markers resulted in a re-classification of this system. In 2007, Spooner et al. (2007) and later Ovchinnikova et al. (2011) re-evaluated cultivated potatoes and grouped them into four species, including: (1) *S. tuberosum*, with the 'Andigenum group' of upland diploids, triploids and tetraploids Andean genotypes and the 'Chilotanum group' of lowland tetraploid Chilean landraces; (2) *S. ajanhuiri* (diploid); (3) *S. juzepczukii* (triploid); and (4) *S. curtilobum* (pentaploid). Overall, during the process of taxonomic classification and re-classification, potato landraces have been assigned to 13 cultivated species (Juzepczuk and Bukasov, 1929), 21 species (Lekhnovich, 1972), 17 species (Bukasov, 1978), 9 species (Ochoa, 1990), 7 species (Hawkes, 1990), one species with eight cultivar groups (Huamán and Spooner, 2002) and, currently, 4 species, with one species including two cultivar groups (Spooner et al., 2007; Ovchinnikova et al., 2011; Spooner et al., 2014).

## 3.2 Nomenclature

The combination of molecular studies and morphological data obtained from different field surveys, herbarium specimens, and plants grown in field pots (Spooner et al., 2004; Spooner et al., 2016; Spooner et al., 2019) led to extensive changes in the taxonomy of the section *Petota* [see Table 2 in Spooner et al. (2014)] subsequent to Hawkes (1990). The re-classification was driven in particular by the difficulty in identifying the species recognized by Hawkes (1990) and the complex biological factors in this section, i.e. the lack of strong biological isolating mechanisms, interspecific hybridization and introgression events, allopolyploidy and a combination of sexual and asexual reproduction. Overall, 107 wild species, instead of 228 species, and four cultivated species, instead of 7 cultivated species, were recognized by Spooner et al. (2014) and the relationship with the Hawkes (1990) system is shown in Table 3.2.1 from Hawkes (1990).

Besides the morphological data, the degree of ploidy and putative phylogenetic relationship are essential taxonomic descriptors (Figure 3.2.1). The ploidy level can support theories about the complex dynamics of polyploid genomes during evolution (Soltis et al., 2004). Polyploidy can be considered either as an evolutionary dead-end (such as the case with triploids) or evolutionarily advanced with enhanced physiological properties, including improved stress tolerance due

to increased genetic variation and the buffer effect of duplicated genes (Van de Peer et al., 2021). In any case, it is one of the most important criteria for plant systematics. The phylogenetic relationship shows the association between ingroups and outgroups, including the division of potato species into three clades. The clades include all tuber-bearing potatoes and are based on a range of phylogenetic studies summarized by Spooner et al. (2014).

- In clade 1+2, diploid species often have non-shiny leaves, white stellate corollas, single tubers at the end of stolons
- In clade 3, diploid species have shiny leaves, blue to purple pentagonal corollas, moniliform tubers
- In clade 4, diploid species have non-shiny leaves, diverse colored pentagonal to rotate corollas, single tubers at the end of stolons

The polyploid wild species are often allopolyploids and difficult to identify based on specific morphological characteristics. Some of them have moniliform tubes. Based on the molecular data, they are grouped into four clades and 19 "informal species groups", including 11 groups for North and Central American species, six groups for southern South American species and three shared groups, i.e. Morelliforme, Conicibaccata and Acaulia group (Spooner et al., 2004; Spooner et al., 2014; Spooner et al., 2016; Spooner et al., 2019; Peralta et al., 2021). Based on morphological characters, molecular data, and phylogenetic relationships, two non-tuber-bearing series of the section *Petota* in the Hawkes (1990) taxonomy – *Etuberosa* Juz. and *Juglandifolia* (Rydb.) Hawkes – were re-classified and are now in the section *Etuberosum* (Bukasov & Kameraz) A. Child and the tomato clade comprising section *Juglandifolia* (Rydberg) A. Child and section *Lycopersicoides* A. Child (Peralta) (Peralta et al., 2008; Spooner et al., 2014).

Cultivated potato species traditionally have been classified as Linnaean taxa according to botanical nomenclature (Juzepczuk and Bukasov, 1929; Hawkes, 1944; Hawkes, 1956; Bukasov, 1978; Hawkes, 1990; Ochoa, 1990). Cultivated species can be distinguished on their morphology and ploidy level. Cultivated landraces were also treated as cultivar groups (Dodds, 1962; Huamán and Spooner, 2002; Spooner et al., 2007; Ovchinnikova et al., 2011). Huamán and Spooner (2002) proposed a key to the differentiation of landrace cultivar-groups. Later, these key and descriptions were modified by Ovchinnikova et al. (2011) as follows:

1. Plants are semi-rosette to semi-erect; pedicel articulation is indistinct to only slightly distinct and located in the upper one-fifth of the pedicel; frost tolerant (of putative hybrid origin with the frost-tolerant species *S. acaule* or *Solanum megistacrolobum* Bitter) …continue with 2
1. Plants are ascending to erect; pedicel articulation is evident and located below the upper one-fifth of the pedicel; not frost tolerant
   ... continue with 4
2. Most distal lateral leaflets are broadly decurrent; plants are diploid.
   See *S. ajanhuiri.*
2. Most distal lateral leaflets are not or only slightly decurrent; plants are triploid or pentaploid
   … continue with 3
3. Plants are low growing, 62 to 98 cm tall and triploid.
   See *S. juzepczukii*
4. Plants are of medium height, 96 to 125 cm tall and pentaploid.
   See *S. curtilobum*
4. Plants are adapted to short-day flowering and tuberization; upper leaves are diverged from stem at 40°–50°; plants are diploid, triploid or tetraploid.
   See *S. tuberosum* 'Andigenum group'
4. Plants are adapted to long-day flowering and tuberization; upper leaves diverged from stem at angle of 50°–90°. Landrace populations is native to south-central Chile.
   See *S. tuberosum* 'Chilotanum group'
5. Modern varieties are commonly breeding populations of the Northern Hemisphere, that are grown worldwide; they may be hybrids of plants of the 'Chilotanum group' and 'Andigenum group' and other cultivar groups
   See *S. tuberosum*

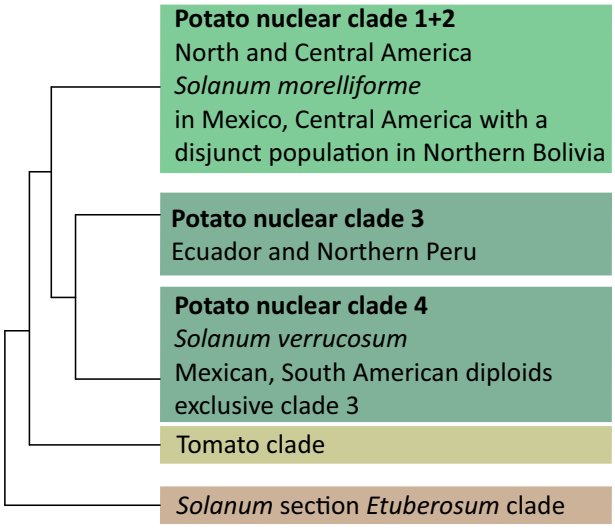



**Figure 3.2.1.** Three nuclear clades and outgroups (tomato and etuberosum) of the diploid species of *Solanum* section Petota. The polyploid species (allopolyploids) combine genomes of the three clades. Figure adapted from Spooner et al. (2014).

**Table 3.2.1.** Accepted species of *Solanum* section *Petota* according to Spooner et al. (2014), (Spooner et al., 2016), (Spooner et al., 2019). Country of occurrence, ploidy level, endosperm balance number (EBN, see chapter 11.2), and nuclear-marker-based cladistic relationships as explained in Spooner et al. (2014) and species and synonyms accepted by Hawkes (1990) or subsequent authors. Genepools and priority levels were assigned based on data of Castañeda-Álvarez et al. (2015). Species that have the highest (H) priority for collecting are highlighted in blue. Medium (M) and low (L) priority are only indicated. More details are provided online on Solanaceae Source (www.http://solanaceaesource.org/).

| Species name according to Spooner et al. (2014) | Genepool | Priority levels | Countries | Ploidy level | Nuclear Clade | Taxon according to Hawkes (1990) or subsequental authors |
|---|---|---|---|---|---|---|
| *Solanum acaule* Bitter | Primary | | ARG, BOL, PER, CHL | 4x (2EBN) | Complex4 | *S. acaule* Bitter |
| | | | | | | *S. acaule f. incuyo* Ochoa (1994b) |
| | | | | | | S. acaule var. punae (Juz.) Hawkes |
| *Solanum acroglossum* Juz. | Secondary | H | PER | 2x (2EBN) | 3 | *S. acroglossum* Juz. |
| *Solanum acroscopicum* Ochoa | Secondary | H | PER | 2x | [4] | *S. acroscopicum* Ochoa |
| | | | | | | *S. lopez-camarenae* Ochoa |
| *Solanum ×aemulans* Bitter & Wittm. | | | ARG | 3x, 4x (2EBN) | [4] | *S. × aemulans* Bitter & Wittm. |
| | | | | | | *S. acaule* subsp. *aemulans* (Bitter & Wittm.) Hawkes & Hjert. |
| | | | | | | *S. ×indunii* K.A. Okada & A.M. Clausen |
| *Solanum agrimonifolium* Rydb. | Secondary | M | GUA, HON, MEX | 4x (2EBN) | 3+4 | *S. agrimonifolium* Rydb. |
| *Solanum albicans* (Ochoa) Ochoa | | L | ECU, PER | 6x (4EBN) | 3+4 | *S. albicans* (Ochoa) Ochoa |
| | | | | | | *S. acaule* subsp. *palmirense* Kardolus (1998) |
| *Solanum albornozii* Correll | Secondary | L | ECU | 2x (2EBN) | 3 | *S. albornozii* Correll |
| *Solanum amayanum* Ochoa | | | PER | 2x (2EBN) | 4 | *S. amayanum* Ochoa |
| *Solanum anamatophilum* Ochoa | Tertiary | | PER | 2x (2EBN) | 3 | *S. anamatophilum* Ochoa |
| | | | | | | *S. peloquinianum* Ochoa |
| *Solanum andreanum* Baker | Secondary | M | COL, ECU | 2x (2EBN), 4x (4EBN) | 3 | *S. andreanum* Baker |
| | | | | | | *S. burtonii* Ochoa |
| | | | | | | *S. correllii* Ochoa |
| | | | | | | *S. cyanophyllum* Correll |
| | | | | | | *S. paucijugum* Bitter |
| | | | | | | *S. regularifolium* Correll |
| | | | | | | *S. serratoris* Ochoa (1990b). |
| | | | | | | *S. solisii* Hawkes |
| | | | | | | *S. suffrutescens* Correll |
| | | | | | | *S. tuquerrense* Hawkes |
| *Solanum augustii* Ochoa | Tertiary | | PER | 2x (1EBN) | 3 | *S. augustii* Ochoa |
| *Solanum ayacuchense* Ochoa | Secondary | H | PER | 2x (2EBN) | 4 | *S. ayacuchense* Ochoa |
| *Solanum berthaultii* Hawkes | Primary | L | ARG, BOL | 2x (2EBN), 3x | 4 | *S. berthaultii* Hawkes |
| | | | | | | *S. flavoviridens* Ochoa |
| | | | | | | *S. tarijense* Hawkes |
| | | | | | | *S. ×litusinum* Ochoa |
| | | | | | | *S. ×trigalense* Cárdenas |

| Species name according to Spooner et al. (2014) | Genepool | Priority levels | Countries | Ploidy level | Nuclear Clade | Taxon according to Hawkes (1990) or subsequental authors |
|---|---|---|---|---|---|---|
| | | | | | | *S.* ×*zudaniense* Cárdenas |
| *Solanum* ×*blanco-galdosii* Ochoa | | | PER | 2x (2EBN) | 3 | *S.* ×*blanco-galdosii* Ochoa |
| *Solanum boliviense* Dunal in DC. | Secondary | L | ARG, BOL, PER | 2x (2EBN) | 4 | *S. boliviense* Dunal in DC. |
| | | | | | | *S. astleyi* Hawkes & Hjert. |
| | | | | | | *S. megistacrolobum* Bitter |
| | | | | | | *S. megistacrolobum f. purpureum* Ochoa (1994b) |
| | | | | | | *S. sanctae-rosae* Hawkes |
| | | | | | | *S. toralapanum* Cárdenas & Hawkes |
| *Solanum bombycinum* Ochoa | Secondary | H | BOL | 4x | [3+4] | *S. bombycinum* Ochoa |
| *Solanum brevicaule* Bitter | Primary | L | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 4 | *S. brevicaule* Bitter |
| | | | | | | *S. alandiae* Cárdenas |
| | | | | | | *S. avilesii* Hawkes & Hjert. |
| | | | | | | *S. gourlayi* Hawkes |
| | | | | | | *S. gourlayi* subsp. *Pachytrichum* (Hawkes) Hawkes & Hjert. |
| | | | | | | *S. gourlayi* subsp. *saltense* A.M. Clausen & K.A. Okada |
| | | | | | | *S. gourlayi* subsp. *vidaurrei* (Cárdenas) Hawkes & Hjert. |
| | | | | | | *S. hondelmannii* Hawkes & Hjert. |
| | | | | | | *S. hoopesii* Hawkes & K.A. Okada |
| | | | | | | *S. incamayoense* K.A. Okada & A.M. Clausen |
| | | | | | | *S. leptophyes* Bitter |
| | | | | | | *S. oplocense* Hawkes |
| | | | | | | *S. setulosistylum* Bitter |
| | | | | | | *S. sparsipilum* (Bitter) Juz. & Bukasov |
| | | | | | | *S. spegazzinii* Bitter |
| | | | | | | *S. sucrense* Hawkes |
| | | | | | | *S. ugentii* Hawkes & K.A. Okada |
| | | | | | | *S. virgultorum* (Bitter) Cárdenas & Hawkes |
| | | | | | | *S.* ×*subandigena* Hawkes |
| *Solanum* ×*brucheri* Correll | | | ARG | 3x | [4] | *S.* ×*brucheri* Correll |
| | | | | | | *S.* ×*viirsoii* K.A. Okada & A.M. Clausen |
| *Solanum buesii* Vargas | Secondary | H | PER | 2x (2EBN) | 4 | *S. buesii* Vargas |
| *Solanum bulbocastanum* Dunal in Poir. | Tertiary | L | GUA, HON, MEX | 2x (1EBN), 3x | 1 | *S. bulbocastanum* Dunal in Poir. |
| | | | | | | *S. bulbocastanum* subsp. *dolichophyllum* (Bitter) Hawkes |
| | | | | | | *S. bulbocastanum* subsp. *partitum* (Correll) Hawkes |

| Species name according to Spooner et al. (2014) | Genepool | Priority levels | Countries | Ploidy level | Nuclear Clade | Taxon according to Hawkes (1990) or subsequental authors |
|---|---|---|---|---|---|---|
| *Solanum burkartii* Ochoa | Secondary | H | PER | 2x | 4 | *S. burkartii* Ochoa |
| | | | | | | *S. irosinum* Ochoa |
| | | | | | | *S. irosinum forma tarrosum* Ochoa (1999) |
| *Solanum cajamarquense* Ochoa | Secondary | H | PER | 2x (1EBN) | 3 | *S. cajamarquense* Ochoa |
| *Solanum candolleanum* Berthault | Primary | L | PER | 2x (2EBN), 3x | 4 | *S. candolleanum* Berthault |
| | | | | | | *S. abancayense* Ochoa |
| | | | | | | *S. achacachense* Cárdenas |
| | | | | | | *S. ambosinum* Ochoa |
| | | | | | | *S. ancoripae* Ochoa (1999) |
| | | | | | | *S. antacochense* Ochoa |
| | | | | | | *S. aymaraesense* Ochoa |
| | | | | | | *S. bill-hookeri* Ochoa |
| | | | | | | *S. bukasovii* Juz. |
| | | | | | | *S. bukasovii* var. *Multidissectum* (Hawkes) Ochoa (1992a) |
| | | | | | | *S. bukasovii forma multidissectum* (Hawkes) Ochoa (1999) |
| | | | | | | *S. canasense* Hawkes |
| | | | | | | *S. canasense* var. *xerophilum* (Vargas) Hawkes |
| | | | | | | *S. chillonanum* Ochoa (1989a) |
| | | | | | | *S. coelestispetalum* Vargas |
| | | | | | | *S. hapalosum* Ochoa |
| | | | | | | *S. huancavelicae* Ochoa (1999) |
| | | | | | | *S. longiusculus* Ochoa |
| | | | | | | *S. marinasense* Vargas |
| | | | | | | *S. multidissectum* Hawkes |
| | | | | | | *S. orophilum* Correll |
| | | | | | | *S. ortegae* Ochoa (1998) |
| | | | | | | *S. pampasense* Hawkes |
| | | | | | | *S. puchupuchense* Ochoa (1999) |
| | | | | | | *S. sarasarae* Ochoa |
| | | | | | | *S. sawyeri* Ochoa |
| | | | | | | *S. saxatile* Ochoa (1992b), as '*saxatilis*' |
| | | | | | | *S. sicuanum* Hawkes (1990) |
| | | | | | | *S. sparsipilum* subsp. *calcense* (Hawkes) Hawkes |
| | | | | | | *S. tapojense* Ochoa |
| | | | | | | *S. tarapatanum* Ochoa |
| | | | | | | *S. ×mollepujroense* Cárdenas & Hawkes |
| *Solanum cantense* Ochoa | Secondary | H | PER | 2x (2EBN) | 3 | *S. cantense* Ochoa |
| *Solanum cardiophyllum* Lindl. | Tertiary | | MEX | 2x (1EBN), 3x | 1 | *S. cardiophyllum* Lindl. |
| | | | | | | *S. cardiophyllum* subsp. *lanceolatum* (Berthault) Bitter |

| Species name according to Spooner et al. (2014) | Genepool | Priority levels | Countries | Ploidy level | Nuclear Clade | Taxon according to Hawkes (1990) or subsequental authors |
|---|---|---|---|---|---|---|
| *Solanum chacoense* Bitter | Secondary | M | ARG, BOL, BRA, PAR, PER, URU | 2x (2EBN), 3x | 4 | *S. chacoense* Bitter |
| | | | | | | *S. arnezii* Cárdenas |
| | | | | | | *S. calvescens* Bitter |
| | | | | | | *S. chacoense* subsp. *chacoense* |
| | | | | | | *S. chacoense* subsp. *muelleri* (Bitter) Hawkes |
| | | | | | | *S. tuberosum* subsp. *Yanacochense* Ochoa (2001); (=*S. yanacochense* (Ochoa) Gorbatenko (2006)) |
| | | | | | | *S. yungasense* Hawkes |
| *Solanum chilliasense* Ochoa | Secondary | H | ECU | 2x (2EBN) | 3 | *S. chilliasense* Ochoa |
| *Solanum chiquidenum* Ochoa | Secondary | M | PER | 2x (2EBN) | 3 | *S. chiquidenum* Ochoa |
| | | | | | | *S. ariduphilum* Ochoa |
| | | | | | | *S. chiquidenum forma amazonense* Ochoa (1994b) |
| | | | | | | *S. chiquidenum* var. *gracile* Ochoa (1994b) |
| | | | | | | *S. chiquidenum* var. robustum Ochoa (1994b) |
| *Solanum chomatophilum* Bitter | Secondary | L | ECU, PER | 2x (2EBN) | 3 | *S. chomatophilum* Bitter |
| | | | | | | *S. chomatophilum forma sausianense* Ochoa (1994b) |
| | | | | | | *S. chomatophilum* var. *subnivale* Ochoa (1994b) |
| | | | | | | *S. huarochiriense* Ochoa |
| | | | | | | *S. jalcae* Ochoa |
| | | | | | | *S. pascoense* Ochoa |
| | | | | | | *S. taulisense* Ochoa |
| *Solanum clarum* Correll | Secondary | H | GUA, MEX | 2x | 1 | *S. clarum* Correll |
| *Solanum colombianum* Dunal | Secondary | L | COL, ECU, PER, VEN | 4x (2EBN) | 3+4 | *S. colombianum* Dunal |
| | | | | | | *S. cacetanum* Ochoa |
| | | | | | | *S. calacalinum* Ochoa |
| | | | | | | *S. jaenense* Ochoa |
| | | | | | | *S. moscopanum* Hawkes |
| | | | | | | *S. nemorosum* Ochoa |
| | | | | | | *S. orocense* Ochoa |
| | | | | | | *S. otites* Dunal |
| | | | | | | *S. pamplonense* L.E. López |
| | | | | | | *S. subpanduratum* Ochoa |
| | | | | | | *S. paramoense* Bitter |
| | | | | | | *S. sucubunense* Ochoa |
| *Solanum commersonii* Dunal | Tertiary | M | ARG, BRA, URU | 2x (1EBN), 3x | | *S. commersonii* Dunal |
| *Solanum contumazaense* Ochoa | Secondary | H | PER | 2x (2EBN) | 3 | *S. contumazaense* Ochoa |
| *Solanum demissum* Lindl. | Secondary | L | GUA, MEX | 6x (4EBN) | Complex[3] | *S. demissum* Lindl. |
| | | | | | | *S. ×semidemissum* Juz. |
| *Solanum ×doddsii* Correll | | | BOL | 2x (2EBN) | 4 | *S. ×doddsii* Correll |

| Species name according to Spooner et al. (2014) | Genepool | Priority levels | Countries | Ploidy level | Nuclear Clade | Taxon according to Hawkes (1990) or subsequental authors |
|---|---|---|---|---|---|---|
| *Solanum dolichocremastrum* Bitter | Tertiary | | PER | 2x (1EBN) | 3 | *S. dolichocremastrum* Bitter |
| | | | | | | *S. chavinense* Correll |
| | | | | | | *S. huanuchense* Ochoa |
| *Solanum* ×*edinense* Berthault | | | MEX | 5x | [4] | *S.* ×*edinense* Berthault |
| | | | | | | *S.* ×*edinense* subsp. *Salamanii* (Hawkes) Hawkes |
| *Solanum ehrenbergii* (Bitter) Rydb. | Tertiary | | MEX | 2x (1EBN) | 1 | *S. ehrenbergii* (Bitter) Rydb. |
| | | | | | | *S. cardiophyllum* subsp. *ehrenbergii* Bitter |
| *Solanum flahaultii* Bitter | Secondary | M | COL | 4x | 3+4 | *S. flahaultii* Bitter |
| | | | | | | *S. neovalenzuelae* L.E.López |
| *Solanum gandarillasii* Cárdenas | Secondary | M | BOL | 2x (2EBN) | 4 | *S. gandarillasii* Cárdenas |
| *Solanum garcia-barrigae* Ochoa | Secondary | H | COL | 4x | 3+4 | *S. garcia-barrigae* Ochoa |
| | | | | | | *S. donachui* (Ochoa) Ochoa |
| *Solanum gracilifrons* Bitter | Secondary | H | PER | 2x | 4 | *S. gracilifrons* Bitter |
| *Solanum guerreroense* Correll | Secondary | | MEX | 6x (4EBN) | [Complex[3]] | *S. guerreroense* Correll |
| *Solanum hastiforme* Correll | Secondary | H | PER | 2x (2EBN) | 4 | *S. hastiforme* Correll |
| *Solanum hintonii* Correll | Secondary | H | MEX | 2x | 1 | *S. hintonii* Correll |
| *Solanum hjertingii* Hawkes | Secondary | H | MEX | 4x (2EBN) | 1+4 | *S. hjertingii* Hawkes |
| | | | | | | *S. hjertingii* var. *physaloides* (Correll) Hawkes |
| | | | | | | *S. leptosepalum* Correll5 |
| | | | | | | *S. matehualae* Hjert. & T.R. Tarn |
| *Solanum hougasii* Correll | Secondary | H | MEX | 6x (4EBN) | Complex[3] | *S. hougasii* Correll |
| *Solanum huancabambense* Ochoa | Secondary | M | PER | 2x (2EBN) | 3 | *S. huancabambense* Ochoa |
| *Solanum humectophilum* Ochoa | Tertiary | | PER | 2x (1EBN) | 3 | *S. humectophilum* Ochoa |
| *Solanum hypacrarthrum* Bitter | Tertiary | | PER | 2x (1EBN) | 3 | *S. hypacrarthrum* Bitter |
| | | | | | | *S. guzmanguense* Whalen & Sagást. |
| *Solanum immite* Dunal | Tertiary | | PER | 2x (1EBN), 3x | 3 | *S. immite* Dunal |
| | | | | | | *S. yamobambense* Ochoa |
| *Solanum incasicum* Ochoa | Secondary | H | PER | 2x (2EBN) | | *S. incasicum* Ochoa |
| *Solanum infundibuliforme* Phil. | Primary | M | ARG, BOL | 2x (2EBN) | 4 | *S. infundibuliforme* Phil. |
| *Solanum iopetalum* (Bitter) Hawkes | Secondary | M | MEX | 6x (4EBN) | 3+4 | *S. iopetalum* (Bitter) Hawkes |
| | | | | | | *S. brachycarpum* (Correll) Correll |
| *Solanum jamesii* Torr. | Tertiary | | MEX, USA | 2x (1EBN) | 1 | *S. jamesii* Torr. |
| *Solanum kurtzianum* Bitter & Wittm. | Secondary | L | ARG | 2x (2EBN) | 4 | *S. kurtzianum* Bitter & Wittm. |
| | | | | | | *S. ruiz-lealii* Brücher |

| Species name according to Spooner et al. (2014) | Genepool | Priority levels | Countries | Ploidy level | Nuclear Clade | Taxon according to Hawkes (1990) or subsequental authors |
|---|---|---|---|---|---|---|
| *Solanum laxissimum* Bitter | Secondary | H | PER | 2x (2EBN) | 4 | *S. laxissimum* Bitter |
| | | | | | | *S. neovargasii* Ochoa |
| | | | | | | *S. santolallae* Vargas |
| *Solanum lesteri* Hawkes & Hjert. | Secondary | M | MEX | 2x | 1 | *S. lesteri* Hawkes & Hjert. |
| *Solanum lignicaule* Vargas | Tertiary | | PER | 2x (1EBN) | 4 | *S. lignicaule* Vargas |
| *Solanum limbaniense* Ochoa | Secondary | H | PER | 2x (2EBN) | 4 | *S. limbaniense* Ochoa |
| *Solanum lobbianum* Bitter | Secondary | H | COL | 4x (2EBN) | 3+4 | *S. lobbianum* Bitter |
| *Solanum longiconicum* Bitter | Secondary | L | CRI, PAN | 4x | 3+4 | *S. longiconicum* Bitter |
| *Solanum maglia* Schltdl. | Secondary | H | ARG, CHL | 2x, 3x | | *S. maglia* Schltdl. |
| *Solanum malmeanum* Bitter | Tertiary | | ARG, BRA, PAR, URU | 2x (1EBN), 3x | | *S. malmeanum* Bitter |
| *Solanum medians* Bitter | Secondary | M | CHL, PER | 2x (2EBN), 3x | 4 | *S. medians* Bitter |
| | | | | | | *S. arahuayum* Ochoa (1994a) |
| | | | | | | *S. sandemanii* Hawkes |
| | | | | | | *S. tacnaense* Ochoa |
| | | | | | | *S. weberbaueri* Bitter |
| *Solanum ×michoacanum* (Bitter) Rydb. | | | MEX | 2x | [1] | *S. ×michoacanum* (Bitter) Rydb. |
| *Solanum microdontum* Bitter | Secondary | L | ARG, BOL | 2x (2EBN), 3x | 4 | *S. microdontum* Bitter |
| | | | | | | *S. microdontum* subsp. *gigantophyllum* (Bitter) Hawkes & Hjert. |
| | | | | | | *S. microdontum* var. *montepuncoense* Ochoa |
| *Solanum minutifoliolum* Correll | Tertiary | | ECU | 2x (1EBN) | 3 | *S. minutifoliolum* Correll |
| *Solanum mochiquense* Ochoa | Tertiary | | PER | 2x (1EBN) | 3 | *S. mochiquense* Ochoa |
| | | | | | | *S. chancayense* Ochoa |
| | | | | | | *S. incahuasinum* Ochoa |
| *Solanum morelliforme* Bitter & Muench | Secondary | M | BOL, GUA, MEX, HON | 2x | 1 | *S. morelliforme* Bitter & Muench |
| *Solanum multiinterruptum* Bitter | Secondary | L | PER | 2x (2EBN), 3x | 4 | *S. multiinterruptum* Bitter |
| | | | | | | *S. chrysoflorum* Ochoa |
| | | | | | | *S. moniliforme* Correll |
| | | | | | | *S. multiinterruptum forma albiflorum* Ochoa |
| | | | | | | *S. multiinterruptum forma longipilosum* Correll |
| | | | | | | *S. multiinterruptum* var. *Machaytambinum* Ochoa (1999b) |
| *Solanum neocardenasii* Hawkes & Hjert. | Secondary | H | BOL | 2x | | *S. neocardenasii* Hawkes & Hjert. |
| *Solanum neorossii* Hawkes & Hjert. | Secondary | L | ARG | 2x | 4 | *S. neorossii* Hawkes & Hjert. |
| *Solanum neovavilovii* Ochoa | Secondary | H | BOL | 2x (2EBN) | 4 | *S. neovavilovii* Ochoa |

| Species name according to Spooner et al. (2014) | Genepool | Priority levels | Countries | Ploidy level | Nuclear Clade | Taxon according to Hawkes (1990) or subsequental authors |
|---|---|---|---|---|---|---|
| *Solanum ×neoweberbaueri* Wittm. | | | PER | 3x | [4] | *S. ×neoweberbaueri* Wittm. |
| *Solanum nubicola* Ochoa | Secondary | H | PER | 4x (2EBN) | 4 | *S. nubicola* Ochoa |
| *Solanum okadae* Hawkes & Hjert. | Primary | M | BOL | 2x | [4] | *S. okadae* Hawkes & Hjert. |
| *Solanum olmosense* Ochoa | Secondary | H | ECU, PER | 2x (2EBN) | 3 | *S. olmosense* Ochoa |
| *Solanum oxycarpum* Schiede | Secondary | M | MEX | 4x (2EBN) | 3+4 | *S. oxycarpum* Schiede |
| *Solanum paucissectum* Ochoa | Secondary | L | PER | 2x (2EBN) | 3 | *S. paucissectum* Ochoa |
| *Solanum pillahuatense* Vargas | Secondary | H | PER | 2x (2EBN) | 4 | *S. pillahuatense* Vargas |
| *Solanum pinnatisectum* Dunal | Teriary | | MEX | 2x (1EBN) | 1 | *S. pinnatisectum* Dunal |
| *Solanum piurae* Bitter | Secondary | H | PER | 2x (2EBN) | 3 | *S. piurae* Bitter |
| *Solanum polyadenium* Greenm. | Secondary | M | MEX | 2x | 1 | *S. polyadenium* Greenm. |
| *Solanum raphanifolium* Cárdenas & Hawkes | Secondary | L | PER | 2x (2EBN) | 4 | *S. raphanifolium* Cárdenas & Hawkes |
| | | | | | | *S. hawkesii* Cárdenas |
| *Solanum raquialatum* Ochoa | Tertiary | | PER | 2x (1EBN) | 3 | *S. raquialatum* Ochoa |
| | | | | | | *S. ingaefolium* Ochoa |
| *Solanum ×rechei* Hawkes & Hjert. | | | ARG | 2x, 3x | [4] | *S. ×rechei* Hawkes & Hjert. |
| *Solanum rhomboideilanceolatum* Ochoa | Secondary | H | PER | 2x (2EBN) | 3 | *S. rhomboideilanceolatum* Ochoa |
| *Solanum salasianum* Ochoa | Secondary | H | PER | 2x | 4 | *S. salasianum* Ochoa |
| *Solanum ×sambucinum* Rydb. | | | MEX | 2x | [1] | *S. ×sambucinum* Rydb. |
| *Solanum scabrifolium* Ochoa | Tertiary | | PER | 2x | 3 | *S. scabrifolium* Ochoa |
| *Solanum schenckii* Bitter | Secondary | M | MEX | 6x (4EBN) | Complex[3] | *S. schenckii* Bitter |
| *Solanum simplicissimum* Ochoa | Tertiary | | PER | 2x (1EBN) | 3 | *S. simplicissimum* Ochoa (1989b) |
| *Solanum sogarandinum* Ochoa | Secondary | M | PER | 2x (2EBN), 3x | 4 | *S. sogarandinum* Ochoa |
| *Solanum stenophyllidium* Bitter | Tertiary | | MEX | 2x (1EBN) | 1 | *S. stenophyllidium* Bitter |
| | | | | | | *S. brachistotrichium* (Bitter) Rydb. |
| | | | | | | *S. nayaritense* (Bitter) Rydb. |
| *Solanum stipuloideum* Rusby | | | BOL | 2x (1EBN) | | *S. stipuloideum* Rusby7 |
| | | | | | | *S. circaeifolium* Bitter |
| | | | | | | *S. circaeifolium* subsp. *quimense* Hawkes & Hjert. |
| | | | | | | *S. capsicibaccatum* Cárdenas |
| | | | | | | *S. soestii* Hawkes & Hjert. |
| *Solanum stoloniferum* Schltdl. | Secondary | | MEX, USA | 4x (2EBN) | Complex[3] | *S. stoloniferum* Schltdl. |
| | | | | | | *S. fendleri* A. Gray |
| | | | | | | *S. fendleri* subsp. *arizonicum* Hawkes |

| Species name according to Spooner et al. (2014) | Genepool | Priority levels | Countries | Ploidy level | Nuclear Clade | Taxon according to Hawkes (1990) or subsequental authors |
|---|---|---|---|---|---|---|
| | | | | | | *S. papita* Rydb. |
| | | | | | | *S. polytrichon* Rydb. |
| | | | | | | *S. stoloniferum* subsp. *moreliae* Hawkes |
| *Solanum tarnii* Hawkes & Hjert. | Tertiary | M | MEX | 2x | 1 | *S. tarnii* Hawkes & Hjert. |
| *Solanum trifidum* Correll | Tertiary | | MEX | 2x (1EBN) | 1 | *S. trifidum* Correll |
| *Solanum trinitense* Ochoa | Tertiary | | PER | 2x (1EBN) | 3 | *S. trinitense* Ochoa |
| *Solanum* ×*vallis-mexici* Juz. | | | MEX | 3x | | *S.* ×*vallis-mexici* Juz. |
| *Solanum venturii* Hawkes & Hjert. | Secondary | H | ARG | 2x (2EBN) | 4 | *S. venturii* Hawkes & Hjert. |
| *Solanum vernei* Bitter & Wittm. | Primary | L | ARG | 2x (2EBN) | 4 | *S. vernei* Bitter & Wittm. |
| | | | | | | *S. vernei* subsp. *ballsii* (Hawkes) Hawkes & Hjert. |
| *Solanum verrucosum* Schltdl. | Secondary | M | MEX | 2x (2EBN), 3x, 4x | 4 | *S. verrucosum* Schltdl. |
| | | | | | | *S. macropilosum* Correll |
| *Solanum violaceimarmoratum* Bitter | Secondary | H | BOL, PER | 2x (2EBN) | 4 | *S. violaceimarmoratum* Bitter |
| | | | | | | *S. multiflorum* Vargas |
| | | | | | | *S. neovavilovii* Ochoa |
| | | | | | | *S. urubambae* Juz. |
| | | | | | | *S. villuspetalum* Vargas |
| *Solanum wittmackii* Bitter | Tertiary | | PER | 2x (1EBN) | [3] | *S. wittmackii* Bitter |
| *Solanum woodsonii* Correll | | | PAN | 4x | 4 | *S. woodsonii* Correll |
| *Solanum tuberosum* L. *Chilotanum* group | | | CHL (Chilean landraces) | 4x (4EBN) | 4 | *S. tuberosum* subsp. *tuberosum* |
| *Solanum tuberosum Andigenum* group | | | Landraces from W Venezuela South to N Argentina | 2x (2EBN), 3x, 4x (4EBN) | 4 | *S. chaucha* Juz. & Bukasov |
| | | | | | | *S. phureja* Juz. & Bukasov |
| | | | | | | *S. phureja* subsp. *estradae* (L. López) Hawkes |
| | | | | | | *S. phureja* subsp. *hygrothermicum* (Ochoa) Hawkes |
| | | | | | | *S. stenotomum* Juz. & Bukasov |
| | | | | | | *S. stenotomum* Juz. & Bukasov subsp. *goniocalyx* (Juz. & Bukasov) Hawkes |
| | | | | | | *S. tuberosum* subsp. *andigenum* Hawkes |
| *Solanum ajanhuiri* Juz. & Bukasov | | | BOL, PER | 2x (2EBN) | 4 | *S. ajanhuiri* Juz. & Bukasov |
| *Solanum curtilobum* Juz. & Bukasov | | | BOL, PER | 5x | 4 | *S. curtilobum* Juz. & Bukasov |
| *Solanum juzepczukii* Bukasov | | | ARG, BOL, PER | 3x | 4 | *S. juzepczukii* Juz. |

Species in brackets have not yet investigated, relationships were proposed by Spooner et al. (2014) based on morphological similarity; Complex[3] and [4] indicate the complex multi-clade hybrid origins of these species.


Potatoes in market, Huancayo, Peru.
Photo: Michael Major/Crop Trust

# 4 POTATO PRODUCTION AND DIVERSITY

After wheat and rice, cultivated potato is the third most important food crop for human consumption (FAOSTAT, 2021b) and source of primary income for many societies around the world. It is primarily grown for direct consumption markets but also provides raw material for processed products such as frozen chips, crisps, preserved potatoes and starch (EUROSTAT, 2021).

## 4.1 Economic importance

Potato is the world's most important non-cereal food crop, with a global production of 370 million tonnes (FAOSTAT, 2021b) (Annex 2, Annex Table 2.1). Most varieties grown (approximately 99%) belong to *S. tuberosum* ssp. *tuberosum* and are produced for local markets as tubers, with their limited storability restricting global distribution (Haverkort and Struik, 2015). However, Haverkort and Struik (2015) reported that companies in the Netherlands export 600,000 to 800,000 t of seed potato annually to Cuba and Bangladesh.

The highest potato production can be found in Asia with 189.9 million t on 9.3 million ha, followed by Europe with 107.3 million t on 4.7 million ha, America with 45.1 million t on 1.54 million ha and Africa with 26.5 million t on 1.76 million ha (Figure 4.1.1 a). Countries with the highest production are China (91.8 million t), India (50.2 million t), Russia (22.1 million t), Ukraine (20.3 million t), USA (19.2) and Germany (10.6 million t) (FAOSTAT, 2021b). Although Eastern Africa, South America and Eastern Europe cultivate potatoes on a wider area, production is more intensive in Northern Africa, America and Western Europe and therefore production volumes are higher (Figure 4.1.1 b) (FAOSTAT, 2021b). However, a large increase in area has been registered over the last 20 years in African countries, and in 2005 the production volume of developing countries, including India and China, exceeded for the first time the developed world, indicating that the importance of the potato for diets, employment and income is increasing in Asia, Africa and Latin America (Devaux et al., 2020).

In the last 60 years, potato production volume increased by 37% (Figure 4.1.1 d), and yield also increased significantly (+75%, Figure 4.1.1 c). On average, the global potato yield was 21.4 t ha$^{-1}$ and achieved the highest values in Kuwait (50.6 t ha$^{-1}$), USA (50.3 t ha$^{-1}$), New Zealand (49.8 t ha$^{-1}$) and Denmark (42.5 t ha$^{-1}$). The highest yields were most likely achieved by large commercial farms using all available inputs optimally in 2019 (FAOSTAT, 2021b). In rainfed agriculture, potatoes have some important advantages over cereals due to their harvest index (ratio of harvested product to total biomass) of 0.75–0.95 (Haverkort and Struik, 2015) compared to cereals of about 0.4–0.6 (Hay, 1995). In addition, potato produces 5,600 kcal per m³ of water, which is +45%, +243% and +280% higher compared to maize, wheat and rice, respectively (Monneveux et al., 2013). Potato is also cultivated at high elevation and poorer soils and contributes substantially to the daily intake of energy and nutrients, especially in remote areas (Scott, 2011). Therefore, as a locally traded product, potato is essential for regional food security and poverty reduction (George et al., 2017).

Potato use and economic importance differ across regions. In Europe, potato was initially a luxury good and yet developed into a crop for the poor due to strong political promotion. This support led to economic growth and welfare over the last two centuries and potato became even a staple inferior good (i.e. its demand decreases when consumer income increases). However, rising income stimulates diversification of food consumption (Salmensuu, 2021). The shift towards cereals in animal feeding and trends for low-calorie diets and to spend less time in cooking led to reductions in the amount of potato consumed in developed countries (EUROSTAT, 2021). By contrast, in developing countries, the level of use is still relatively low. Here, potato is slowly establishing as a staple food and, therefore, the price levels are still higher (Salmensuu, 2021). However, promoting policies, such as those conducted in China (Liu et al., 2021), could stimulate sustainable potato farming systems and the economy and welfare of the country.

Cultivated potato is produced for different types of markets. These include specific table varieties used at home and in restaurants which show specific skin type and flesh and skin coloration. The French-fry industry asks for elongated tubers with long dormancy. The chip-processing industry is interested in a high starch content and low accumulation of reducing sugar at 10°C storage to avoid Maillard reactions and browning (Hirsch et al., 2013). As the '*Petota*' group is very

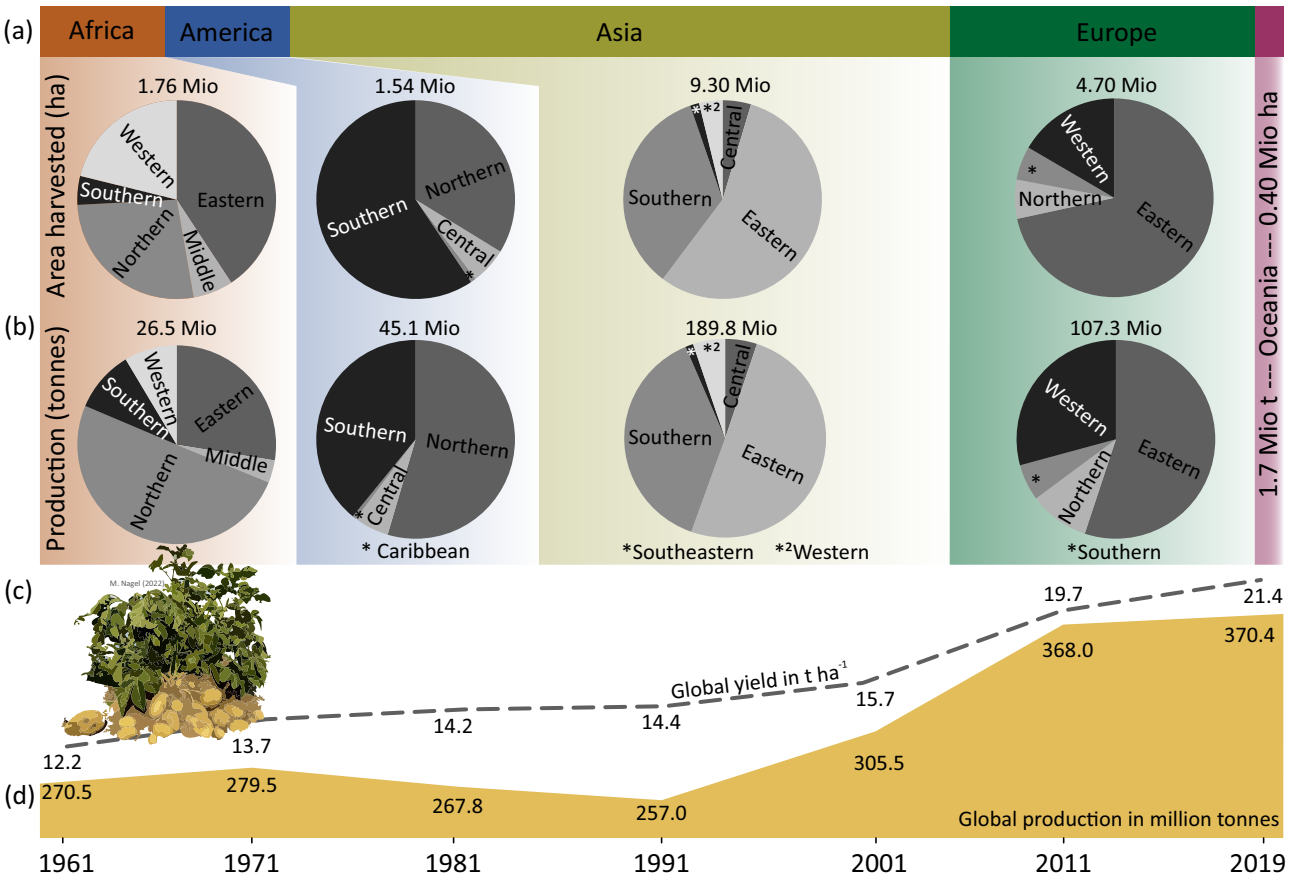



**Figure 4.1.1.** Global potato production and area harvested. (a) Area harvested and (b) production volume shown for different regions on five continents in 2019. Development of (c) yield and (d) global potato production over the last 60 years. Source: FAOSTAT, 2021b, *as explained in the figure.

diverse, potato genetic resources can have a valuable impact on these industries. However, in order to assess these genetic resources, they need to be comprehensively described, evaluated and integrated into breeding programs.

## 4.2 Potato development, descriptors and potato diversity

Potatoes are herbaceous perennial plants grown in different temperate climates. **Potato growth and developmental stages** can be divided into four major phases (Figure 4.2.1) **a)** the vegetative growth with the development of shoots and leaves; **b)** tuber initiation with the emergence of tubers at the end of the stolons; **c)** the growth of tubers and their significant increase in size; and **d)** final maturation, when the leaves senesce and tuber skin thickens. Depending on the environmental conditions, the genotype used, and hence the specific production system (see below), the developmental period can last between 90–180 days and can be divided into specific stages according to the Biologische Bundesanstalt für Land- und Forstwirtschaft, Bundessortenamt und CHemische Industrie (BBCH) scale (Figure 4.2.1).

For **optimum growth** (George et al., 2017), most potatoes require a minimum temperature of 6°C for sprouting and show optimal tuber development in a range between 18–20°C, a soil temperature between 15- 18°C and a water potential of -25 kPa. Intense drought stress impairs cellular functions and occurs when water potential is at or below – 0.8 MPa. Higher soil temperatures in combination with elevated air temperatures can also cause severe stress. At temperatures above 38°C, photosystem II is irreversibly destroyed.

Depending on the climatic conditions in the areas of cultivation, production has been adapted to the most appropriate season. Thereby, Haverkort and Struik (2015) identified six cropping systems:

**Rainy summer:** production occurs during the frost-free period under rain-fed conditions, occasionally irrigation is used. Long growing seasons (180 days) and long

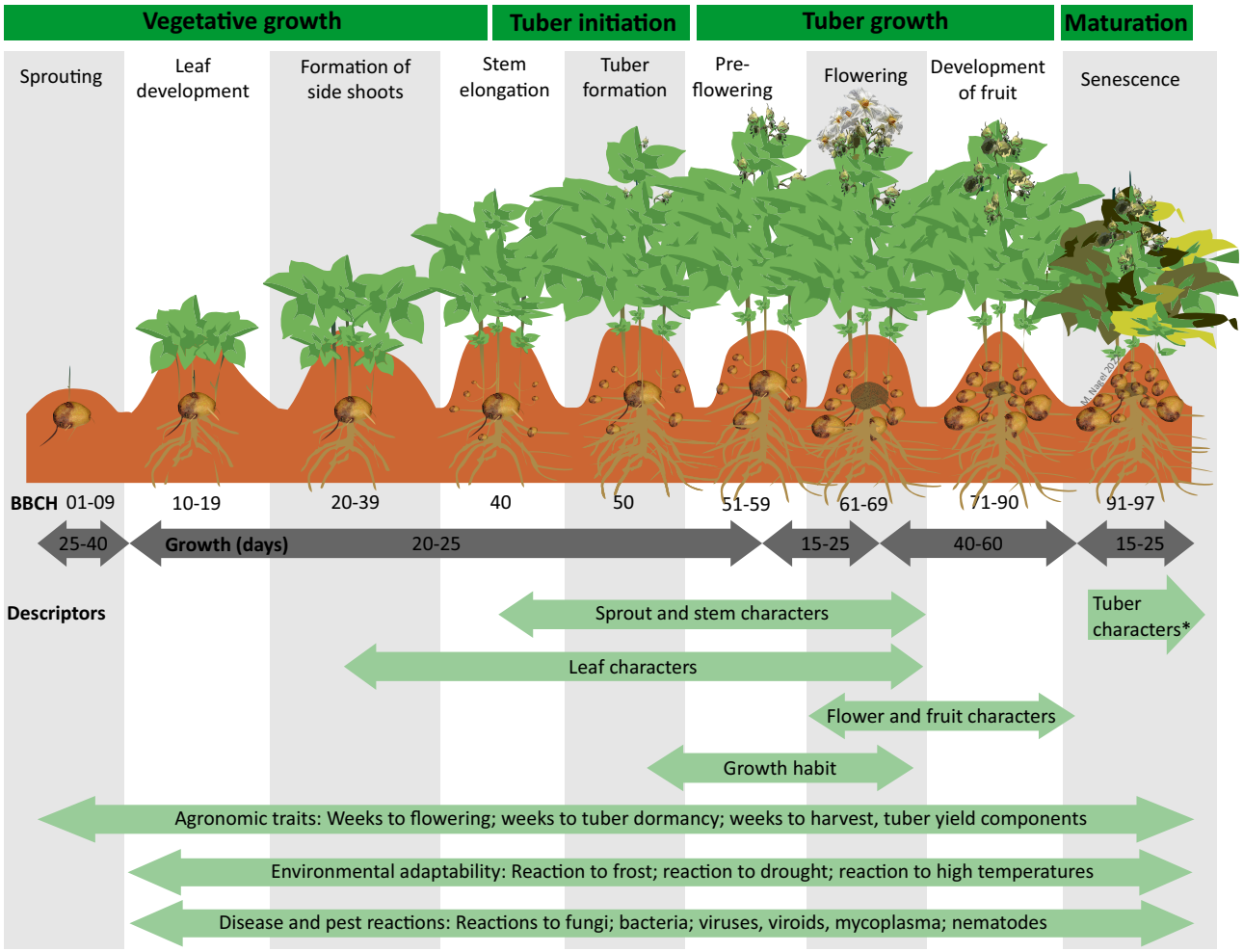



**Figure 4.2.1.** Stages of potato development and applied descriptors to characterise and evaluate potato genetic resources. Data on growth stages are based on Nemes et al. (2008) and descriptors are based on Huaman et al. (1977). * Tubers are characterized on basis of their morphology [color, shape, skin, flesh) and can be evaluated on basis of their biochemical traits (dry matter content, total nitrogen content, relative nutritive value, total glycoalkaloids (TGA)].

day-lengths lead to high yields, e.g. in Europe and South Africa's High Veld.

**Dryland summer:** high solar radiation in combination with optimum irrigation achieve highest potato yields; in the north western United States and Kuwait.

**Partly irrigated spring**: potatoes grow over winter (110 days) and are harvested in spring, e.g. in Mediterranean climates, North Africa, South America and South Africa.

**Irrigated autumn**: after the hot summers, potatoes are cultivated over autumn (100 days) and are harvested before winter, yields are usually low due to low solar radiation; e.g. in Mediterranean climates.

**Irrigated winter**: cultivation after the rainy summer (90–100 days) during the heat-free period; found in areas with monsoon climate.

**Equatorial highlands**: production under rain-fed conditions in two main growing seasons (100 days each); above 1,800 m in East and Central Africa.

In order to identify and describe potato genetic resources suitable for the different production systems and climatic conditions, a descriptor list for potato was developed at the planning conference of on "Utilization of the genetic resources of the potato II" held at CIP in October 1977 (Huaman et al., 1977). The descriptors involve a list of relevant passport information, data on germplasm collections and morphological traits to be phenotyped during and after the growing season. In addition, to describe the detailed characteristics of potato varieties, a form has been developed by the International Union for the Protection of New Varieties of Plants (UPOV). Comparable to the descriptor list for potato genetic resources (Huaman et al., 1977), the UPOV list (UPOV, 2004) includes sprout, stem, tuber, leaf, flower, fruit, plant type and growth habit characters (Figure 4.2.1). Furthermore, disease and pest resistances are often evaluated using standardized tests, or responses to other abiotic and biotic stresses are documented through additional experimental setups. However, most potato collections have chosen to use their own specific list of descriptors. Examples of described traits at the different stages of development are provided Figure 4.2.2 to 4.2.5).

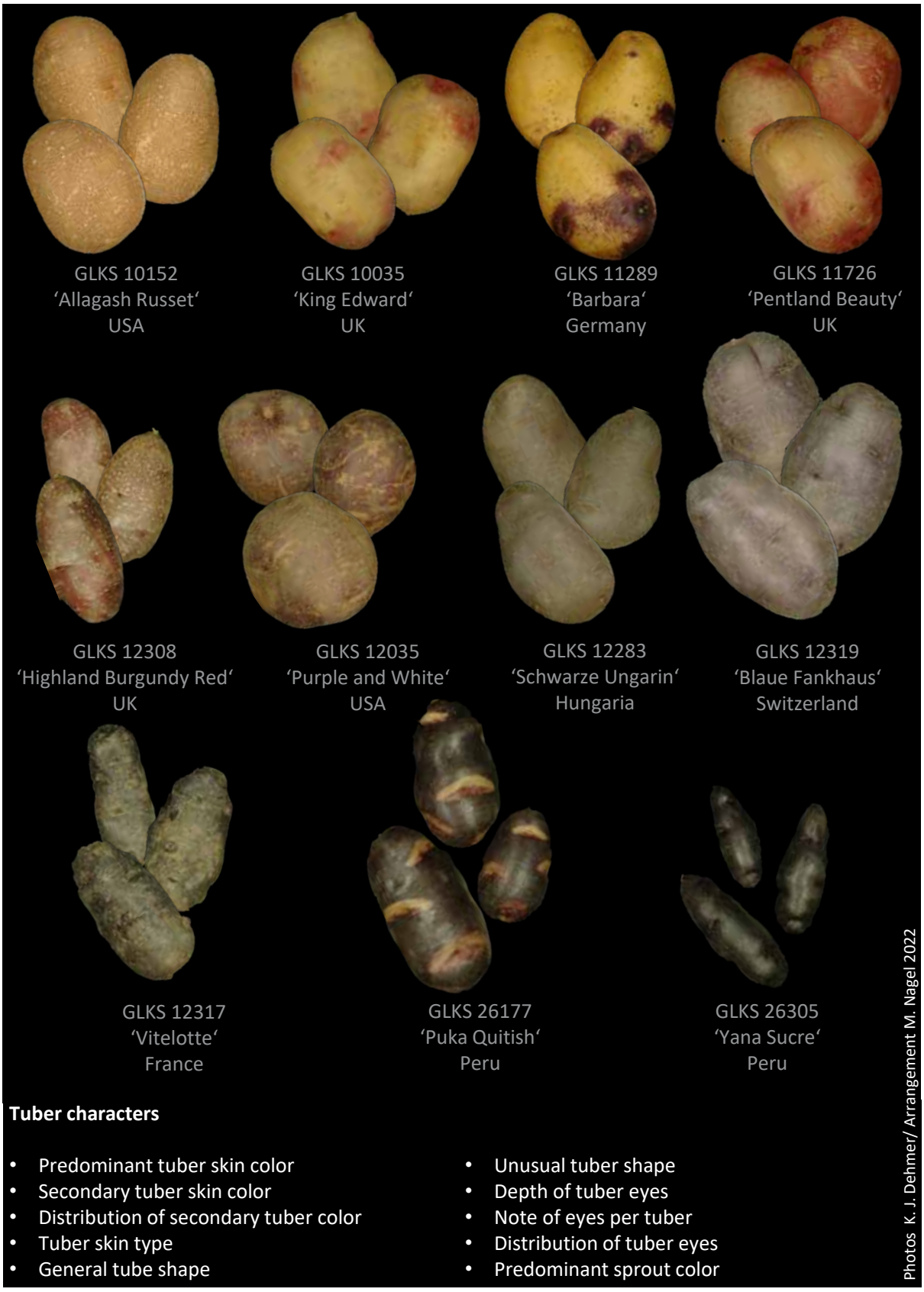



**Figure 4.2.2.** Cultivated potatoes differing in tuber skin color, type, shape and tuber eye distribution (Photos: Klaus J. Dehmer; Photo arrangement: Manuela Nagel, IPK, 2022).

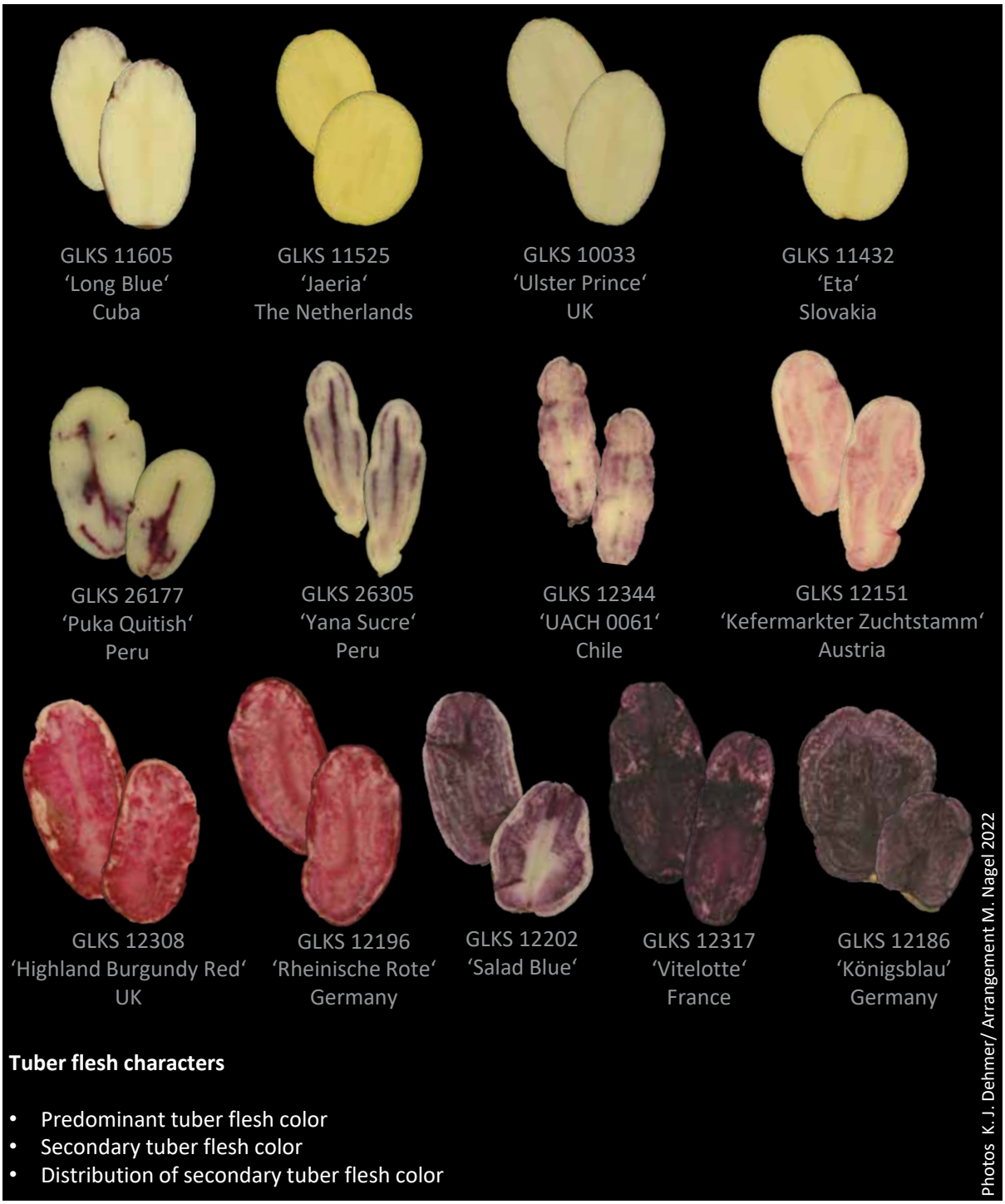



**Figure 4.2.3.** Cultivated potatoes differing in tuber flesh color and distribution of flesh color (Photos: Klaus J. Dehmer; Photo arrangement: Manuela Nagel, IPK, 2022).

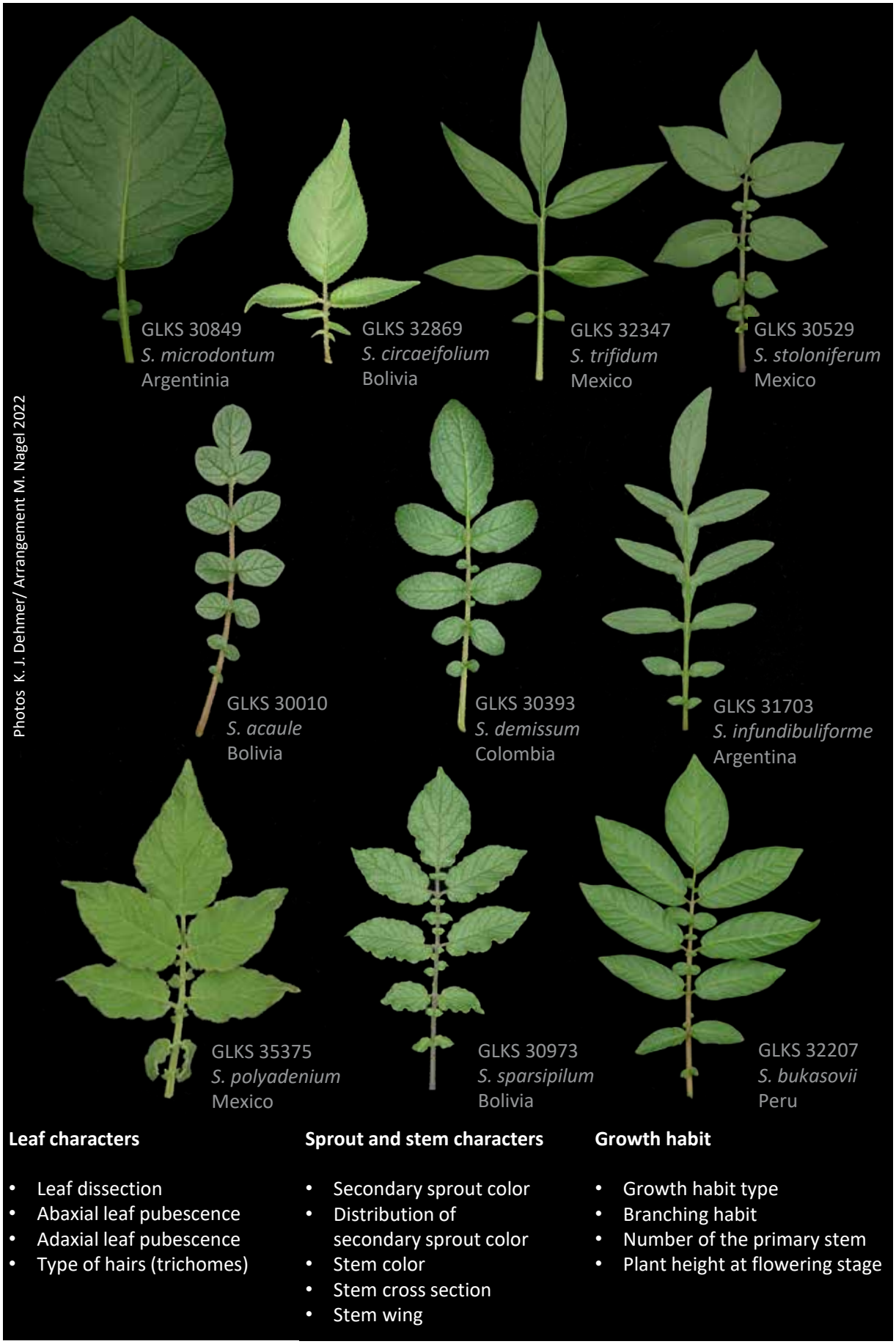



**Figure 4.2.4.** Wild potatoes differing in leaf dissection, pubescence and type of hair on the leaf surfaces (Photos: Klaus J. Dehmer; Photo arrangement: Manuela Nagel, IPK, 2022).


**Figure 4.2.5.** Cultivated and wild potatoes differing in flower and fruit characters (Photos: Klaus J. Dehmer; Photo arrangement: Manuela Nagel, IPK, 2022).

Field work of Aguapan farmers in the Andean highlands at 3,500 m. Photo: Manuela Nagel/IPK

# 5 *IN SITU* CONSERVATION OF NATIVE POTATO VARIETIES

Traditional landraces of potato have been cultivated in South America for millennia and are still grown by smallholder farmers between western Venezuela and northern Argentina and along the coast of Chile (De Haan and Rodriguez, 2016). Most landraces are cultivated in the Andes (Cadima et al., 2014). Farmers, their families and communities aim to preserve these valuable food resources in combination with traditional cultivation practices, uses, cultural traditions and beliefs (Scott, 2011; Lüttringhaus et al., 2021). The wild relatives of *S. tuberosum* are restricted to an area between the southwestern United States and the southern end of South America (Spooner et al., 2014). The local landraces and the wild species occurring across their natural range represent a huge reservoir of genetic and morphological diversity important for potato breeding, for the adaptation to environmental changes and for resistance to pest and diseases. The conservation of the genetic resources of native potato germplasm *in situ* and on farm is critically important to sustain the productivity of this major global crop.

## 5.1 Threats to native potato diversity

### Potato landraces

Indigenous farmers, in particular in Argentina, Bolivia, Chile, Ecuador and Peru, grow more than 3,000 native potato varieties in South America (Spooner et al., 2014), many of which are threatened by various recent developments. In northern **Argentina**, the number of local varieties grown is declining in some areas, due to: (i) displacement by other crops, (ii) threats from pests and diseases, (iii) low accessibility of clean virus-free material of local varieties, and (iv) the migration of the farmers and their families towards urban centers (Ispizúa et al., 2007). In **Ecuador**, local landraces of potato are threatened with extinction because traditional varieties are being replaced by new high-yielding varieties, more pest and disease pressure and the lack of market opportunities (Unda et al., 2005). In **Chile**, indigenous and peasant communities grew between 800 to 1,000 native potato varieties; nowa-

days, only 270 local varieties are cultivated according to the Austral University of Chile. In **Peru**, a total of 42 landraces were identified in the communities Haquira – Pauchi, Queuñapampa and Huancacalla Chico, of which 13 were considered as threatened, eight were conservation-dependent and three were not at risk of loss. Among the reasons for this, many young farmers abandon agriculture and search for attractive options with higher income (Valdivia-Díaz et al., 2015). However, local traditions and customs have maintained the local diversity of potato landraces relatively well, and heavy declines as seen for other crops have not been observed yet (De Haan and Rodriguez, 2016).

The diversity of potato resources is also severely threatened by the effects of climate change, including increases in temperature, change in spatial and temporal patterns of precipitation and phenomena associated with El Niño. Hijmans (2003) assessed the impact of climate change on global potato production and predicted that between 1961–1999 and 2040–2069, global potato yield potential could decrease by 18% (without adaptation), especially in lower latitude areas. Some of the risks to the production of rain-fed potato crop in Peru include climatic disasters, e.g. the El Niño drought in the southern highland in 1983 and severe flooding near Cusco in 2010 (Scott, 2011). Furthermore, the potato wild relatives are under enormous pressure from habitat loss and environmental degradation, as a result of climate change, which makes habitats unsuitable for these species and could cause their extinction. About 16–22% of wild populations of potato species are predicted to go extinct, with possibly losing 50% of their range size by 2055 (Jarvis et al., 2008).

## Wild potato species

At the global level, 26 wild potato species have been assessed by the International Union for Conservation of Nature (IUCN) Red List, of which 19 are considered as priority potato crop wild relatives (Vincent et al., 2013). Among the assessed species, 16 are classified as Least Concern (61.5%), four as Endangered (15.4%), two as Near Threatened (7.7%), two as Vulnerable (7.7%) and two as Data Deficient (7.7%) (Table 5.1.2.1). In **Argentina**, seven endemic wild potato species were assessed according to the IUCN Red List and *S.* x*brucheri* was classified as Near Threatened, *S.* x*rechei* as Vulnerable and the remaining five as of Least Concern (Palchetti et al., 2020).

In **Bolivia,** the assessment of the vulnerability of the 21 endemic potato wild relatives (Cadima et al., 2014) revealed that five endemic potato species (24%) are classified as Critically Endangered, four as Endangered (19%), six as Vulnerable (28%) and the remaining six as either Near Threatened or of Least Concern (28%). Human access, fire and livestock pressure were reported as the main threats, substantially impacting all the species. The most threatened species were *S. achacachense* (EN), *S. arnezii* (VU), *S. brevicaule* (LC), *S. flavoviridens* (CR), *S. hoopesii* (EN), *Solanum ugentii* Hawkes & K.A. Okada (EN) and *S. sucrense* (NT). Four of these seven species were spotted in only a few areas. Therefore, Cadima et al. (2014) identified sites of approximately 50 km$^2$ to conserve all 21 endemic wild potato relatives of Bolivia, including *S. achacachense* (EN) in La Paz and the endangered *S. hoopesii* and *S. ugentii* in Chuquisaca.

**Table 5.1.2.1**. The IUCN Red List categories of priority *Solanum* section *Petota* crop wild relatives (https://www.iucnredlist.org/, accessed on 21st April 2020). Priority *Solanum* crop wild relatives according to Vincent et al. (2013) are indicated by **. LC, least concern species; EN, endangered species; NT, near threatened; VU, vulnerable species; DD, data deficient.

| Scientific name | IUCN status | Scientific name | IUCN status |
|---|---|---|---|
| *Solanum agrimonifolium*** | LC | *Solanum jamesii* | LC |
| *Solanum albornozii* ** | EN | *Solanum lesteri*** | DD |
| *Solanum bulbocastanum*** | LC | *Solanum minutifoliolum* | LC |
| *Solanum cardiophyllum* | LC | *Solanum morelliforme*** | LC |
| *Solanum chilliasense*** | VU | *Solanum oxycarpum*** | EN |
| *Solanum clarum*** | VU | *Solanum pinnatisectum* | LC |
| *Solanum demissum*** | LC | *Solanum polyadenium*** | LC |
| *Solanum ehrenbergii* | LC | *Solanum schenckii*** | EN |
| *Solanum guerreroense*** | DD | *Solanum stenophyllidium* | LC |
| *Solanum hintonii*** | NT | *Solanum stoloniferum*** | LC |
| *Solanum hjertingii*** | LC | *Solanum tarnii*** | EN |
| *Solanum hougasii*** | LC | *Solanum trifidum* | NT |
| *Solanum iopetalum*** | LC | *Solanum verrucosum*** | LC |

## 5.2 *In situ* conservation projects in Latin America

### Peru

Peru has the largest number of landraces and wild species of potato. Following the classification of Hawkes (1990), seven domesticated species with 3,000 landraces/native varieties and 91 wild species are native to Peru. Since 1990, the conservation of native potatoes in Peru has been supported by a series of *in situ* conservation projects. Non-governmental organization (NGO) groups, scientists and research organizations (Scott, 2011) work closely with farmers on *in situ* conservation of native potato varieties. In particular, NGOs provide technical assistance, training in conservation approaches, support exchange of native varieties and create community-based diversity repositories. They also help repatriate varieties collected in local communities and support the development of new/improved products from indigenous potato varieties. The NGO Centro IDEAS in Cajamarca, for example, supports local farmers in the *in situ* conservation of over 130 varieties. They register and utilize local native potatoes and document traditional cultivation approaches and local knowledge (Scott, 2011). Within the local communities, there are some farmers, also known as stewards or "conservacionistas" or "cuidadores" of biodiversity who pursue many of the traditional conservation practices. Further studies and inventories of plant genetic resources including potato local varieties have also been carried out in the regions of Cusco, Huánuco, San Martín, Apurímac, Piura, Arequipa, Cajamarca, Lima, Puno, Loreto and Ucayali (Gallardo et al., 2009).

The most important *in situ* project, implemented by the Instituto Nacional de Innovación Agraria (INIA), the Peruvian Amazon Research Institute (IIAP), and the NGOs ARARIWA Association, Agrarian Services Center, Proyecto of Campesino Technological Alternatives and Coordinator of Andean Science and Technology, is the UNDP/GEF funded project "*In Situ* Conservation Project for Native Crops and their Wild Relatives". It ran between 2001–2006 and supported the national *in situ* conservation of several crops, including potatoes. The project has contributed to conserving plant genetic resources as an important natural heritage by

- preserving agrobiodiversity in farmers' fields,
- protecting wild relatives,
- strengthening peasant organizations,
- raising awareness about the ecological, cultural and nutritional value of crops,
- developing policies to support *in situ* conservation,
- developing and consolidating markets, and
- developing an information and monitoring system, as a tool for planning and coordinating agrobiodiversity conservation activities in Peru.

The project participants have also established microgene centers of biodiversity of Andean tubers and maintain an inventory of 11 priority crops, among them potato, in 472 conservationist farms involving 154 communities from 53 districts in 12 regions.

The 'Potato Park' (Parque de la Papa), a well-known project supported by the International Treaty (FAO, 2009a), conserves native potato diversity in combination with its cultural landscape, including its agrobiodiversity, wild relatives and associated knowledge (see also chapter 5.3.2). The Potato Park comprises a high elevation valley of an area of 15,000 ha outside Cusco, Peru and is organized by five different farming communities. The communities maintain their own genebank to foster diversity awareness and exchange of landraces.

The International Potato Center (CIP, PER00) in Lima has also provided significant support for *in situ* conservation of landraces since 1998 (Scott, 2011) and works with farmers in the Cusco region and other highland regions known to have high diversity of native potatoes, including the Potato Park. CIP provides clean virus-free native varieties, information and support to improve potato cultivation. Over 9,400 high quality samples of more than 1,300 native potatoes have been repatriated to more than 94 Andean farm communities in 12 regions of Peru during this period (Gomez et al., 2018; Lüttringhaus et al., 2021).

CIP has been actively documenting the diversity of native potato landraces in key hotspots in Peru as part of the CGIAR research program on Roots, Tubers and Bananas (CRP-RTB). The program aims to promote an integrated and complementary approach to the conservation and the use of the genetic diversity of five priority crops, including potato. A detailed study on the diversity of potato landraces in the Bolivian Altiplano and in Peru (Apurimac and Huancavelica) as well as in Pasco department was carried out. In particular, the Pasco department has a great geographical and ecological diversity ranging from altitudes of 5,723 m down to the Amazon basin. Overall, nine communities participated in the Pasco region. In each of the communities, so-called guardians maintain *in situ* between 49–81 different landraces/native varieties representing 3–5 different potato species. Following legal procedures and with the agreement of the indigenous communities, CIP managed to introduce 544 accessions into the international potato genebank.

Another CRP-RTB project led by CIP established a hotspot-based *in situ* network called 'Chiripaq Nan network' for a systematic monitoring of potato landraces (De Haan and Rodriguez, 2016). This involved the identification of landrace diversity hotspots within the native potato center of diversity in Argentina

(Jujuy Province), Bolivia (Department of La Paz), Chile (Chiloe Province), Colombia (Department of Nariño, Cauca Province), Ecuador (Chimborazo) and Peru (Departments of Cusco, Apurimac, Huancavellica and Huacanuco). The project documented total, relative and spatial diversity and collective knowledge.

### Bolivia

Bolivia is a country rich in traditions and cultures with *in situ* conservation and on farm management practices dependent on the indigenous knowledge of its people (Bolivia, 2009). Within the framework of the National System of Genetic Resources for Food and Agriculture (SINARGEAA), a complete inventory of potatoes, oca, papalisa and isaño was carried out in 2002, in the Candelaria microcenter of the municipality of Colomi, department of Cochabamba (Bolivia, 2009). In the North Potosí-Oruro microcenter, an inventory of native potatoes was made in eight communities of the Ayllus Chullpa, Aymaya, Thayaquira and Sullka region. These registers constitute varietal records or censuses containing information on the local names of the varieties, their distribution, frequency, and abundance. Inventories have also been made in other micro-centers around Lake Titicaca, such as Titijoni (Ingavi province), Cachilaya (Los Andes province) and Cariquina Grande (Camacho province).

PROINPA in Bolivia has also been active in implementing *in situ* conservation activities in microcenters of diversity detected in the Andean zone and covering the entire value chain from agricultural production, to transformation and marketing. For example, *in situ* conservation of the genetic diversity of native tubers in Candelaria, Cantón of Colomi, in the Department of Cochabamba is supported by the Belgian Government and executed by PROINPA, the Catholic University of Louvain la Nueva and Gembloux of Belgium, the Bolivian Private University, the municipality of Colomi, AIDAA, the Association of Andean Tubers Producers of Colomi (APROTAC) and other organizations. The results have been published in a book on the 'Promotion of the Diversity of Andean Tubers and their Products Transformed' (Bolivia, 2009).

The Bolivian Ministry of Environment and Water, Vice Ministry of the Environment, Biodiversity and Climate Change (MMAyA-VMABCC) has undertaken different actions related to research and conservation of crop wild relatives as a partner in the UNEP/GEF Global Project "*In Situ* Conservation of the Wild Relatives of Crops through the Strengthening of Information Management and its Application in the Field" during the period 2005–2009 (Hunter and Heywood, 2011). As an outcome, a Red Book of the crop wild relatives of Bolivia was published (Mora et al., 2009) that prioritized research work and generated considerable knowledge about the crop wild relatives of 16 genera of food crops, including potato. Furthermore, capacities and a national information system on crop wild relatives was developed that integrates the information dispersed among national institutions and manages information for spatial analysis.

### Ecuador

In Ecuador, 23 wild species, and 3 cultivated species, *S. phureja*, *S. chaucha* and *S. tuberosum* subsp. *andigena* (Monteros-Altamirano, 2011), including more than 400 landraces of native potatoes, have been reported (Unda et al., 2005; Monteros-Altamirano, 2018). The number of landraces grown for subsistence purposes is hardly known but perhaps only 5% is offered in markets (Unda et al., 2005). Two improved varieties (INIAP 'Gabriela' and 'Superchola') occupy more than half of the cultivation area (Andrade et al., 2002). To study the dynamics of potato cultivation in the provinces of Carchi, Chimborazo and Loja, the potato diversity was compared between the 1970s, the 1980s and 2006–2008 (Monteros-Altamirano, 2011; Monteros-Altamirano, 2018). Potato farmers were interviewed and new landraces and names were discovered indicating change of the contemporary system. However, potato farmers highly appreciate current developments of diversity fairs and re-introduction of landraces to maintain cultural heritage.

### Argentina, Chile, Brazil

In **Argentina**, much efforts have been expended towards the on farm conservation of plant genetic resources, which include important crops for subsistence agriculture such as potato (Argentina, 2008). In Puna and Prepuna, organizations such as Instituto Nacional de Tecnología Agropecuaria (INTA), Universidad Nacional de Mar del Plata (UNMdP), National University of Jujuy (UNJu) and Universidad Nacional de Salta and different NGOs work collaboratively for the *in situ* conservation of local potato varieties and their traditional knowledge, with a particular focus on culinary properties in combination with traditional and new recipes. The different organizations support also the fairs of different communities that take place once a month. Here, local farmers interchange crops and seeds for their own consumption and cultivation. Obtaining healthy seeds continues to be a problem, but INTA recently set up a laboratory for the production of healthy seed potatoes in the Abra Pampa station (personal communication Ariana Digilio, Argentina, 2022).

**Chile** is considered a center of origin of the cultivated potato and has important traditional varieties (Seguel and Agüero, 2008). In five Chilean regions, civil society organizations support the rescue of local seeds and

indigenous knowledge. The organizations promoted the concept of women guardians of local traditions to save, cultivate and exchange the seeds of ancient varieties. There have also been national initiatives for the rescue, protection, sanitation and commercialization, of value chains for the native potato varieties of Chiloé, executed by the Austral University of Chile with financial support of the Foundation for Agrarian Innovation (FIA) and participation of many local public and private partners. Furthermore, INIA (CHL071) has promoted the production of certified native seed potatoes from Chile through the delivery of healthy, pathogen-free tubers to custodian farmers interested in commercial seed production.

In **Brazil**, Heiden et al. (2017) have made a taxonomic revision of the wild species of potato to map the geographic distribution of herbaria samples and genebank accessions, and to identify gaps in *ex situ* collections. A total of 655 distribution data points were collected for the native potato species in Brazil. The accessions of potato and their wild relatives maintained at the Embrapa Clima Temperado genebank were evaluated for their morphological and agronomical characteristics. Their analysis showed that there are more taxa native to the country than previously recognized.

## 5.3 Complementarity with *ex situ* conservation

For successful conservation of all wild relatives of potato across their distribution range, it is important that *in situ* activities are complemented by *ex situ* conservation, as some of the endemic and rare crop wild relatives face serious threats that could imminently drive them to extinction. Threatened sites and species should be prioritized for collecting missions to retrieve germplasm accessions to be preserved in genebanks.

### *AGUAPAN* guardians in Peru

The Association of Guardians of the Native Potato of Central Peru (AGUAPAN), founded in Huancayo in 2014, is a self-organized association of potato farmers that strives to raise the wellbeing of their members while conserving this biodiversity (Naranjo, 2019). The farmers are known as 'guardians' and are passionate and show special interest in maintaining a collection of unique varieties, inherited from their families. However, they live in conditions of poverty, with limited access to health, education and value markets. AGUAPAN tries to raise support from the private sector and others and share benefits to improve farmers' living conditions. The association initially grouped 50 families from equal numbers of communities from five regions of Peru (Huánuco, Junín, Pasco, Huancavelica and Lima), who partnered to promote the conservation and use of the vast diversity of native potatoes from central Peru. Each AGUAPAN member cultivates between 50–300 varieties of native potatoes through sustainable management practices. This includes planting in *chaqru* or *wachuy* (variety mixtures) and uses technologies such as the *chakitaklla* plow that allows direct sowing, thus reducing soil erosion. AGUAPAN also promotes cooperation and solidarity among its associates, as well as the exchange of seeds, knowledge and experiences.

AGUAPAN is guided by five key principles: (1) **Openness**: Members of the association are those farmers who keep more than 50 varieties of native potato for more than two generations (father-son, mother-daughter) and are recognized by their community; (2) **Direct Deal**: Dialogue and investment between farmers and companies to share benefits without transaction costs; (3) **Self-determination**: They are their own custodians, who know the needs and what benefits they require; (4) **Trust and Transparency**: The information has to be shared among all partners; (5) **Good Governance**: The elected managers have clear responsibilities, promote gender equity and continually improve management.

The 'guardian' farmers live in geographically isolated communities and are not familiar with the international treaties which are in place to protect farmers' rights. AGUAPAN helps to raise awareness and knowledge of these custodian farmers on the role they play


Figure 5.3.1.1. AGUAPAN Guardians maintain unique native potato varieties in Peru. (Photo: Stephany Naranjo, 2019)

in conserving biodiversity for the whole of humanity and helps to find ways to improve their living conditions while conserving biodiversity.

AGUAPAN has been financially supported by a Dutch potato seed company (HZPC) and a Dutch cooperative (AGRICO) dedicated to potato breeding and seed production. The main investment has gone to support each farmer in the education of their children, agricultural inputs or family health. The rest of the funds are invested in paying for the annual assembly of AGUAPAN, a health fund to support farmers who need medical attention and the quarterly sessions of the board of directors.

### Parque de la Papa in Peru

The Parque de la Papa (Potato Park) was created in 1998 as a bio-cultural territory focused not only on the conservation of native potatoes but also on the conservation of the heritage of the six indigenous communities who inhabit the high elevation valley, 3,200–5,000 meters above sea level, outside of Cusco, Peru. The Potato Park is managed using the Indigenous Biocultural Heritage Area (IBCHA) model developed by Asociación ANDES, which incorporates contemporary science and conservation models with a rights-based governance built on the *ayllu* political and socio-economic system. The *ayllu* can be thought of as a community linked through mutual and shared respect of all elements in the natural surroundings, such as humans, animals, rocks, spirits, rivers, lakes, plants life, etc. (personal communication David Ellis, 2022).

The Potato Park and CIP have had a long-term collaborative agreement which includes the integration of science-based knowledge with the traditional knowledge of the five indigenous communities which make up the Potato Park and has involved a lasting relationship for the blending of *ex situ* and *in situ* conservation. The communities maintain the diversity of over 1,000 potato landraces, about 450 of which were repatriated from the CIP genebank as disease-free planting materials. CIP and the Papa Arariwa, or "Guardians of the Potato," have collaborated over the years in scientific experiments to understand, and develop lasting tools to ensure, sustainability in the park, considering very rapid climatic changes. Most recently, using disease-free material maintained *ex situ* at CIP, these experiments have looked at the effects of planting native landraces along an elevational gradient up to 4,500 meters above sea level. Experiments start with meetings between CIP scientists and community members to design the experiments and determine the landraces that will be used. This collaborative effort extends from planning to planting, monitoring, harvesting and evaluating the experiments. By this joint effort between an *ex situ* genebank and the native farmers who protect and maintain the culture and diversity *in situ*, the harmony of closing the gap between *ex situ* and *in situ* conservation is brought closer, with an enhanced understanding of the value to both (personal communication David Ellis, 2022).

### *In situ* conservation of wild potato germplasm in Argentina

To determine and prioritize specific sites as genetic reserves in Argentina, a literature search was combined together with field-based research (Marfil et al., 2015). *S. kurtzianum* was used as an example of a wild relative of potato in a protected nature reserve to devise a protocol for active monitoring of the populations in selected sites to ensure long-term conservation. Further, Garavano (2018) investigated *in situ* conservation to protect *S. commersonii* in the Paititi Private Natural Reserve (Buenos Aires). *S. commersonii* is known for its genes for resistance/tolerance to biotic and abiotic stresses and is thus important for genetic improvement. Sajama (2017) ranked this wild species as the one with the highest priority for conservation actions as it is one of the wild potato species losing the most geographical range.

The geographic data retrieved for wild potato species accessions from the INTA Active Germplasm Bank, Balcarce (ARG1347) revealed that 67% of the Argentine species of *Solanum* section *Petota* occurred in 18 protected areas distributed in 11 Argentinian prov-

**Figure 5.3.2.1**. Potato diversity during a celebration of Dia de la Papa at the Potato Park. (Photo: Dave Ellis, 2013)

inces, with higher species richness in the Northwest areas (Clausen et al., 2018). The following parameters were monitored for *S. kurtzianum* during 2006–2014: number of plants per population, tuber sprouting behaviour, pollen viability, seed germination, Amplified Fragment Length Polymorphism (AFLP) markers. Over the nine years of monitoring, pests (*Epicauta* spp.) causing plant defoliation were detected. The sprouting of tubers was found to be asynchronous, which could be an escape strategy for pest and disease resistance. Population counts and pollen viability showed significant variation between the years (Marfil et al., 2015). This work supports the revision and improvement of management plans and conservation of these genetic resources.

Furthermore, Kozub et al. (2019) identified specific characteristics during monitoring of four wild potato species (*S. acaule, S. boliviense*, *S. brevicaule*, *S. vernei*) in Los Cardones National Park (LCNP). However, for comprehensive conservation, the consolidation of a single genetic reserve for all the wild potato species in LCNP is necessary. First steps have already been taken and a nature trail called "Sendero de la papa" has been established in the Valle Encantado sector, where the local communities but also tourists can visit and learn about wild potato species (Kozub et al., 2020).

## 5.4 Current challenges of *in situ* conservation

Although many programs and projects have been initiated in the last decades, there are still major challenges and limitations for supporting *in situ* conservation of traditional landraces and wild species of potato in the countries of origin. These include the following:

**More inventories required.** Lack of information about number of distinct landraces, wild species and their ecogeographic distribution, including missing information about genotype, economic value (tuber flavor, texture, stress resistances) and vulnerability status of wild relatives and their habitats limits the possibilities for *in situ* conservation. Therefore, comprehensive inventories are needed, and data must be publicly accessible in databases.

**Support for on farm and *in situ* conservation.** Specific areas need to be identified as priority sites for wild species and considered for national genetic reserves. Marketing strategies and additional economic support can compensate for lower profitability of products derived from varieties preserved on farm, and stimulate farmers to grow traditional varieties and conserve wild relatives in nearby areas.

**Increase of training possibilities.** Technical expertise of farmers and guardians for *in situ* conservation and knowledge transfer must be improved among the plant genetic resources community.

**Availability of virus-free plant material.** The availability of healthy propagules is severely limited and chains must be improved to provide clean tubers of local varieties to interested farmers.

International Potato Center genebank. Lima, Peru. Photo: Luis Salazar/Crop Trust

# 6 POTATO *EX SITU* COLLECTIONS

## 6.1 *Ex situ* conservation and priorities in genebanks

Although genebanks represent a very cost-efficient conservation approach, genebank operations can face several challenges, including the loss of unique material and the risk of genetic erosion if germplasm cannot be maintained and/or regenerated under optimal conditions and/or other political or environmental circumstances require re-organization (Fu, 2017). Following and complementing Fu (2017), Figure 6.1.1 represents a prioritization of the genebank's most important activities if processes have to be rationalized. Germplasm maintenance has the highest priority, followed by germplasm regeneration and duplication, data management, germplasm distribution, acquisition, gap analysis and collecting, germplasm evaluation and characterization and supportive research to improve germplasm collections. Depending on the type of accession (variety, breeding line, landrace, wild species), the management of potato collections is linked to the corresponding plant organ to be preserved (seed, tubers, *in vitro* plantlets, shoot tips) and the aspects are addressed in the listed chapters.

## 6.2 Historic potato collection missions

**Russia (RUS001)**. The first missions to systematically collect potato genetic resources in South America were carried out by Russian scientists involving Yurii Voronov and Sergei Bukasov in 1925–1926, Sergei Juzepczuk between 1926–1928 and Nikolai Vavilov in 1930–1933 (Loskutov, 1999). The material was collected in Colombia, Ecuador, Peru, Bolivia and Chile (Ovchinnikova et al., 2011; Spooner et al., 2014) and was the basis for the first potato germplasm collection of the N. I. Vavilov Institute of Plant Industry (VIR) in Leningrad, today the N. I. Vavilov Institute of Plant Genetic Resources (VIR) in St. Petersburg (Ovchinnikova et al., 2011). After detailed analysis, Juzepczuk and Bukasov (1929), Bukasov (1933) and Vavilov (1935 ) concluded that potato was domesticated independently in the Peruvian-Bolivian plateau and in southern Chile, and they proposed about 20 wild potato species progenitors that are endemic to these countries. Later, between 1955–1990 Russian scientists systematically collected more than 6,100 further accessions of wild and cultivated potato species in ten South American countries (Gorbatenko, 2006).

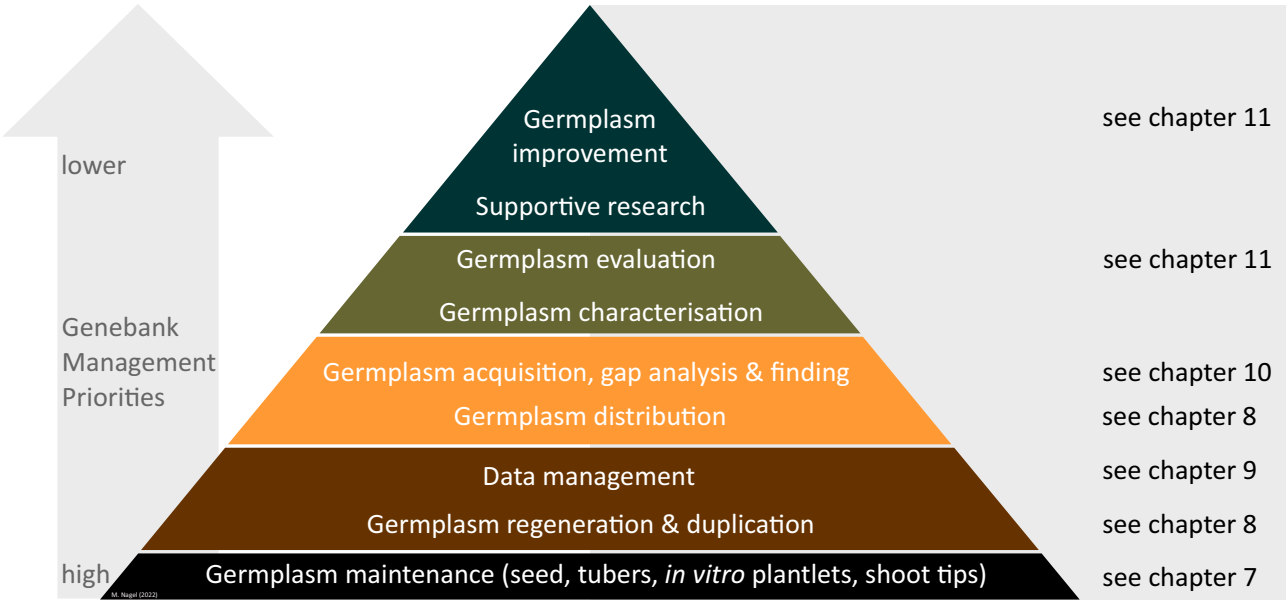



**Figure 6.1.1.** Management priorities in genebanks and relevant chapters for potato conservation management. Adapted and modified from Fu (2017).

**Germany (DEU159)** organized several expeditions to collect potatoes, among other crops, including missions to Chile and Bolivia in 1930–31 (Müntz and Wobus, 2013), 1958 to Central America, 1988 to Peru and Colombia and 1989 to Peru. Since 1949, the material has been maintained at the Groß Lüsewitz Potato Collections (GLKS) near Rostock, and in 1998 the potato varieties collection of Braunschweig Genetic Resources Center (BGRC, DEU001), were integrated with this. Currently, the GLKS comprise 2,845 accessions from South and Central America and over 2,800 accessions of cultivated potatoes from Europe and North America. Intensive work on the taxonomy of *S. tuberosum* L. was carried out in particular by S. Danert in the 1950s and 60s (Gäde, 1998).

**United Kingdom (GBR251).** Parts of Scotland were severely affected by late blight in the 1840s. When blight-resistant hybrids were discovered in the Royal Botanic Garden in Edinburgh, British expeditions were sent to Mexico and South America between 1938–1939. The collectors, including the British taxonomist Jack G. Hawkes, were particularly interested in the cultivation of potatoes from true seeds in southern Colombia and northern Ecuador. A total of 1,164 accessions of wild and cultivated potato species were collected in Argentina, Bolivia, Peru, Ecuador, Colombia and Mexico (Hawkes, 1941) and formed the basis of the so-called Commonwealth Potato Collection (CPC), which is now held at the James Hutton Institute at Invergowrie Dundee, Scotland.

USA (USA004). The U.S. Potato Genebank was established in the late 1940s with the aim of avoiding the import of varieties from abroad that might pose a threat to the potato industry or endemic wild species. Two species were found to originate in the USA (Bamberg et al., 2003). Therefore, collecting missions were conducted within the USA. Since the 1990s, the late D.M. Spooner contributed significantly to the taxonomic classification of Solanaceae species and organized several collecting missions, together with colleagues from Guatemala, the Netherlands (NLD037) and Germany (DEU159) (Spooner and Hijmans, 2001). Wild potato germplasm was collected in almost all Latin American countries including Guatemala (Spooner et al., 1998), Argentina, Bolivia, Chile, Colombia, Costa Rica, Ecuador, Honduras, Mexico, Panama, Peru, and Venezuela (Spooner and Hijmans, 2001).

**Netherlands (NLD037)**. The CGN potato collection is the successor of the German-Dutch potato collection at DEU001, which was established in 1974 by merging the 'Erwin Baur Sortiment' from DEU063 (Max-Planck Institute in Cologne) and the Wageningse Aardappel Collectie (WAC) from NLD002. It includes germplasm from the Dutch expeditions in 1955 and 1974 and material from missions of DEU063 collecting wild and native Andean potatoes in Argentina, Bolivia, Peru and Ecuador in 1959 (Ross, 1960; Ross and Rimpau, 1960).

It was substantially expanded with germplasm from the Argentine genebank of INTA-Balcarce, mainly collected by K.A. Okada, and by a collecting mission in Bolivia in 1980 by DEU001 (Soest et al., 1983). Further collecting missions were conducted together with the USA (Spooner et al., 1998). Today, the collection holds 2,700 potato accessions from 12 American countries. About 55% of this collection meets EU plant health requirements for distribution of germplasm. Limited phytosanitary testing capacity at the Dutch Plant Health Service hampers rejuvenation. In 2004, some

of this material was repatriated to the potato collection of the National Gene Bank of Andean Tubers and Roots, maintained by PROINPA in Bolivia (Cadima Fuentes et al., 2017).

**International Potato Center (PER001).** The International Germplasm Bank for potato was established at the International Potato Center (Centro Internacional de la Papa, CIP) in Lima, Peru in the early 1970s. In close collaboration with the Peruvian National Institute for Agricultural Research (INIA) (Huaman et al., 2000) and well-known international scientists like J.B. Bamberg, J.G. Hawkes, A.M. Van Harten, J.P. Hjerting, W. Hondelmann, R. Hoopes, K.A. Okada, A. Salas, D. Spooner, and J.J.C. Van Soest, more than 300 systematic exploration missions (Spooner et al., 2014) and more than 100 collecting missions in more than 12 countries were carried out (Huaman et al., 2000). Many of these were funded by the International Board for Plant Genetic Resources (later the International Plant Genetic Resources Institute). Carlos M. Ochoa of CIP spent his entire career working on the systematics of wild potatoes and, with Alberto Salas, led many missions for the Universidad Nacional Agraria La Molina, and later for CIP (Spooner et al., 2014). More recently (2017–2018), in collaboration with INIA, CIP co-led 18 collecting missions for potato crop wild relatives throughout Peru, which yielded 322 potato accessions of 26 species according to Spooner taxonomy.

## 6.3 Information on the potato germplasm collections and the survey

The World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture (WIEWS) assesses the status of conservation and use of plant genetic resources (WIEWS, 2021) and provides contact information and collection data of participating genebanks. According to these data, 86 institutes preserve between 1 and 12,100 potato accessions. To increase our knowledge of the composition, safety, data availability and conservation challenges and objectives of the different potato germplasm collections and to update the first global strategy for the conservation of potato (van Soest, 2006), 48 institutes were contacted and a survey was conducted. A questionnaire (Annex 1) was sent out in 2020 and 2021. A total of 24 participants completed the survey in 2020 and eight participants in 2021 from the germplasm collections of:

- Asia: India (1 institution), China (2), Japan (1)
- Europe: Belgium (1), Bulgaria (1), Czech Republic (1), Estonia (1), France (1), Germany (1), Ireland (2), Netherlands (1), Latvia (1), Romania (1), Russia (1), Slovenia (1), Spain (1), Sweden (1), United Kingdom (2)
- Latin America: Argentina (1), Brazil (1), Chile (1), Colombia (1), Cuba (1), Ecuador (1), Guatemala (1), Peru (1),
- North America: Canada (1), USA (1)
- International Center: CIP (1)

The information collected was processed by the lead coordinator (as data controller) and carried out as scientific research in the public interest. Upon completion, all data was transferred to the Crop Trust. In accordance with Regulation 2016/679 (GDPR) and local data protection law (in the EU), participants have the rights to access, modify, erase and transfer (when applicable) personal data, as well as the right to restrict and object to its processing. They also have the right to withdraw their consent at any time and to submit a complaint directly to the appropriate data protection supervisory authority.

National germplasm banks are often embedded in institutional and departmental structures, and it can be difficult to contact curators. Therefore, contacts for potato germplasm collections are provided here, based on information from websites or from participants who consented to the publication of these data (Table 6.3.1).

## 6.4 *Ex situ* collections

Worldwide, a total of 82,293 potato accessions are maintained in 89 institutions and four international/regional centers in 59 countries (Figure 6.4.1; WIEWS (2021) and survey data). The active conservation of potato accessions is the result of numerous missions to collect landraces and wild species in Latin America between 1930–2020. In addition, improved varieties and breeding lines have been added to the published inventory of national and international genebanks. Forty-seven institutes in 36 countries keep more than 100 accessions and just five countries (France, Germany, India, Russia, USA) together with the International Potato Center (CIP, PER001) in Peru hold more than 50% of all potato accessions.

Most, and the largest, collections are found in Europe (Table 6.3.1), with 12,120 accessions preserved at the Institute for Genetics, Environment and Plant Protection in France (INRAE, FRA010), 8,150 accessions at the N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR, RUS001) in Russia, 6,289 accessions at the Leibniz-Institute of Plant Genetics and Crop Plant Research (IPK, DEU159) in Germany, 2,638 accessions at the Potato Research Institute Havlickuv Brod in the Czech Republic (CZE027), 1,634 accessions at the Center for Genetic Resources (CGN, NLD037) of the Netherlands, and 1,523 accessions at the James Hutton Institute (GBR251) in UK.

**Table 6.3.1.** International and national potato germplasm collections and curator contacts based on the survey data, publicly available websites and information from WIEWS (2021).

| Code | Institution | Curator | Organization | Number of Accessions |
|---|---|---|---|---|
| **ARG1347** | Instituto Nacional de Tecnología Agropecuaria (INTA)<br>Banco Activo de Germoplasma, Agricultural Experimental Station Balcarce<br>Ruta 226 km 73,5<br>Balcarce 7620<br>Argentina<br>https://inta.gob.ar/documentos/banco-activo-de-germoplasma-de-la-eea-balcarce | Ariana Digilio<br>digilio.ariana@inta.gob.ar | Governmental | 1,550 |
| **BEL023** | Walloon Agricultural Research Center (CRA-W)<br>Le laboratoire Pomme de Terre In Vitro<br>Rue du Serpont, 100<br>Libramont 6800<br>Belgium<br>https://www.cra.wallonie.be/en | Alice Soete<br>a.soete@cra.wallonie.be | Governmental | 123 |
| **BGR001** | Institute of Plant Genetic Resources "Konstantin Malkov" (IPGR)<br>National Genebank<br>2 Druzhba Str.<br>Sadovo 4122<br>Bulgaria<br>http://ipgrbg.com/en/ | Stanislava Stateva<br>stanislava.stateva@gmail.com | Research<br>Institute | 431 |
| **BLR016** | Republican Unitary Enterprise 'Research and Practical Center of the National Academy of Sciences of Belarus for Potato, Fruit and Vegetable Growing'<br>2-a Kovalev street, 2a 223013<br>Samokhvalovichy, Minsk district, Minsk Region<br>Belarus<br>https://nasb.gov.by/eng/about/otdeleniya-nauk/agro.php | belbulba@belbulba.by | | 1,570* |
| **BOL317** | National Institute for Agricultural and Forestry Innovation (INIAF)<br>Calle Cañada Strongest, Zona San Pedro<br>casi esquina Otero de la Vega, N°1573<br>La Paz<br>Bolivia<br>https://www.iniaf.gob.bo | contacto@iniaf.gob.bo | | 1,567* |
| **BRA020** | Embrapa Clima Temperado<br>Rodovia BR 392, Km 78, 9º Distrito, Monte Bonito<br>Pelotas / RS 96015-420<br>Brazil<br>https://www.embrapa.br/clima-temperado | Caroline Marques Castro<br>caroline.castro@embrapa.br | Governmental | 389 |
| **CAN064** | Agriculture and Agri-Food Canada (AAFC)<br>Fredericton Research and Development Center (Fredericton RDC), Canadian Potato Genetic Resources<br>850 Lincoln Road, P.O. Box 20280<br>Fredericton E3B 4Z7<br>Canada<br>https://pgrc-rpc.agr.gc.ca/gringlobal/search.aspx | Benoit Bizimungu<br>Benoit.Bizimungu@canada.ca | Governmental | 193 |

| Code | Institution | Curator | Organization | Number of Accessions |
|---|---|---|---|---|
| **CHL071** | Instituto de Investigaciones Agropecuarias (INIA)<br>Ruta 5 Sur, Km 8 Norte<br>Osorno, Los Lagos<br>Chile<br>http://www.recursosgeneticos.com/ | Manuel Andrés Muñoz David<br>manuel.munozd@inia.cl | Governmental | 866 |
| **CHL179** | Universidad Austral de Chile (UACh)<br>Institute of Plant Production and Protection<br>Potato Germplasm Bank<br>Valdivia<br>Región de Los Rios<br>Chile<br>http://www.potatogenebank.cl/ | Anita Pia Behn<br>anita.behn@uach.cl | | 837* |
| **CHN116** | Heilongjiang Academy of Agricultural Sciences (HAAS)<br>Keshan branch of HAAS, Potato Resources Institute<br>Keshan<br>161606<br>China<br>http://www.hljnkyksfy.cn/ | Liu Xicai<br>kslxc@sina.com | Governmental | 2,206 |
| **CHN122** | Chinese Academy of Agricultural Sciences (CAAS)<br>Institute of Vegetable and Flowers (IVF)<br>12 Zhongguancun Nandajie<br>Beijing<br>100081<br>China<br>http://ivf.caas.cn | Liping Jin<br>jinliping@caas.cn | Governmental | 2,064 |
| **COL017** | Corporación colombiana de investigación agropecuaria (AGROSAVIA)<br>Banco de Germoplasma Vegetal<br>Km 14 vía<br>Mosquera - Bogotá, Cundinamarca<br>250047<br>Colombia<br>https://www.agrosavia.co/ | Zahara Lasso Paredes<br>zlasso@agrosavia.co<br>Paula Helena Reyes<br>phreyes@agrosavia.co | Governmental, & Research Institute<br>Mixed<br>organization | 1,570 |
| **CUB005** | Instituto Nacional de Ciencias Agrícolas<br>Carretera Tapaste Km 3.5<br>San José de las Lajas<br>Mayabeque<br>32700<br>Cuba<br>www.inca.edu.cu | Jorge Luis Salomon Diaz<br>salomon@inca.edu.cu | Governmental | 1,206 |
| **CZE027** | Potato Research Institute Havlickuv Brod<br>Department of Genetic Resources<br>Dobrovskeho 2366<br>Havlickuv Brod<br>58001<br>Czech Republic<br>https://www.vubhb.cz/en | Jaroslava Domkarova<br>domkarova@vubhb.cz | Private | 2,638 |

| Code | Institution | Curator | Organization | Number of Accessions |
|---|---|---|---|---|
| **ECU023** | Instituto Nacional de Investigaciones Agropecuarias (INIAP)<br>Departamento Nacional de Recursos Fitogenéticos (DENAREF)<br>Panamerica sur km 1 - Vía a Tambillo, Cantón Mejía, Provinz Pichincha<br>Quito 170401<br>Ecuador<br>http://www.iniap.gob.ec/ | Álvaro Monteros<br>alvaro.monteros@iniap.gob.ec | Governmental | 1,341 |
| **EST019** | Estonian Crop Research Institute<br>M. Pilli haru 1<br>Jõgeva 48309<br>Estonia<br>https://etki.ee/en/ | Kristiina Laanemets<br>kristiina.laanemets@etki.ee | Governmental | 786 |
| **FRA010** | INRAE, IGEPP, the Institute for Genetics, Environment and Plant Protection<br>Amélioration de la Pomme de Terre, 29260 Domaine de Keraïber<br>Ploudaniel 29260<br>France<br>https://www6.rennes.inrae.fr/igepp_eng/ | Esnault Florence<br>florence.esnault@inrae.fr | Governmental | 12,120 |
| **DEU159** | Leibniz Insitute of Plant Genetics and Crop Plant Research (IPK)<br>Groß Lüsewitz Potato Collection (GLKS)<br>Parkweg 3a<br>Sanitz OT Gross Luesewitz 18190<br>Germany<br>https://www.ipk-gatersleben.de/en/research/genebank/satellite-collections-north | Klaus J. Dehmer<br>dehmer@ipk-gatersleben.de<br>gbis-info@ipk-gatersleben.de | Non-university<br>Research<br>Institute<br>Publicly funded | 6,247 |
| **GBR251** | The James Hutton Institute<br>Potato Germplasm Collection<br>Invergowrie<br>Dundee DD2 5DA<br>Great Britain<br>https://potato.hutton.ac.uk/topics/resources | Gaynor McKenzie<br>gaynor.mckenzie@hutton.ac.uk | Governmental | 1,523 |
| **GBR165** | Science & Advice for Scottish Agriculture (SASA)<br>Roddinglaw Road<br>Edinburgh EH12 9FJ<br>Great Britain<br>https://www.sasa.gov.uk/ | Heather Campbell<br>heather.campbell@sasa.gov.scot | Governmental | 1,475 |
| **GTM001** | Instituto de Ciencia y Tecnología Agrícolas (ICTA)<br>Banco de Germoplasma<br>Km. 21.5 Carretera hacia el Pacifico<br>Bárcena, Villa Nueva 09001<br>Guatemala<br>https://www.icta.gob.gt/ | María de los A. Mérida Guzman<br>mmerida@icta.gob.gt<br>Eleonara Ramírez<br>eleonoraramirez@icta.gob.gt<br>Osman Cifuentes<br>osmancifuentes@icta.gob.gt | Governmental | 242 |
| **IND665** | ICAR-Central Potato Research Institute (CPRI)<br>Central Potato Research Institute<br>Himachal Pradesh<br>Shimla 171001<br>India<br>https://cpri.icar.gov.in/ | Vinay Bhardwaj<br>vinay.bhardwaj@icar.gov.in | Governmental | 4,257 |

| Code | Institution | Curator | Organization | Number of Accessions |
|---|---|---|---|---|
| **IRL036** | Department of Agriculture, Food & the Marine<br>Raphoe Potato Labratory<br>Raphoe Co. Donegal F93 HV02<br>Ireland<br>https://www.gov.ie/en/organization/department-of-agriculture-food-and-the-marine/ | Gerry Doherty<br>gerry.doherty@agriculture.gov.ie | Governmental | 700 |
| **IRL012** | The Agriculture and Food Development Authority (Teagasc)<br>Oak Park<br>Carlow R93 XE12<br>Ireland<br>https://www.teagasc.ie/ | Denis Griffin<br>denis.griffin@teagasc.ie | Governmental | 600 |
| **JPN183** | Research Center of Genetic Resources<br>National Agriculture and Food Research Organization (NARO)<br>2-1-2 Kannondai<br>Tsukuba, Ibaraki 305-8602<br>Japan<br>https://www.naro.go.jp/english/laboratory/ngrc/ | www@naro.affrc.go.jp | Governmental | 1,890 |
| **LVA006** | Institute of Agricultural Resources and Economics<br>Priekuli Research center<br>Zinātnes 2<br>Priekuli LV 4126<br>Latvia<br>https://www.arei.lv/lv | Ilze Dimante<br>ilze.dimante@arei.lv | Research Institute | 155 |
| **PER001** | International Potato Center (CIP)<br>Genetic Resources Unit<br>Avenida La Molina 1895<br>Lima 12<br>15023<br>Peru<br>https://cipotato.org | Vania Azevedo (Genebank Head)<br>vania.azevedo@cgiar.org<br>Julian Soto (Potato CWR curator)<br>j.soto@cgiar.org<br>Rene Gomez (Cultivated potato curator)<br>r.gomez@cgiar.org | NGO | 7,467 |
| **PER860** | Instituto Nacional de Innovación Agraria (INIA)<br>Av la Molina N° 1981<br>Lima 2791<br>Peru<br>https://www.inia.gob.pe | Elizabeth Fernandez Huaytalla (in vitro)<br>fcarrillo@inia.gob.pe | Governmental | 559 |
| **POL002** | Bonin Research Center<br>Potato Gene Resources and Tissue Culture Laboratory Plant<br>Oddział w Boninie Bonin 3<br>Bonin 76-009<br>Poland<br>www.ziemniak-bonin.pl | Włodzimierz Przewowski<br>w.przewodowski@ihar.edu.pl | | 1,395* |
| **ROM007** | Banca de Resurse Genetice Vegetale „Mihai Cristea" (BRGV)<br>Bdul 1 Mai, Banca de Gene, 17<br>Suceava 720224<br>Romania<br>https://svgenebank.ro/ | Dana Constantinovici<br>dana.constantinovici@svgenebank.ro<br>svgenebank@upcmail.ro | Governmental | 153 |

| Code | Institution | Curator | Organization | Number of Accessions |
|---|---|---|---|---|
| **RUS001** | N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR)<br>Bolshaya Morskaya st., 42, 44<br>St. Petersburg<br>190031<br>Russian Federation<br>http://www.vir.nw.ru/en/ | Elena Rogozina (field)<br>erogozina@vir.nw.ru<br>Tatjana Gavrilenko (in vitro & cryo)<br>tatjana9972@yandex.ru | Governmental | 8,150 |
| **SVN019** | Kmetijski inštitut Slovenije<br>Hacquetova ulica 17<br>Ljubljana 1000<br>Slovenia<br>https://www.kis.si/en/ | Peter Dolničar<br>peter.dolnicar@kis.si | Governmental | 32 |
| **ESP016** | NEIKER - Basque Research and Technology Alliance<br>Arkaute Agri-food Campus<br>Vitoria 01192<br>Spain<br>https://neiker.eus/en/ | Jose Ignacio Ruiz de Galarreta<br>jiruiz@neiker.eus | Governmental | 292 |
| **SWE054** | The Nordic Genetic Resource Center (NordGen)<br>Växthusvägen 12<br>Alnarp<br>234 56<br>Sweden<br>https://www.nordgen.org/en/ | Pawel Chrominski<br>pawel.chrominski@nordgen.org | Governmental | 94 |
| **NLD037** | Wageningen University & Research (WUR)<br>Center for Genetic Resources the Netherlands<br>P.O. Box 16<br>Wageningen 6700 AA<br>The Netherlands<br>https://www.wur.nl/en/Research-Results/Statutory-research-tasks/Center-for-Genetic-Resources-the-Netherlands-1/Genebank/CGN-crop-collections/CGN-potato-collection.htm | Roel Hoekstra<br>roel.hoekstra@wur.nl | Research Institute | 1,634 |
| **USA004** | US Department of Agriculture (USDA)<br>US Potato Genebank<br>4312 Highway 42<br>Sturgeon Bay, Wisconsin 54235<br>USA<br>https://www.ars.usda.gov/midwest-area/madison-wi/vegetable-crops-research/people/john-bamberg/bamberg-lab/ | John Bamberg<br>John.Bamberg@usda.gov<br>Alfonso Del Rio<br>adelrioc@wisc.edu | Governmental | 5,900 |
| **UKR026** | Ukrainian Academy for Agricultural Sciences<br>Ukrainian Institute for Potato Research<br>22 Chkalov Street<br>Nemishaevo<br>Borodyanka, Kiev region 7853<br>Ukraine | Mykola Furdyga<br>upri@visti.com | | 2,229* |

Important collections are also held in **Latin American** countries, in the countries of origin, representing 15% of the global total. Thereby, 1,555 accessions are maintained in Chile at the Instituto de Investigaciones Agropecuarias (INIA, CHL071) and the Universidad Austral de Chile (UACH, CHL179), 1,570 accessions in Colombia at the Corporacion Colombiana de Investigacion Agropecuaria (CORPOICA, COL017), 1,561 accessions in Argentina at the Instituto Nacional de Tecnología Agropecuaria (INTA, ARG1347), 1,567 accessions in Bolivia at the Instituto Nacional de Innovación Agropecuaria y Forestal (INIAF, BOL317) and 1,754 accessions in Peru at the Instituto Nacional de Innovación Agraria (INIA, PER860) and the Asociación para la Naturaleza y el Desarrollo Sostenible, an NGO (ANDES, PER867). The US Potato Genebank at the USDA (USA004) is the largest holder in **North America** with 5,934 accessions.

In **Asia**, China preserves 4,270 accessions at the Heilongjiang Academy of Agricultural Sciences (HAAS, CHN116) and the Chinese Academy of Agricultural Sciences (CAAS, CHN122), India 4,259 accessions at the ICAR-Central Potato Research Institute (CPRI, IND665) and Japan 1,890 accessions at the Research Center of Genetic Resources, National Agriculture and Food Research Organization (NARO, JPN183).

The uneven distribution of potato accessions in *ex situ* genebanks on different continents may reflect the need of the potato industry for plant genetic resources for their breeding programs.

The number of accessions maintained has increased by 42.0% (WIEWS (2021) and survey data) compared to the last survey (van Soest, 2006) (Table 6.4.1). Significant increases were recorded by:

- France (FRA010; +88%; +5,670 accessions)
- India (IND665; + 62%, +1,629 accession)
- China (CHN122; +143%, +1,214 accessions)
- Peru (PER867, +89.7%; +565) accessions)

In contrast, some countries/institutions showed decreases in the number of accessions. CIP (PER001) preserved 10,308 accessions in 2006 and 7,467 accessions in 2020 (-28%), due to a rationalization of the collection and elimination of duplicates. CGN (NLD037) reduced its collection by 1,082 (-40%) and in Bolivia the potato collection was transferred from PROINPA (BOL055) to INIAF (BOL317) and shows an overall reduction of 640 accessions (-29%). However, in some countries, e.g. Bolivia, the transfer of potato collections between institutions is difficult to track and the current status may not be fully reflected by the available numbers.

## 6.5 Biological status of potato accessions

Overall, most accessions are breeding lines (27%), followed by landraces (23%) and improved varieties (25%) and wild species (20%) (Figure 6.5.1). Institutions holding a large number of breeding lines, landraces, improved varieties and wild species in parallel are located in Russia (RUS001), Germany (DEU159), Peru (CIP, PER001), USA (USA004) and the Netherlands (NLD037) (Figure 6.5.2), and are mainly collections that were established in the early 20th century. Compared to the last survey (van Soest, 2006) (Table 6.4.2), the numbers of breeding lines (+107%) and improved

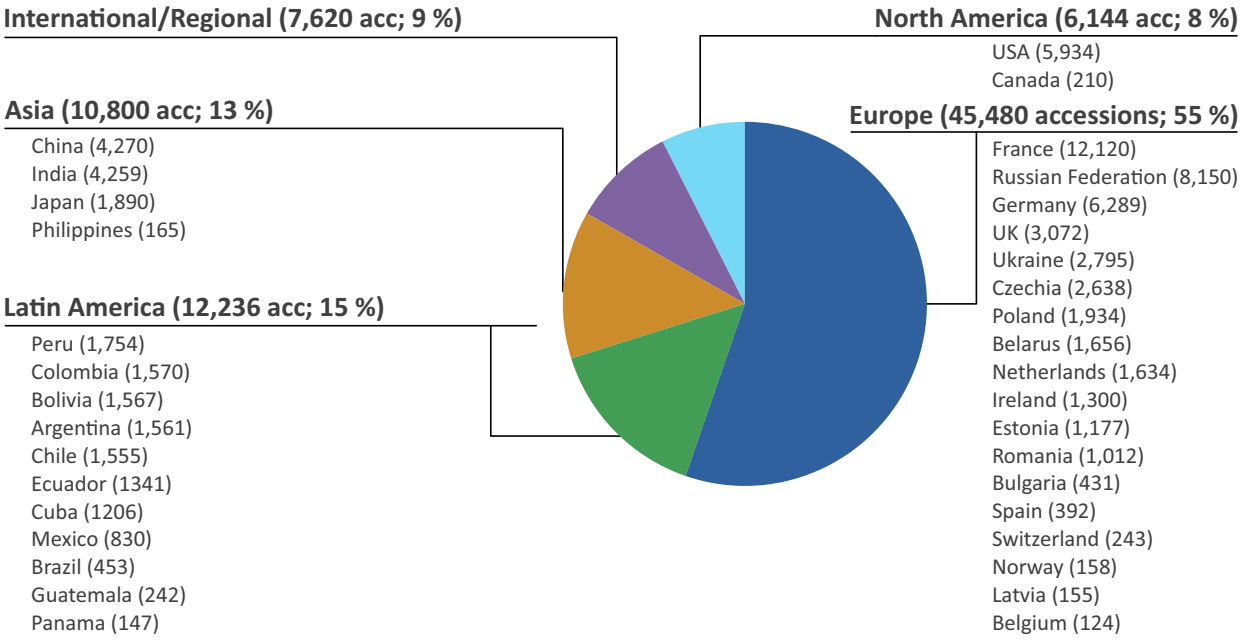



**Figure 6.4.1.** Overview of potato collections by continent and country. Countries preserving more than 100 accessions are shown. Data include survey data and institutes listed in the World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture (WIEWS). WIEWS ©FAO 2021, http://www.fao.org/wiews/en/, accessed on 20th Sept 2021.

**Table 6.4.1.** Number of potato accessions, number of species for each category and changes in percentage compared to the last survey (van Soest, 2006) are listed for each institution contributing to the survey (*). In addition. data the World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture (WIEWS). WIEWS ©FAO 2021, http://www.fao.org/wiews/en/. accessed on 20 September 2021.

| Institute code | Country | Wild species | % | Landrace | % | Breeding line | % | Improved variety | % | unknown | Total | % |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| FRA010* | France | 620 (26) | 3.3 | 300 (1) | 20.0 | 10000 | 117.4 | 1200 (1) | 20.0 | | 12120 | 87.9 |
| RUS001* | Russian Federation | 1990 (98) | -35.8 | 3200 (11) | -5.9 | 600 | 200.0 | 2360 (1) | 12.4 | | 8150 | -7.4 |
| PER001* | International | 2596 (144) | 9.9 | 4468 (7) | 0.2 | 31 | -99.0 | 372 (?) | 18.5 | | 7467 | -27.6 |
| DEU159* | Germany | 1357 (130) | 0.6 | 2270 (7) | 32.7 | 638 | -19.9 | 1943 (2) | -2.3 | 39 | 6247 | 6.0 |
| USA004* | USA | 4044 (90) | 6.7 | 1177 (5) | 15.2 | 371 | -30.5 | 308 (1) | -1.3 | | 5900 | 4.3 |
| IND665* | India | 340 (105) | -13.9 | 107 (?) | -88.4 | 96 | 1143.5 | 2952 (?) | 138.1 | 762 | 4257 | 62.0 |
| CZE027* | Czechia | 136 (23) | -53.6 | 20 (1) | 566.7 | 933 | 75.7 | 1361 (2) | 22.5 | 188 | 2638 | 29.0 |
| UKR026 | Ukraine | 455 (60) | | 23 (1) | | 846 | | 352 (2) | | 553 | 2229 | |
| CHN116* | China | 12 (?) | | 43 (?) | | 1451 | | 700 (?) | | | 2206 | |
| CHN122* | China | 54 (14) | -64.0 | 23 (1) | | 1600 | 300.0 | 387 (1) | 29.0 | | 2064 | 142.8 |
| JPN183* | Japan | 37 (17) | -70.9 | 42 (5) | 68.0 | 1476 | 4667.7 | 333 (1) | -79.9 | 2 | 1964 | 2.6 |
| NLD037* | Netherlands | 1302 (118) | -33.6 | 298 (4) | -59.7 | 5 | 126.7 | | | 29 | 1634 | -39.8 |
| COL017* | Colombia | 274 (9) | 153.7 | 1196 (1) | 30.7 | 44 | -42.0 | 42 (1) | 16.7 | | 1570 | 35.5 |
| BLR016 | Belarus | 577 (78) | | | | 138 | | 855 (1) | | | 1570 | |
| BOL317 | Bolivia | | -100.0 | 1567 (9) | 11.9 | | -100.0 | | -100.0 | | 1567 | -29.0 |
| ARG1347* | Argentina | 1060 (31) | -27.4 | 411 (3) | -25.4 | 67 | | 12 (1) | | 0 | 1550 | -22.9 |
| GBR251* | UK | 686 (86) | -24.8 | 340 (4) | -50.9 | | | | | 497 | 1523 | -5.0 |
| GBR165* | UK | | | | | 25 | | 1450 (1) | | | 1475 | |
| POL002 | Poland | | | | | | | 1395 (1) | | | 1395 | |
| ECU023* | Ecuador | 166 (10) | -39.6 | 602 (3) | 171.2 | 550 | | 23 (3) | 64.3 | 0 | 1341 | 162.4 |
| CUB005* | Cuba | 63 (12) | | 16 (1) | | 650 | | 438 (2) | | 39 | 1206 | |
| PER867 | Peru | | | 785 (5) | 153.2 | 410 | 36.7 | | -100.0 | | 1195 | 89.7 |
| CHL071* | Chile | | | 486 (1) | | 287 | | 13 (1) | | 80 | 866 | |
| MEX208 | Mexico | 9 (4) | | | | | | 96 (1) | | 708 | 813 | |
| EST019* | Estonia | 1 (1) | | 55 (1) | | 310 | | 400 (1) | | 20 | 786 | |
| ROM018 | Romania | 12 (1) | | | | | | 704 (1) | | | 716 | |
| IRL036* | Ireland | | | | | | | 700 (1) | | | 700 | |
| CHL179 | Chile | | -100.0 | | -100.0 | | -54.1 | | -100.0 | 689 | 689 | -67.1 |
| IRL012* | Ireland | | | | | 100 | | 500 (90?) | | 0 | 600 | |
| UKR008 | Ukraine | | | 7 (1) | | 10 | | 537 (1) | | 12 | 566 | |

| Institute code | Country | Wild species | % | Landrace | % | Breeding line | % | Improved variety | % | unknown | Total | % |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PER860* | Peru | 322 (55) | | 237 (1) | | | | | | | 559 | |
| POL047 | Poland | 8 (2) | | | | 422 | | | | 5 | 435 | |
| BGR001* | Bulgaria | | | 89 (1) | | 336 | | 6 (1) | | 0 | 431 | |
| EST006 | Estonia | 1 | | 73 | | 17 | | 300 | | | 391 | |
| BRA020* | Brazil | 92 (3) | | | | 153 | | 127 (1) | | 17 | 389 | |
| ESP016* | Spain | 32 (28) | | 92 (2) | -20.7 | 20 | | 148 (2) | | 0 | 292 | 151.7 |
| GTM001* | Guatemala | 12 (5) | | 35 (2) | | 28 | | 153 (1) | | 14 | 242 | |
| CAN064* | Canada | | | | | 21 | 71.6 | 78 (1) | 50.0 | 94 | 193 | 62.2 |
| PHL303 | Philippines | | | | | 80 | | 13 (1) | | 66 | 159 | |
| LVA006* | Latvia | | | 12 (1) | | 89 | | 54 (1) | | 0 | 155 | |
| ROM007* | Romania | 2 (1) | | 150 (1) | 0.0 | 0 | | 1 (1) | | 0 | 153 | 2.0 |
| PAN147 | Panama | 1 (1) | | 3 (1) | | 119 | | 24 (1) | | | 147 | |
| ROM028 | Romania | | | | | 8 | | 134 (1) | | | 142 | |
| BEL023* | Belgium | 14 | | 36 | | 42 | | 10 | | 21 | 123 | |
| CHE001 | Switzerland | | | | | | | | | 121 | 121 | |
| NOR061 | Norway | | | | | | | | | 111 | 111 | |
| POL003 | Poland | 104 (28) | | | | | | | | | 104 | |
| ESP172 | Spain | 1 (1) | | 93 (4) | | | | | | 6 | 100 | |
| MNG030 | Mongolia | | | 8 (1) | | 19 | | 72 (1) | | | 99 | |
| SWE054* | Sweden | | | 39 (1) | | 9 | 28.6 | 46 (1) | -19.3 | | 94 | 46.9 |
| BLR029 | Belarus | | | | | 86 | | | | | 86 | |
| GBR004 | UK | 73 (14) | | | | | | | | 1 | 74 | |
| CHE063 | Switzerland | | | | | | | | | 65 | 65 | |
| BRA003 | Brazil | 37 (2) | | | | | | 7 (1) | | 20 | 64 | |
| CHE002 | Switzerland | | | | | | | | | 57 | 57 | |
| FJI049 | Fiji | | | 54 (2) | | | | | | | 54 | |
| MNE001 | Montenegro | | | 52 (1) | | | | | | | 52 | |
| LKA036 | Sri Lanka | 1 (1) | | 6 (1) | | 30 | | | | 12 | 49 | |
| NOR035 | Norway | | | | | | | | | 47 | 47 | |
| KGZ040 | Kyrgyzstan | | | | | | | 45 (2) | | | 45 | |
| ARM059 | Armenia | | | | | 15 | | 6 (1) | | 20 | 41 | |
| PRT102 | Portugal | | | 32 (1) | | 8 | | | | | 40 | |
| SVN019* | Slovenia | | | | | | -100.0 | 32 (1) | -47.5 | | 32 | -64.8 |

| Institute code | Country | Wild species | % | Landrace | % | Breeding line | % | Improved variety | % | unknown | Total | % |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| USA016 | USA | 11 (2) | | | | | | | | 10 | 21 | |
| BGD215 | Bangladesh | | | 9 (1) | | 11 | | | | | 20 | |
| DEU401 | Germany | | | | | | | 18 (1) | | | 18 | |
| MEX006 | Mexico | 17 (8) | | | | | | | | | 17 | |
| CAN004 | Canada | 16 | | | | | | | | 1 | 17 | |
| ITA368 | Italy | | | 16 (1) | | | | | | | 16 | |
| DEU483 | Germany | | | | | | | 14 (1) | | | 14 | |
| LTU001 | Lithuania | | | | | 14 | | | | | 14 | |
| ARG1342 | Argentina | 8 (3) | | 2 (1) | | | | 1 (1) | | | 11 | |
| ZAF062 | South Africa | 1 (1) | | 8 (1) | | | | | | | 9 | |
| USA995 | USA | 1 (1) | | | | | | | | 7 | 8 | |
| URY003 | Uruguay | | | | | 7 | | | | | 7 | |
| DEU567 | Germany | | | | | | | 6 (1) | | | 6 | |
| PHL131 | Philippines | | | | | | | | | 6 | 6 | |
| TWN001 | International | | | | | | | | | 5 | 5 | |
| USA176 | USA | 5 (1) | | | | | | | | | 5 | |
| HRV041 | Croatia | | | 4 (1) | | | | | | | 4 | |
| DEU526 | Germany | | | | | | | 4 (1) | | | 4 | |
| HND029 | Honduras | | | | | | | 2 (1) | | | 2 | |
| IND001 | India | | | | | | | | | 2 | 2 | |
| LSO015 | Lesotho | | | | | | | | | 2 | 2 | |
| AZE007 | Azerbaijan | | | | | 1 | | | | | 1 | |
| BEL002 | Belgium | | | | | | | | | 1 | 1 | |
| SWZ015 | Eswatini | | | 1 (1) | | | | | | | 1 | |
| GUY021 | Guyana | | | | | | | | | 1 | 1 | |
| LBN020 | Lebanon | | | 1 (1) | | | | | | | 1 | |
| MLT001 | Malta | | | 1 (1) | | | | | | | 1 | |
| ROM023 | Romania | | | 1 (1) | | | | | | | 1 | |
| TJK027 | Tajikistan | | | | | | | 1 (1) | | | 1 | |
| TZA016 | Tanzania | | | 1 (1) | | | | | | | 1 | |
| | WIEWS 2021 | 1338 | | 2747 | | 2241 | | 4586.0 | | 2528.0 | 13440 | |
| | Survey Data | 15212 | | 15744 | | 19932 | | 16149.0 | | 1816.0 | 68853 | |
| | **Total** | **16550** | **-5.8** | **18491** | **7.4** | **22173** | **107.1** | **20735** | **100.2** | **4344** | **82293** | **42.0** |

varieties (+100%) in particular has increased, while the number of accessions of landraces has increased only a little (+7%) and has decreased by -5.8% for wild species. However, if data are only obtained through WIEWS (2021) (see also Figure **Annex A3**), a lower number of breeding lines (only one third) and improved varieties (only half) and a higher number of unknown accessions are visible in the system (Figure 6.5.1, Figure **Annex A3**).

Analysis of data on biological status and the number of species is hampered by the different taxonomic classification systems currently in use. Although RUS001 applies the classification system of Bukasov (1978), most genebanks follow the Hawkes (1990) taxonomy, which accepts 228 wild species. However, some genebanks, e.g. the USA, have already changed to the classification system proposed by Spooner et al. (2014), which allows 107 wild species. For cultivated species, Spooner et al. (2014) accepts four species instead of seven, namely: (1) *S. tuberosum* including the 'Andigenum group' and the 'Chilotanum group'; (2) *S. ajanhuiri*; (3) *S. juzepczukii*; and (4) *S. curtilobum*. For comparisons, taxonomic classification of the genebank accessions listed in WIEWS (2021) were transferred to the system used by Spooner et al. (2014) (Table **Annex A4**).

### Wild species

In total, 20% of all potato collections (16,550 accessions) consist of wild species classified into 223 species (WIEWS (2021) plus survey data), which are commonly conserved through seeds (Table 6.3.1; Table Annex A3). The largest collections of wild potato species, with the highest number of different species, are held by CIP (PER001; 144 species; 2,596 accessions), Germany (DEU159; 130 species; 1,357 accessions), the Netherlands (NLD037; 118 species; 1,302 accessions) and Russia (RUS001; 89 species; 1,990 accessions) (Figure 6.4.2). The USA (USA004) follows the Spooner et al. (2014) classification and has a collections of 90 species and 4,044 accessions. Compared to the last survey (van Soest, 2006), only a few institutions have increased or maintained the number of accessions preserved. The largest increase was recorded in the USA (USA004) with 253 accessions (+7%) and CIP (PER001) with 233 accessions (+10%) in 2020. In most countries, a reduction in the number of accessions of wild species was reported. In Russia (RUS001), the number of wild accessions reduced by -1,100 accessions (-36%), in Czechia (CZE027) -157 fewer accessions were registered (-54%). In other countries, e.g. Bolivia, it is not clear whether the collections have been transferred and maintained in another institution. In summary, the conservation of wild species has mostly experienced negative changes, and it is not clear whether the decline in numbers is due to rationalization processes, loss or a transfer of material.

The highest number of different wild species is still maintained by CIP (PER001; 95 species) when only the classification of Spooner et al. (2014) is used and data available from WIEWS (2021) are considered (Table **Annex A4**). According to these criteria (which differ slightly from (WIEWS (2021) plus survey data), other collections with a high number of different species are the USA (USA004; 79 species), Russia (RUS001; 70 species), Germany (DEU159; 66 species) and the Netherlands (NLD037; 60 species), which largely confirms

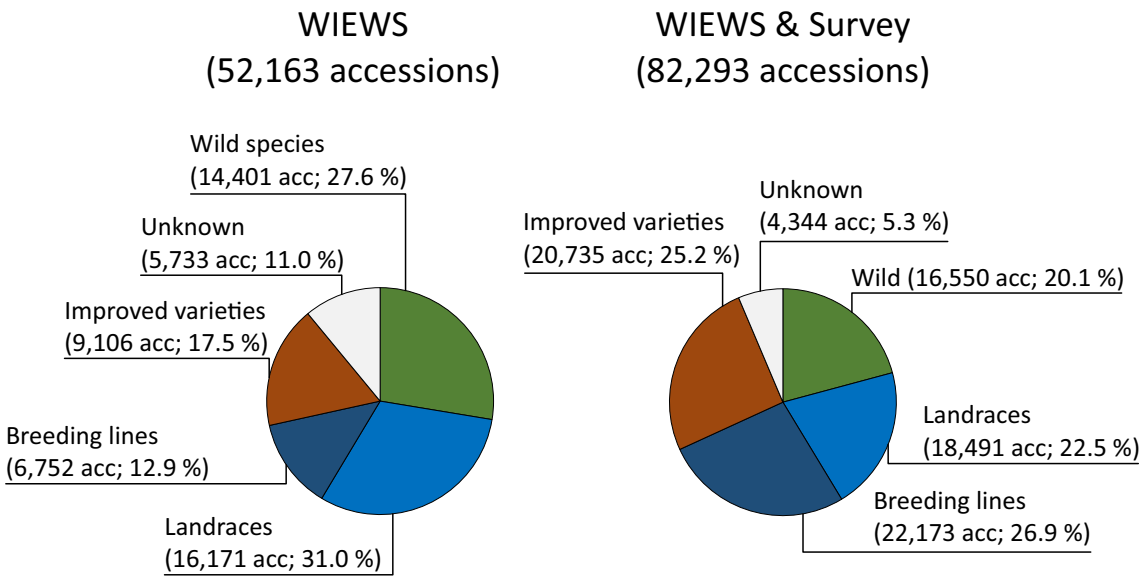



**Figure 6.5.1.** Biological status of the potato collections listed in the World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture (WIEWS) (left) ©FAO 2021, http://www.fao.org/wiews/en/, accessed on 20 Sept 2021 and additional data obtained by the survey (right).

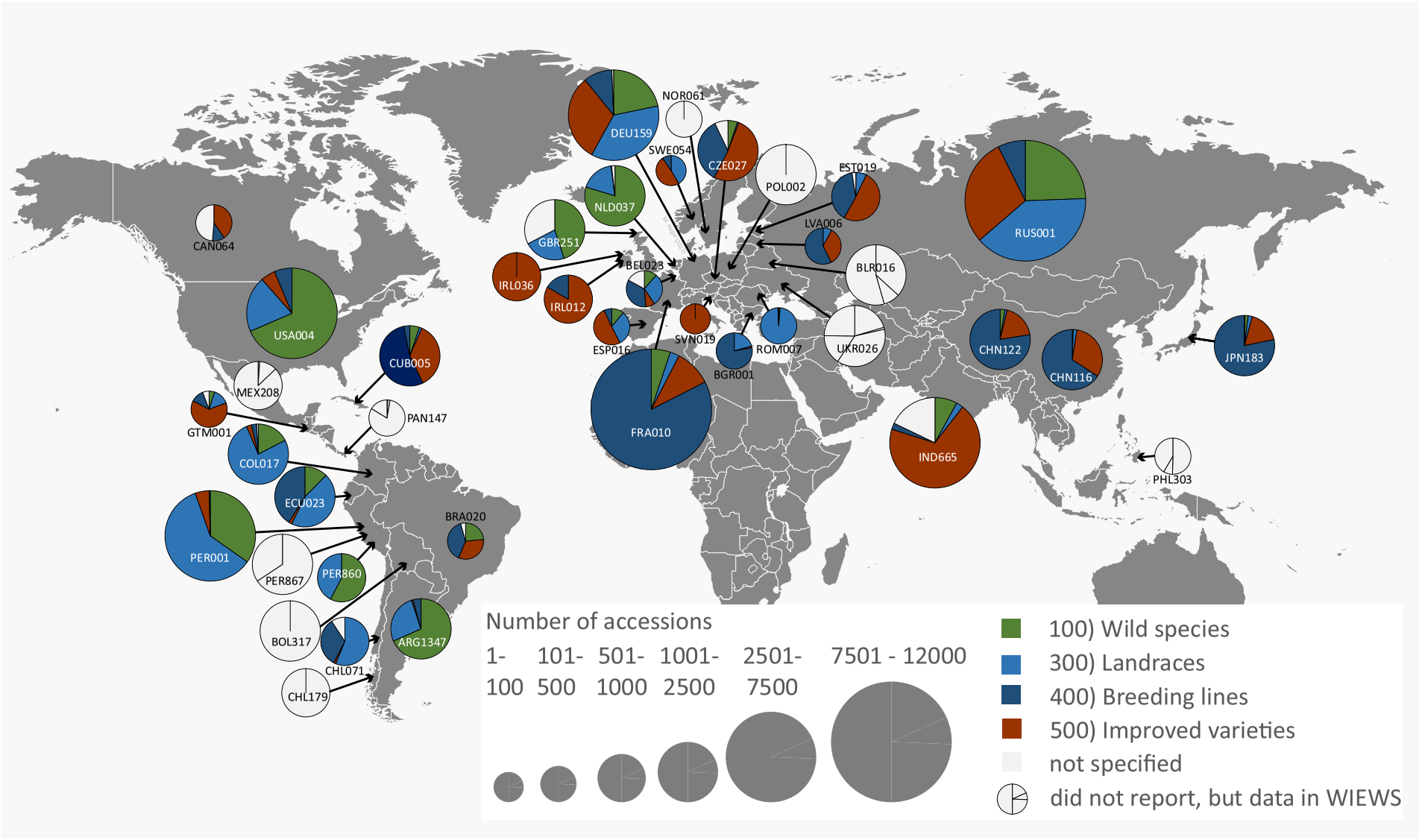



**Figure 6.5.2.** Number and category of potato accessions listed for each institute contributing to the survey. In addition, institutes listed in the World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture (WIEWS) having > 150 accessions are shown. WIEWS ©FAO 2021, http://www.fao.org/wiews/en/, accessed on 20 Sept. 2021.

the data generated by the survey. Most accessions belong to *S. brevicaule* Bitter (1,896 accessions), which were combined from 19 different species accepted by Hawkes (1990). Among these species, *S. brevicaule* (632 accessions), *Solanum gourlayi* Hawkes (229 accessions) and *Solanum sparsipilum* (Bitter) Juz. & Bukasov (220 accessions) are the largest groups and are mainly held by the USA (USA004, 551 accessions), Russia (RUS001; 119 accessions) and CIP (PER001; 58 accessions), respectively. *S. acaule* (1,491 accessions), the second largest group, represents *S. acaule* and two non-accepted species (*Solanum schreiteri* and *Solanum uyunense*) according to Hawkes (1990) and is preserved in the USA (USA004, 421 accessions), Russia (RUS001;336 accessions) and CIP (PER001; 377 accessions). The third largest group (*S. stoloniferum*; 1,255 accessions) is represented by four accepted species and five non-accepted species according to Hawkes (1990) and the largest collections are in the USA (USA004, 520 accessions) and Russia (RUS001; 271 accessions). In summary, five potato genebanks (PER001, USA004, RUS001, DEU159, NLD037) maintain 75% of the collection of wild species and cover 105 of the 107 wild species accepted by Spooner et al. (2014). However, the number of duplicates or unique accessions in these collections is not clear.

## Landraces

About 18,491 accessions are landraces and represent 23% of the total (WIEWS (2021) plus survey data), and are commonly preserved through clonal plants in the field or *in vitro* (Table 6.4.1; Figure 6.5.1). By definition, the landrace collections comprise South American cultivated material, but also selected landraces adapted to specific ecogeographic areas after potatoes were distributed globally, and heirloom varieties (see definition Chapter 1). Most landraces are maintained in CIP (PER001; 7 species; 4,468 accessions), Russia (RUS001; 11 species following the taxonomic treatment of Bukasov (1978); 3,200 accessions), Germany (DEU159; 7 species; 2,270 accessions), Bolivia (BOL317; 9 species; 1,567 accessions), Colombia (COL017; 1 species; 1,196 accessions) and the USA (USA004; 5 species; 1,177 accessions), (Figure 6.5.2). Compared to the last survey (van Soest, 2006), Germany (DEU159) increased the collection of landraces by +33% (+559 accessions) and the USA (USA004) by +15% (+155 accessions). In Peru, Ecuador, Colombia and Bolivia, the landrace collections increased by +153% (PER867; +475 accessions), +171% (ECU023; +420 accessions), +31% (COL017; +281 accessions) and +12% (BOL317; +167 accessions) (Table 6.4.1). These increases are often due to the integration of landraces obtained from farmers or additional accessions from collecting missions. In other countries, however, the number of landraces declined, i.e. in the Netherlands (NLD037) by -442 accessions (-60%), in the UK (GBR251) by -352 accessions (-50%), in Argentina (ARG1347) by -140 accessions (-25%) and in Russia by -200 accessions (-6%). In some cases, the reduction of landraces was reported to be due to a rationalization processes (NLD037) or loss of material (ARG1347) and indicates that the maintenance of clonal plants is a challenge in terms of cost and plant health status.

*S. tuberosum* is thought to have evolved from the *S. brevicaule* complex (Figure 3) and the three rarer domesticated species (i.e. *S. juzepczukii*, *S. ajanhuiri* Juz. & Bukasov and *S. curtilobum* Juz. & Bukasov) from the *S. acaule* complex. However, to analyse the diversity of the landraces present in potato collections, the taxonomic names available from WIEWS (2021) were transferred to the taxonomy of Spooner et al. (2014) and unknown species names were searched in the Solanaceae database. Overall, 32 taxonomic names were listed in WIEWS (2021) and were combined into 27 available names due to spelling issues, of which nine were *S. tuberosum*, seven *S. tuberosum* 'Andigenum group', two *S. tuberosum* 'Chilotanum group' and another two *S. juzepczukii* (Table Annex A4). Together with *S. ajanhuiri* Juz. & Bukasov, 16,121 accessions were listed (WIEWS, 2021) as landraces. Most accessions (9,622 accessions) belong to the *S. tuberosum* 'Andigenum group' and 1,290 accessions to *S. tuberosum* 'Chilotanum group' (Table 6.5.2.1). About 4,800 *S. tuberosum* accessions are not further categorized and may be improved landraces. In addition, some species were misclassified and are listed in the landrace group: i.e. two accessions of *S. boliviense*; one accession of *Solanum campylacanthum* Hochst. ex A. Rich., one accession of *S. candolleanum*. Furthermore, 30 accessions of *Solanum* x *curtilobum,* which are according to Dodds (1962) most likely *S. curtilobum* Juz. & Bukasov, and 16 accessions of the *Solanum etuberosum* Lindl. outgroup are listed. Overall, these results show that most landraces in collections belong to *S. tuberosum* 'Andigenum group', which originated between western Venezuela and northern Argentina and are di-, tri-, tetra- or hexaploid.

Most landraces of *S. tuberosum* 'Andigenum group' are categorized as *S. tuberosum* subsp. *andigena* (7,845 accessions) and are maintained at CIP (PER001; 3,308 accessions), Germany (DEU159; 1,215 accessions), Bolivia (BOL317; 975 accessions) and the USA (USA004; 940 accessions) (WIEWS, 2021) (**Table Annex A5**). Landraces from *S. stenotomum* subsp. *stenotomum* are maintained at CIP (PER001; 287 accessions), Germany (DEU159; 86 accessions) and Peru (PER867; 77 accessions). For the *S. tuberosum* 'Chilotanum group', most landraces have been described as *S. tuberosum* subsp. *tuberosum* and are found in Chile (CHL071; 492 accessions), Germany (DEU159; 405 accessions) and CIP (PER001; 173 accessions). The largest group

within *S. tuberosum* belongs to *Solanum andigenum* (*S. tuberosum* ssp. *andigena*, *S. tuberosum* 'Andigenum group') and is held in Russia (RUS001; 2,701 accessions). The rare domesticates of *S. ajanhuiri*, *S. curtilobum* and *S. juzepczukii* are mainly kept in Bolivia and are represented by 64, 80 and 128 accessions, respectively. Considering the small number of rare domesticates available in the Bolivian genebank, it is probable that there are gaps in the collections.

## Improved varieties

The category of improved varieties consists of *S. tuberosum* varieties that were broadly commercially available and often provided by breeding companies for a limited period of time (dependent on consumer preferences and intellectual property protection). This group includes 20,735 accessions, representing 25.2% of the total potato collection (Figure 6.5.1). Five institutions hold 50% of all improved varieties, with 2,952 accessions at IND665, 2,360 accessions in RUS001, 1,943 accessions in DEU159, 1,450 accessions at GBR165 and 1,395 accessions at POL002 (Figure 6.5.3.1 a). Some institutions are strongly focused on improved varieties, and more that 50% of their collections consist of such material, i.e. 100% of POL002 (1,395 accessions) in Poland, 100% of IRL036 (700 accessions), and 83% of IRL012 (500 accessions) in Ireland, 98% of ROM018 (704 accessions) in Romania, 98% of GBR165 (1450 accessions) in UK, 94% of UKR008 (537 accessions) in Ukraine, 69% of IND665 (2,952 accessions) in India, 55% in BLR016 (855 accessions) in Belarus, 51% of CZE027 (1,361 accessions) in Czechia, 51% of EST019 (400 accessions) in Estonia (Figure 6.5.2 and 6.5.3.1). These institutes often have close contacts with breeding companies or actively participate in breeding programs.

The group of improved varieties has increased considerably (+100%) in the last 15 years. Compared with the last survey (van Soest, 2006), more than 10,000 additional accessions of this type are maintained (Table 6.4.1). In particular, IND665 have increased the number of accessions by 138% (1,712 accessions),

**Table 6.5.2.1** Total number of landraces maintained in genebanks and listed in the World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture (WIEWS). WIEWS ©FAO 2021, http://www.fao.org/wiews/en/, accessed on 20 Sept. 2021. Species name according to WIEWS (2021) have been transferred to the taxonomy of Spooner et al. (2014) including country of origin, ploidy level. not found = name not present in the https://solanaceaesource.myspecies.info/ database.

| Accepted by Spooner et al. (2014) | Code | Country | Ploidy | Total |
|---|---|---|---|---|
| *Solanum ajanhuiri* Juz. & Bukasov | ahj | BOL, PER | 2x (2EBN) | 98 |
| *Solanum curtilobum* Juz. & Bukasov | cur | BOL, PER | 5x | 121 |
| *Solanum juzepczukii* Bukasov | juz | ARG, BOL, PER | 3x | 191 |
| *Solanum tuberosum* | | | | 4799 |
| *Solanum tuberosum* 'Andigenum group' | tub | Landraces from W Venezuela South to N Argentina | 2x (2EBN), 3x, 4x (4EBN) | 9622 |
| *Solanum tuberosum* 'Chilotanum group' | tub | CHL (Chilean landraces) | 4x (4EBN) | 1290 |
| *Solanum boliviense* Dunal in DC. | blv | ARG, BOL, PER | 2x (2EBN) | 2 |
| *Solanum campylacanthum* Hochst. ex A.Rich. | | | | 1 |
| *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 1 |
| *Solanum x curtilobum* (not found) | | | | 30 |
| *Solanum etuberosum Lindl.* | | | | 16 |
| **Total** | | | | **16171** |

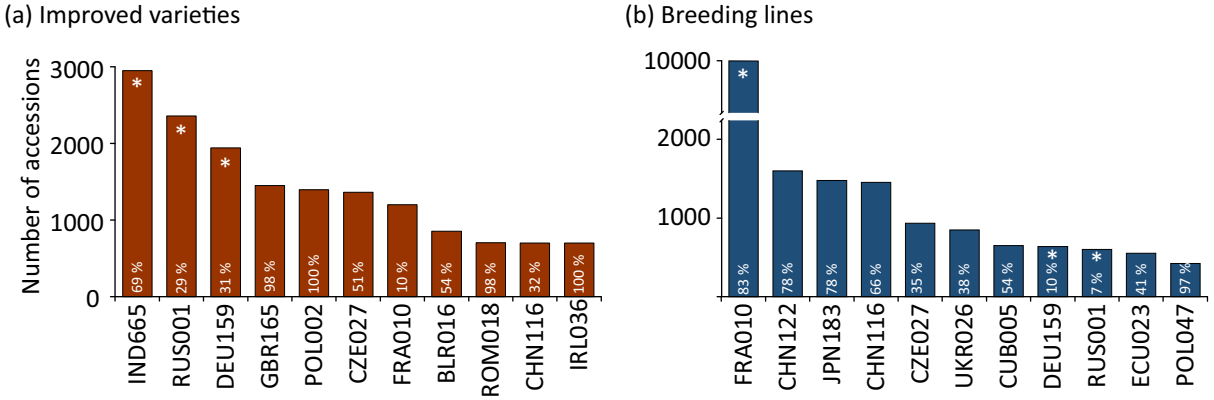



**Figure 6.5.3.1**. Top 11 largest potato collections maintaining a) improved varieties and b) breeding lines. Asterisks mark the largest potato collections holders and percentages in each show proportion of the respective collection.

RUS001 by 12% (260 accessions), FRA010 by 20% (200 accessions) and CHN122 by 29% (87 accessions). In contrast, the number of accessions decreased in JPN183 by -80% (1,327 accessions), DEU159 by -2% (46 accessions) and PER867 by 100% (20 accessions), suggesting that some collections have focused, rationalized or re-structured this part of the collection or may have lost clonal plants.

### Breeding lines

Breeding lines are the result of intensive crossing and selection processes, with the aim of developing potato varieties with higher yields and greater tolerances to stress and diseases. This material may also include lines from mapping population panels used for genetic analysis and other research material. In any case, breeding lines are an important source for further breeding processes and research and comprise a collection of 22,173 accessions, representing 26.9% of all potato accessions worldwide (Figure 6.5.1). The country with the highest number of breeding lines is France (FRA010), which maintains 10,000 accessions as clonal plants *in vitro* and/or in fields, accounting for about 50% of the total breeding line collection (Table 6.4.1). Other countries with large collections are China with CHN122 (1,600 accessions) and CHN116 (1,451 accessions) and Japan (JPN183, 1476 accessions). Institutions with a strong focus on breeding lines (more that 50% of collections) are POL047 with 97% (422 accessions), FRA010 with 83% (10,000 accessions), PAN147 in Panama with 81% (119 accessions), JPN183 with 78% (1,476 accessions), BGR001 with 78% (336 accessions), CHN122 with 78% (1,600 accessions), CHN116 with 53% (1,451 accessions) and CUB005 in Cuba with 54% (650 accessions) (Figure 6.5.2 & 6.5.3.1). The number of breeding lines may indicate the great importance of potato breeding in these countries.

The number of breeding lines has developed similarly to the number of improved varieties, increasing by +107% and 13,711 accessions in the last 15 years (van Soest, 2006). Compared to the last survey, FRA010 has increased the number of breeding lines by 117% (5,400 accessions). JPN183 maintained 31 breeding lines in 2005 and increased by 1,445 accessions, CHN122 by 300% (1,200 accessions) and RUS001 by 200% (400 accessions). (Table 6.4.1). However, comparable to the improved varieties, some institutions reduced the number of breeding lines, in particular PER001 by -99% (3,139 accessions), DEU159 by -20% (207 accessions), BOL317 by -100% (300 accessions) and USA004 by -30% (163 accessions). Again, it is likely that the decline in breeding lines is due to rationalization or re-structuring of the collection or that clonal plants have been lost.

In summary, the institutes that participated in the survey maintain about 69,000 potato accessions and represent more than 80% of the global potato collections in North and Latin America, Europe and Asia. In general, the Latin American countries and CIP but also countries that initiated the first collecting missions, i.e. Russia, Germany, the Netherlands, UK and the USA, maintain comprehensive collections of wild species and landraces. In the last 15 years, the number of accessions of wild species has decreased and the number of accessions of landraces has increased only marginally, indicating that there are some challenges in conserving this material. Assessing the composition of the wild species and landraces collections is hampered by the different taxonomic classification systems applied in the different genebanks. After transferring the available data into the classification system from Spooner et al. (2014), it appears that of the 107 known wild species, accessions of only 105 wild species can be found in genebanks. However, it is not clear if this observation is biased by the simple transformation. By contrast, the number of improved varieties and breeding lines in genebanks has increased massively, e.g. in France and China, over the last 15 years. This increase may reflect the importance of the potato for these countries or new strategic goals for developing their agricultural systems.

## 6.6 Challenges of differences in potato classification systems

The taxonomic group *Solanum* section *Petota* is a very complex and difficult group shaped by interspecific hybridization, introgression, polyploidy and the mix of sexual and asexual reproduction. The taxonomic classification systems have changed considerably over time. The most important changes were that the complex Russian systems, which were based on ploidy levels, morphological and eco-geographic characters and date back to Vavilov (1922); (1935 ), Juzepczuk and Bukasov (1929), Lekhnovich (1972) and Bukasov (1978) was simplified by Hawkes (1990). He used morphological parameters, biogeography, crossability and ploidy levels as the main determinants and incorporated results of (Correll, 1962) and (Ochoa, 1962). However, genetic variation in *ex situ* collections may not be comprehensively explained by morphological characters (Tanksley and McCouch, 1997) and conversely, genetic markers may not predict specific traits either. Therefore, David Spooner and collaborators have worked intensively on an integrative taxonomy which aimed to combine evidence from natural history, botany, biogeography, ecology and genetics (Spooner et al., 2004; Spooner et al., 2007; Ovchinnikova et al., 2011; Spooner et al., 2014; Spooner et al., 2016; Spooner et al., 2019). Their goal was to develop a complementary perspective that includes a predictive

classification, proposing provisional taxonomic groups based on hypotheses of phylogenetic relationships among species that reflect the evolutionary history of potatoes, and pending more data to elucidate interrelationships. In addition, this classification aimed to be useful for conservation and breeding (personal communication Iris Edith Peralta, 2021).

Extensive taxonomic work was conducted on 7,641 specimens in 74 herbaria, plus field work, experimental trials, and the evaluation of quantitative, qualitative and molecular characters (Spooner et al., 2014). As a result, the 228 wild potato species, seven cultivated species and 19 taxonomic series recognized by Hawkes (1990) were combined into 107 wild and four cultivated species (Spooner et al., 2014). Nowadays, most genebanks still apply the Hawkes (1990) taxonomy, VIR (RUS001) applies the classification system according to Bukasov (1978), while those which use GRIN, such as the US potato genebank (USA004), apply the classification system of Spooner et al. (2014). Unfortunately, the three classification systems used can be problematic for users of the collections and pose challenges for database searches, 'gap analysis' and the identification of duplicates. Therefore, the community needs to develop a way to combine the benefits of the two taxonomic classification systems.

Although both systems have a rational and well-developed basis, the classification according to Hawkes (1990) is very useful in managing *ex situ* collections due its precise species characterization and detailed and comprehensive morphological descriptions. However, the revision by Spooner et al. (2014) is considered an advance in the field (Ellis et al., 2020) as morphological descriptors are qualitative but do not necessarily show the underlying variation in diverse collections, e.g. the large phenotypic diversity in tuber traits does not reflect the allelic diversity for disease resistance and stress tolerance (Jansky et al., 2015). As a consequence of DNA marker analysis, many species categorized by their phenotype have been merged because they could not be clearly distinguished in genetic analysis. While the lumping of species eliminated intermediates, it resulted in specific problems in the management of genebank collections. Some of these issues can particularly create confusion for germplasm users and were communicated by John Bamberg (curator of the US potato collection, USA004, 2022):

1. A new lumped species often does still have empirically distinguishable "old" species types within. *Solanum fendleri* A. Gray, *S. stoloniferum*, and *Solanum polytrichon* Rydb., for example, can be clearly distinguished by morphological characters. By combining them into *S. stoloniferu*m, the usefullness of the identities of these types has been lost, sometimes in a misleading way. For example, all of the hundreds of collections of the *S. fendleri* type from the USA are now called *S. stoloniferum*, although none of them look like the classic *stoloniferum* known from Mexico.
2. A new species name may now represent a very minor fraction of the accessions. For example, approxiately 20 accessions of the original *Solanum boliviense* had been in the US collection before Spooner et al. (2014) lumped them with approximately 200 additional accessions of *Solanum astleyi* Hawkes & Hjert.*, S. megistacrolobum, Solanum sanctae-rosae* Hawkes and *Solanum toralapanum* Cárdenas & Hawkes in this group. As a result, the identities of many *S. megistacrolobum* accessions have disappeared and been replaced with *S. boliviense,* which was originally only 10% of the accessions. This is because accessions are not synonimized according to the name which has any logical dominance in numbers of accessions in genebanks or size of geographic natural distribution, but only on the historic precidence of the taxonomic name.
3. The *S. tuberosum* 'Andigenum group' now comprises landraces with different ploidy levels. But breeders are often quite interested in knowing if stocks will cross readily with their diploid or tetraploid material. So, it is an extra step to download a list of available *andigenum* accessions as a jumble of ploidies, then use a secondary ploidy datafield to sort them to the previously familiar diploid *phureja* or tetraploid *andigena* accessions.

**The overall proposals towards a harmonization of taxonomy includes**

1. **Subdivision of large groups.** Large species groups of Spooner et al. (2014) may need to be sub-divided based on their genetic diversity because identification of gaps is more likely in smaller groups. Where appropriate, Hawkes (1990) or other classification for grouping may be used for sub-division.
2. **Predictive taxonomy** should be considered and names to be associated with traits; when grouping is necessary, sub-groups need to be identified by modern technologies and may be predictive for specific traits.
3. **Intermediate forms** might be given a standard name other than "unknown" or "spp." so that users of the germplasm have some idea about their background.
4. **The Intergenebank Potato Database** (Huamán et al., 2000) already matches wild species accessions between eight genebanks based on collector/accession numbers or digital object identifiers (DOI). The database should be revised and linked to or integrated into other platforms, i.e. Genesys and EURISCO.
5. **Genebank databases** should also include references to the taxonomic framework used. Changes to the taxonomic description should be stored in

the database, including infraspecific categories.

6. **Identification of taxonomic preferences** of users, genebank curators and taxonomists.
7. **Comprehensive DNA marker sequencing** would provide additional information about accessions and support taxonomists, genebank curators, and users. Agreements on standardized marker systems and establishment of user-friendly analysis platforms would be required.
8. **More information** is needed about natural populations and hybrids, more collections of wild species are required because they are threatened by habitat modifications or introduction of invasive species
9. **Digitization of herbaria.** Support the work of taxonomist through digitization and expansion of herbaria.
10. **Evaluation and characterization** data will support the work of taxonomists and help to identify useful accessions for users. Consider establishing core sets for detailed characterization

Cryopreservation at IPK genebank, Gatersleben, Germany. Photo: Lynn Maine/IPK

# 7 POTATO GERMPLASM MAINTENANCE

## 7.1 *Ex situ* maintenance of potato

The conservation of potato accessions is varied and depends on the type of material (Figure 7.1.1). Accessions of wild species are collected as populations and are mostly preserved as orthodox seeds in cold storage facilities. For landraces and improved varieties, the specific allele combination of each genotype needs to be maintained as a clonal accession in the field, *in vitro* or in cryopreservation (*in cryo*). The following data summarize the conservation practices of 32 collections, comprising more than 80% of potato germplasm and located in Asia (3 collections), Europe (17 collections), Latin America (8), North America (2 collections), plus the International Center CIP (PER001).

## 7.2 Field maintenance and short-term warehouse storage of seed potato

Field maintenance is the traditional approach to maintaining clonal plant genetic resources. The benefit is that the accessions are easily accessible, can be described and images and voucher specimen can be prepared easily (Panis et al., 2020). Therefore, most or even all collections have the potential to reproduce and conserve their germplasm in the field, usually in locations that are less susceptible for pests and diseases. CIP (PER001) grows out and maintains tubers from the landrace collection in a 3 ha field in Huancayo, Peru at an altitude of 3200 m (Huaman et al., 2000). The US potato genebank (USA004) uses fields at the Hancock Agricultural Research Station, the central potato production area in Wisconsin (Bamberg, 2021). The potato field collection of IPK (DEU159) is located at the Groß Lüsewitz station (GLKS) in Mecklenburg Vorpommern and VIR (RUS001) uses experimental stations in different geographic areas such Saint Petersburg, Murmansk, Moscow, Tambov region, and Krasnodar (Kiru et al., 2007). Usually, up to 10 tubers are planted in the field and the emerging plants are described and characterized. A list of descriptors (see chapter 4.2) has been elaborated by FAO and IPGRI (Alercia et al., 2018) and between different genebanks (Huaman et al., 1977; Gomez, 2000) to exchange germplasm information and provide breeders with a preliminary set of characterization and evaluation data.

Storage of tubers is essential for further tuber evaluation, characterization and distribution, and to bridge the gap between growing seasons. To avoid quality

losses during storage due to mobilization of starch and proteins (Sonnewald and Sonnewald, 2014), tuber dormancy is essential and can be partly controlled by environmental conditions. In this state, the buds that contain the meristems show no visible signs of growth, whereas the remaining part is still metabolically active yet at a reduced rate (Viola et al., 2007; Sonnewald and Sonnewald, 2014). The most important post-harvest environmental factor to affect tuber dormancy (ecodormancy) is temperature, which is inversely related to the duration of dormancy and optimally lies in a range of 3–20°C. In addition, humidity control as well as controlled gas composition help maintain dormancy (Wiltshire and Cobb, 1996). External physiological factors such as the application of chlorpropham (CIPC) or other chemical alternatives (Alamar et al., 2017) stimulate paradormancy (Suttle, 2007). In addition, the length of tuber dormancy is under genetic control and involves the interaction of plant growth regulators such as abscisic acid (ABA), auxins, cytokinins (CKs), gibberellins (GAs), ethylene, and strigolactones (SLs), as well as other compounds such as carbohydrates and organic acids (Viola et al., 2007)

In general, the application of controlled tuber storage depends on the country and the intended use, e.g. tubers for the processing market require higher temperatures between 8–13°C to maintain frying quality while temperatures below 7°C can be applied for potatoes for the fresh market or for storing tuber as propagules for the next planting season. Depending on the variety and the location of production, excessively low temperatures can cause the accumulation of reducing sugars and lead to 'cold-induced sweetening' (Alamar et al., 2017). In countries where warehouse systems are poorly developed, tubers are often stored in wooden boxes with air-circulation. However, these can promote the spread of fungal diseases. For example, monitoring airborne elements showed elevated amounts of fungal spores from *Cladosporium* followed by *Aspergillus*/*Penicillium*, *Helminthosporium* and *Alternaria* during potato storage in warehouses without control. In storage systems with cooling conditions, the most abundant fungal spores were from

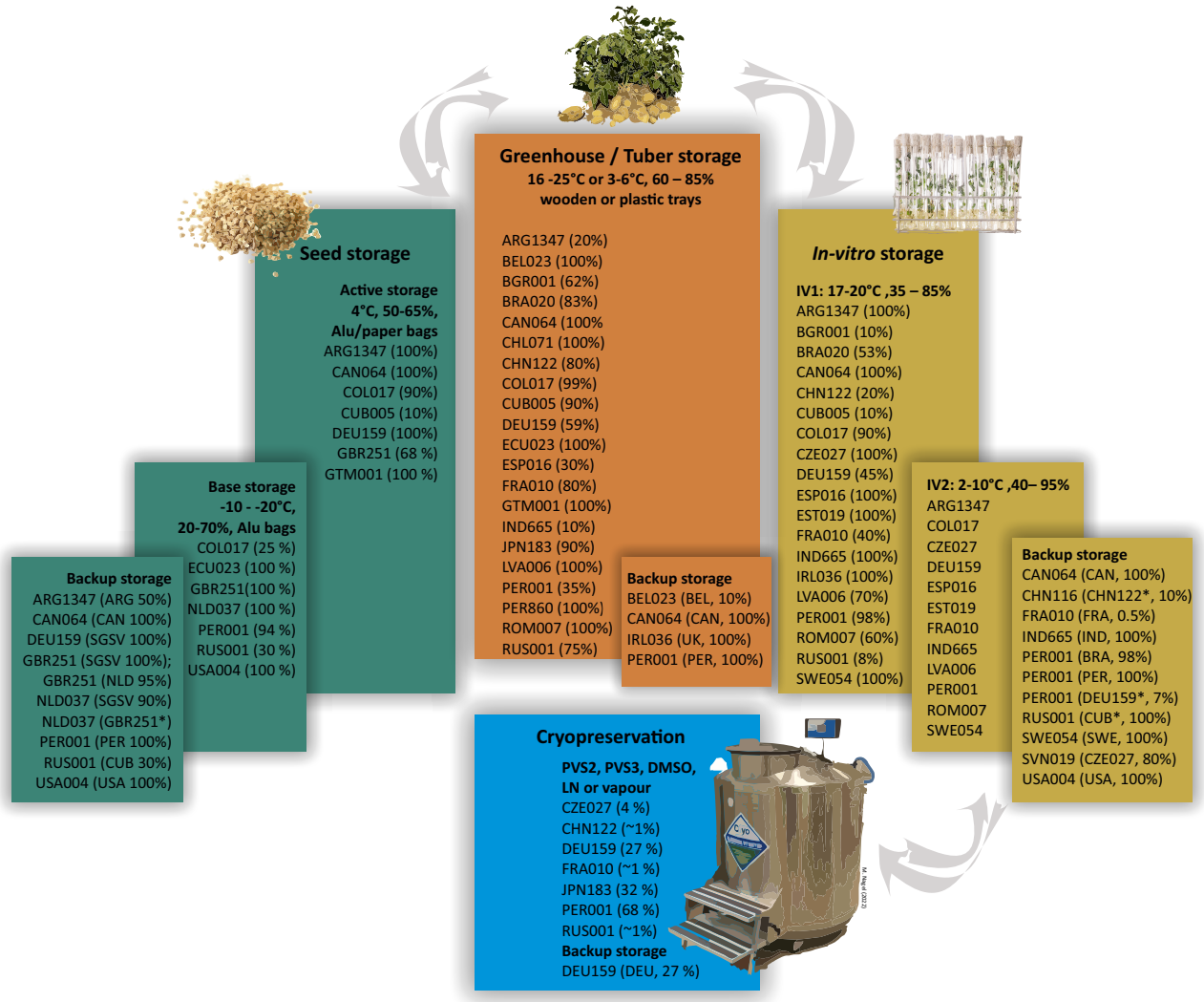



**Figure 7.1.1.** Potato *ex situ* storage approaches applied by 32 potato collection holders participating in the survey. Percentages in brackets describes the estimated proportion of the collection maintained under each storage condition. For the backup repositories, the country and percentage of collections located outside the respective institute are indicated in brackets. *Numbers provided by the institution where the backup repository is located.

*Aspergillus*/*Penicillium*, *Cladosporium*, *Fusarium* (Meno et al., 2021). Interestingly, the production of potato tubers from true potato seeds prolonged significantly the period of tuber dormancy, and also the days to tuber shrinkage, compared to plants grown from tubers. If this is a viable alternative, this approach has important benefits in countries which cannot apply refrigeration storage, passive cooled water or sprouting inhibitors (Roy et al., 2006). However, in potato collections, where genotypes need to be maintained, tubers are commonly stored for extended short-term periods, at low temperatures and higher humidities.

Most collections maintain and reproduce between 20–100% of their material in the field or in the greenhouse (survey data). In the Northern Hemisphere, tubers are planted in spring, grown and characterized during the year, harvested at the end of summer and stored until the next growing season. For CHL071, COL017, ECU023, GTM001, PER860 and CUB005, more than 90% of the collection is preserved in the field, while other collections keep a smaller proportion for national distribution, characterization and evaluation in the field. These include DEU159, ESP016, IND665 and PER001, with between 10–60% field reproduction. For storage, tubers are stocked in plastic boxes at low temperatures between 3–6°C, and 60% relative humidity (RH). Storage at higher temperature in wooden boxes is often applied when cold storage facilities are not available, e.g. GTM001. To avoid the risk of losing accessions during the year, clonal potato collections in the field are often backed up by *in vitro* slow growth storage.

## 7.3 Medium-term storage through *in vitro* slow-growth maintenance

Clonal *in vitro* plants can be kept disease-free under sterile conditions for a longer period under slow-growth storage conditions. To reduce metabolic activity and thus plant growth, lower temperatures and lower light intensities are commonly applied. The procedures, parameters and media are very species and institute specific. For slow-growth storage of *S. tuberosum* at IPK (DEU159), a combination of warm (20°C for 2–3 months) and cold phases (9°C for 2–4 months, low light intensity) is used to induce microtubers, followed by cold storage (4°C, low light intensity) for 16–18 months (Keller et al., 2006). At USA004, plants are sub-cultured, grown at 20–22°C for 2 weeks and stored at 8–10°C and low light intensity for 12–18 months (Bamberg et al., 2016). The growth medium contains MS medium supplemented with 6% sucrose and in some cases sorbitol (Sarkar et al., 2001). However, large variations exist between different institutions.

When plants are introduced into *in vitro* culture, combinations of chemo-, and thermotherapy followed my meristem isolation ensure virus-free stocks (Keller et al., 2006; Keller et al., 2012). However, the US potato collection is screened every five years for Potato Virus A (PVA), PVM, PVS, PVX, PVY, Potato Leaf Role Virus (PLRV), Potato Spindle Tuber Viroid (PSTVd), and bacteria such as *Clavibacter sepedonicus* causing potato ring rot (Bamberg et al., 2016). For CIP (PER001), the relevant viruses for import/export are the Andean potato latent virus (APLV), Andean potato mild mosaic virus (APMV), the Arracacha virus B, Oca strain (AVB-O), Potato Virus T (PVT), PVS, PVX, PVY, PLRV and PSTVd (Ellis et al., 2020). At IPK (DEU159), the collections are regularly tested for the common virus strains PVA, PLRV, PVM, PVS, PVX, and PVY. Furthermore, accessions are screened for the absence of PSTVd and bacterial quarantine diseases caused by *Clavibacter sepedonicus* and *Ralstonia solanacearum* upon entry to the collections. Entries of Southern American origin are additionally screened for Andean Potato Latent Virus (APLV-Col, APLV-Col 2, APLV-Hu), Andean Potato Mottle Virus (APMoV-B, APMoV-H), Potato Black Ringspot Virus (PBRSV), AVB-O, PVT, Potato Virus V (PVV) and Potato Yellowing Virus (PYV). For distribution, test certificates for the absence of *Clavibacter*, *Ralstonia* and PSTVd not older than three years have to be provided (personal communication Klaus J. Dehmer 2021). Although plants are maintained under sterile conditions and screened regularly for potential diseases, growth retardation, cellular ageing and endophytic contaminations can affect the viability of *in vitro* plant and thus their survival (Panis et al., 2020). In combination with potential infections of mites and/or other insects, the collections can be severely compromised.

Of the 32 survey participants, 21 collections are fully or partly maintained in slow growth storage (survey data). Between 90–100% of the collection are maintained *in vitro* by ARG1347, CAN064, COL017, CZE027, ESP016, EST019, IND665, IRL036, PER001 and SWE054. Other institutions, such as BRA020, DEU159, FRA010, LVA006 and ROM007, store between 40–90% *in vitro,* and BGR001, CHN122 and CUB005 between 10–20%. In the collections where there is a lower proportion of accessions in *in vitro* storage, the remaining portion of the collection is either maintained as true potato seeds or as clonal plants in the field. However, only 12 participants indicated that they have cold rooms available. Therefore, nine respondents may not be able to induce and maintain shoot cultures or microtubers at lower temperatures, and therefore the intervals for sub-culturing are shorter and the workload much higher. Notably, curators from Latin America reported that they rely on older equipment and technologies and have no resources to replace them. If the equipment breaks down, there is the risk of losing the

entire *in vitro* collection. This partly explains the 30% decline in the ARG1347 landrace collection, which should be considered as severe risk.

Only nine survey participants have the possibility to back-up at least part of their collection at another site. Among these, CAN064, IND665, PER001, SWE054, SVN019 and USA004 have between 80–100% of their collections safely duplicated. For example, CIP (PER001) backs up its *in vitro* collection at a distant site within Peru (Huancayo) as well as internationally at BRA020 in Brazil. With other genebanks, it is common practice to back-up, i.e. minitubers at 5°C. Overall, only a part of the world's *in vitro* potato collection is securely maintained and backed-up and significant infrastructure improvements are needed, in particular in Latin American countries, for in tissue culture and cold storage facilities.

## 7.4 Long-term storage via cryopreservation

Although *in vitro* preservation offers some benefits because the plants are available immediately and throughout the year for research and distribution, cryopreservation is the only approach for secure long-term storage of clonal plant genetic resources collection and thus minimizes the risk of loss (Panis et al., 2020). Most methods use the process of vitrification for cryopreservation, which involves reducing water activity to a minimum and rapid cooling with liquid nitrogen (LN), such that the cytoplasm vitrifies. In this state, the molecular mobility of the water molecules is reduced and metabolic processes are greatly slowed down, allowing long-term survival of the biological material. Depending on the species, organ and the technical background and experiences of the laboratory, protocols may vary and the individual steps differ (Panis et al., 2020).

Sakai (1960) was the first to succeed in ensuring the survival of plants at ultra-low temperature using dormant bud cryopreservation. Over the years, other approaches, such as slow freezing (also known as 2-step cooling), encapsulation-dehydration and dimethylsulfoxide (DMSO) droplet freezing were developed. However, the introduction of plant vitrification solutions (PVS), including PVS2 composed of 30% glycerol, 15% ethylene glycol, 15% DMSO and sucrose (Sakai et al., 1990), and PVS3, composed of 50% glycerol and 50% sucrose (Nishizawa et al., 1993), have opened a range of possibilities for rapid cryopreservation of shoot tips with high survival rates. The main challenge is to adapt the different species and even sub-species groups to these methods, which may require changes in pre-culture and cryoprotection treatments as well as in the composition of solutions and media.

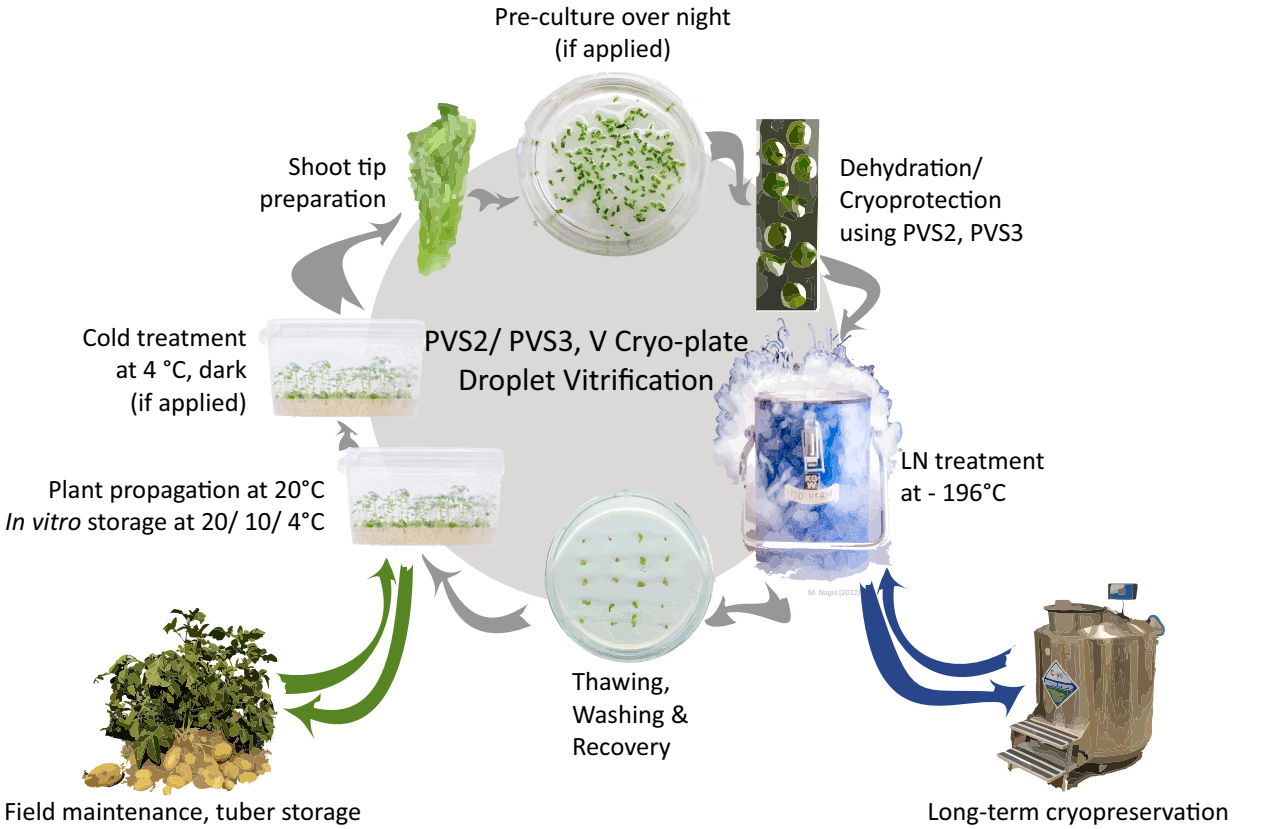



**Figure 7.4.1.** Principal procedure during PVS2, PVS3, V Cryo-plate droplet vitrification cryopreservation. PVS, plant vitrification solution; LN, liquid nitrogen

The number of potato landraces cryopreserved has increased considerably in the last 15 years (van Soest, 2006). Landraces and improved varieties have been cryopreserved mainly at CIP (PER001), IPK (DEU159) and NARO (JPN183) by using PVS2, PVS3 and the V cryo-plate approach, respectively. All approaches involve the propagation and cold acclimation of the *in vitro* donor plants, the excision of shoot tips followed by a loading and cryoprotectant step using PVS2, PVS3 or a cryo-plate and rapid immersion in LN (Figure 7.4.1). By using PVS2 droplet vitrification, CIP (PER001) has cryopreserved more than 4,000 cultivated potato accessions over the last 20 years (Vollmer et al., 2021) (personal communications Rainer Vollmer, 2021). IPK (DEU159) initially used DMSO droplet freezing (Kaczmarczyk et al., 2011) but has since changed to PVS3 droplet vitrification and has cryopreserved about 1,900 accessions located at IPK and in a backup storage facility at Leibniz-DSMZ in Braunschweig, Germany (Köpnick et al., 2018; Panis et al., 2020; Senula and Nagel, 2021). NARO has cryopreserved more than 640 accessions (personal communications Shin-ichi Yamamoto, 2022) using the V-cryo plate with PVS2 (Yamamoto et al., 2015). Other institutes, such as CZE027, CHN122, FRA010 and RUS001 [for RUS001 see Gavrilenko et al. (2019a); Efremova et al. (2021)] have started to cryopreserve their material. However, due to the increasing number of clonal plants in *in vitro* collections and field genebanks, combined with an increasing workload and limited funding for potato genebanks, specifically in Latin America, the risk of losing unique accessions is increasing. Cryopreservation can ensure a long-term conservation at minimum cost. Therefore, the Global Plant Cryopreservation Initiative, which is currently proposed (personal communication David Ellis, 2022), is urgently needed to help securely back up potato collections.

The Global Plant Cryopreservation Initiative is targeting the secure, long-term cryopreservation of at risk clonal and recalcitrant seed crop genetic resources collection, including potato. This initiative is a follow-up to the Feasibility Study for a Safety Back-up Cryopreservation Facility (Acker et al., 2017), which concluded that there was an urgent need for a global effort to operationalize cryopreservation as a long-term conservation strategy for genetic resources collections which cannot be backed up at the Svalbard Global Seed Vault (SGSV). The initiative proposes the establishment of regional centers of cryo excellence that can provide cryopreservation training, cryo back-up facilities, operational cryopreservation of genetic resources collections and establishment of a plant cryopreservation community of practice. The intent is to raise awareness of plant conservation and facilitate the development of expertise, protocols, guidelines, international standards and networks. Genetic resources collections of 10 crops are initially targeted, including potato, and hence this initiative could play a role in securely backing up all potato genetic resources collections.

## 7.5 Storage of orthodox potato seed

The majority of plants studied on Earth produce orthodox seeds that are desiccation tolerant and storable at low temperatures over long periods of time. In contrast, a smaller amount of angiosperms and gymnosperms produce 'recalcitrant' seeds, which are desiccation- and chilling sensitive and have short life spans (Kew, 2018). As orthodox seeds have the ability to survive extraordinary long periods of storage, e.g. seeds of *Nelumbo nucifera* Gaertn. found in north-eastern China germinated after about 1,300 years (Shen-Miller et al., 1995), they are ideal for the preservation of plant genetic resources. Most *Solanum* species of the *Petota* group produce fertile orthodox seeds. However, due to high heterozygosity, seeds cannot be used to store the allele combination of a particular genotype, but are very suitable for the conservation of individual genes or haplotypes or seed populations of wild species. Unfortunately, when summarizing the findings on storability of *S. tuberosum* seeds, it must be noted that the literature lacks current research results, and the terminology is confusing because small potato tubers are also considered as "seeds" for planting. Therefore, orthodox seeds of potato plants are also called 'true potato seed' or TPS.

Over the last decades, 'Genebank Standards for Plant Genetic Resources for Food and Agriculture' have been developed and repeatedly revised. A group of experts agreed on the ABS (Active-Base-Security) system and proposed to dry orthodox seeds between 5–20°C and 10–25% RH and to store only material with an initial germination of >85%. Seeds in (A) active storage are held at 5–10°C and 15% RH for about 30 years, from which distribution are made. Seeds in (B) long-term base storage, and (S) security back-up storage are often packed in airtight containers and stored between -20--15°C, under which the seed should remain in high quality for more than 30 years. In the case of (S), the cold storage rooms should be at a geographically far location from (B), preferably one back-up nationally and another internationally, such as the SGSV. Additionally, to ensure that accessions are rejuvenated before viability drops below 85% of the initial viability, an active viability monitoring program should be implemented (FAO, 2014). Since 2008, SGSV has stored a backups of many of the major collections of plant genetic diversity and more than one million samples from more than 89 genebanks have been deposited so far.

The true potato seeds of *Solanum* wild species are considered to be very long-lived. Towill (1983) showed

that 92% of the *S. demissum* seeds, 100% of *Solanum hjertingii* Hawkes seeds and more than 96% of the seeds of the *S. tuberosum* groups *Andigenum* and *Phureja* germinated after more than 26 years of storage at 1–3°C and 5% seed moisture content. In contrast, a more detailed study of true potato seeds from cultivated potato measured germinability of 159 *S. tuberosum* accessions stored at the USDA National Center for Genetic Resources Preservation, the same center which Towill worked at. These data measured a decline by an average of 57% within 24 years of storage at -18°C and undefined "low seed moisture content", resulting in an estimated half-viability period (P50) of 22 years (Walters et al., 2005). Seeds stored under ambient storage conditions at an experimental station in France had a P50 of 9.4 years (Priestley et al., 1985). These results led to the consideration that *S. tuberosum* seeds might have a 'medium short' longevity (Walters et al., 2005). Overall, there are few reports on germination after long-term storage or species-specific information. Therefore, further research is needed to draw comprehensive conclusions about the seed storage behaviour of all wild as well as cultivated potato seed.

Most true potato seeds, from both wild and cultivated species, exhibit physiological dormancy which can be broken either by a treatment of GA (2000 ppm $GA_3$), by alternating temperatures using 21°C and 6°C for 8 and 16 h, respectively (Bamberg, 2018), or by high storage temperatures and elevated moisture contents (Pallais, 1995; Pallais et al., 1996). For example, freshly harvested true potato seeds of the Peruvian variety 'Ccompis' were dried to 3.4, 4.2, 5.1, 6.1, and 7.3% moisture content (dry weight basis) and hermetically stored at 15, 30, and 45°C for 6 months. Seed dormancy was released, and germination increased during 4 months of storage at 3% and, more rapidly, at 5% moisture content and 45°C. When seeds were stored at a moisture content of 7% and 45°C, deteriorative processes occurred and germination decreased within the first month and was lost after 3 months (Pallais, 1995). In general, germination depends on seed quality, which is influenced by many other factors, including nitrogen levels during seed production (Pallais and Espinola, 1992) and the position in the inflorescence from which seeds originate. Larger seeds with higher germination and better seedling growth have been obtained from late-harvested primary inflorescences (Almekinders and Wiersema, 1991). Beside the reproduction of wild species, seed quality and dormancy breaking are of great relevance in the production of potato tubers from true potato seeds, such as in the production of an inbred hybrid potato system. Further studies and developments are necessary in the future to produce large quantities of high-quality seeds with lower dormancy level.

Storage of true potato seed is usually favored for accessions of wild species, but occasionally landraces are also maintained as seed, especially in Latin American countries. The survey results show that 12 participants (ARG1347, CAN064, COL017, CUB005, DEU159, ECU023, GBR251, GTM001, NLD037, PER001, RUS001, USA004) preserve true potato seeds. Unfortunately, the survey could not fully clarify whether true potato seeds belong to wild potato species or cultivated potato and whether the ABS system is applied in the different genebanks. The responses indicate that seven genebanks actively store their material in (A) in aluminum or paper bags at 4° and 50–65% RH. Only seven collections holders have the option of storing (B) samples in sealed aluminum bags at various temperature between -10--20°C, and eight genebanks have backed up at least 50% of their collections at the SGSV or elsewhere. To apply the 'Genebank Standards for Plant Genetic Resources for Food and Agriculture', most genebanks need to improve their facilities (e.g. by additional installation of cold storage and drying facilities), equipment (e.g. vacuum sealers) and consumables (e.g. aluminum foil bags).

## 7.6 Challenges of potato germplasm maintenance and steps to improve

The application of best storage and maintenance practice is the foundation for the long-term conservation of potato genetic resources to maintain the full genetic potential for future generations. High priorities should be given to storage conditions and handling to ensure a long-term survival of this valuable material.

**Field maintenance.** Most national genebanks in Latin American countries, but also genebanks in Europe, maintain up to 100% of their collections in the field, where the material is exposed to severe environmental risks. The chances of genetic drift and also loss are high. In addition, optimum tuber storage facilities with controlled cold rooms and cleanable plastic trays are not always available. High priority should be given to adequate conditions for tuber storage and optimal field management. It is highly recommended to duplicate and/or back up field collections *in vitro* or *in cryo* both on site and in a geographically distinct location.

***In vitro* slow growth (medium-term) storage.** Overall, 21 genebanks fully or partially conserve the material through slow growth storage. Of those, only 12 genebanks reported having cold storage facilities available and only nine have backed up their collections elsewhere. Priorities include research to improve the methodology of slow growth storage, additional cold storage facilities, and an *in vitro* back up system for safety duplicates.

**Cryopreservation.** Cryopreservation enables the long-term conservation of clonal potato accessions, and possibly true potato seeds, at minimal costs. However, currently only three genebanks (PER001, DEU159, JPN183) are intensively cryopreserving their collections. To avoid the loss of unique material in the field or *in vitro*, further cryopreservation efforts are needed. In parallel, standards for 'best practice' have to be established and research on optimum cryo-preservation conditions, fundamental processes, and the effects of long-term cryopreservation have to be intensified. If material is stored only *in cryo*, an Active-Base-Safety (ABS) system should also be considered involving different storage sites and secure back up storage. The Global Plant Cryopreservation Initiative focuses on all these aspects and needs to be supported to ensure a long-term conservation of potato.

**Seed storage.** Although the storage of orthodox seeds has been extensively studied, information on the species of the *Solanum* group *Petota* is very rare. The long-term viability of seed of cultivated and wild species and their optimum storage conditions have not been sufficiently studied, and as indicated earlier there is good evidence that true potato seeds and seed from potato wild relatives may not store as long as originally thought. Although cryopreservation of true potato seeds is an option, this has not been researched. Further, not all genebanks are currently capable of adhering to the Genebank Standards, including the ABS system. Therefore, there is an urgent need to: 1) back up high-quality seeds under dry conditions in aluminum foil bags and low temperatures at different sites, including the SGSV, 2) provide infrastructure to those genebanks which do not have cold storage capacities, and 3) initiate research into long-term seed storage behaviour and cryopreservation of true potato seeds.

Maintenance of potato landrace and other Andean crops at the Parque de la Papa in Cusco. Photo: Manuela Nagel/ IPK

# 8 MANAGEMENT OF THE COLLECTIONS

## 8.1 Establishment of procedures and protocols

Detailed written procedures and protocols are essential for the safe and effective transfer and exchange of experience and knowledge between staff and genebanks, and for assuring the best possible storage, regeneration and distribution of high-quality seed and clonal material. Out of 32 genebanks, 26 reported having established protocols and documents for fundamental processes of 'storage and maintenance' of accessions as well for 'characterization' (Figure 8.1.1). Twenty-four genebanks have written procedures for 'regeneration' available and 21 genebanks have procedures for 'health of germplasm' and 'documentation'. Protocols for 'distribution', 'safety duplication', 'acquisition' are only reported by 18, 17 and 16 genebanks, respectively, and only 16 genebanks can provide a copy of their protocols. However, half of participants (15 genebanks) follow protocols for six to eight functions, and of those, nine genebanks (DEU159, ESP016, EST019, NLD037, PER001, RUS001, SVN019, SWE054, USA004) have protocols for all functions. Two genebanks (DEU159, NLD037) are ISO 9001/2015 certified. In the last survey (van Soest, 2006), half of the participants reported keeping protocols for two to six genebank functions, indicating

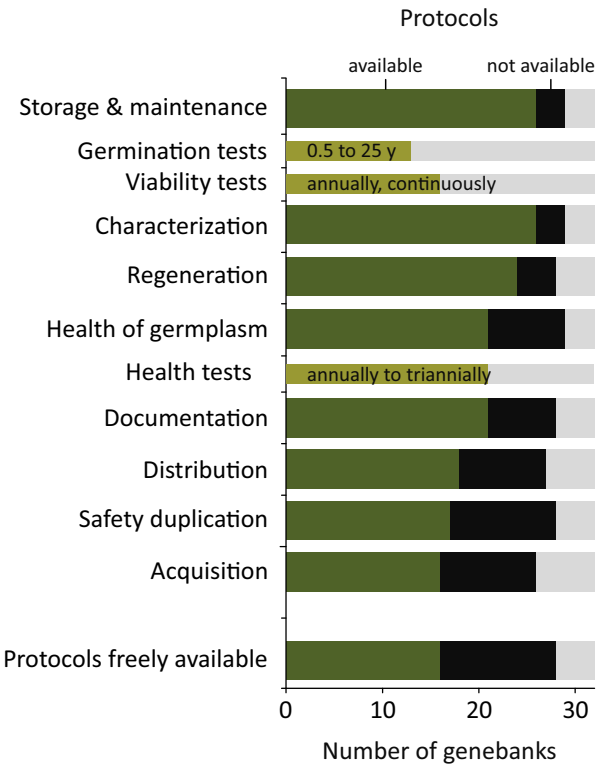



**Figure 8.1.1.** Availability of germination, viability and health tests protocols and written procedures in genebanks responding to the survey (see chapter 6.3). Green, protocols available and test performed; black, protocols not available; grey, no information provided.

an increased awareness of the importance of written procedures. In summary, fundamental aspect of potato germplasm storage and maintenance are documented by the majority of genebanks. However, for at least one function, most genebanks cannot provide protocols. To ensure high quality seed and clonal material, and adequate guidance for technical staff, it is highly recommended that all procedures are fully and clearly documented.

## 8.2 Regeneration

Most conservation approaches require frequent regeneration, but at different intervals. In general, the frequency of regeneration is as follows: field maintenance > slow growth storage > seed storage > cryopreservation. Field maintenance usually requires annual and slow growth storage an annual/biennial regeneration. Depending on seed quality, quantity and storage conditions, seed regeneration may be considered after decades. Routine monitoring of potato in cryostorage is being done by CIP (PER001) and DEU159. However, it is too early to say when cryopreserved material will need to be renewed. To date, there has been no decline observed but it will be prudent for future generations to continue to monitor the material to ensure it is renewed prior to a decline in viability. In this respect, cryopreserved material can be viewed as very analogous to long-term orthodox seed banks where routine monitoring is needed. The difference with the cryopreserved material is that "extra" vials of randomly selected accessions may need to be cryopreserved so that material is available to future generations for monitoring viability (personal communication David Ellis and Manuela Nagel, 2022).

**Wild species.** The participants of the survey reported that overall about 1,260 accessions (8.3%) of the 16,550 accessions maintained require urgent regeneration (Figure 8.2.1). As most wild species are conserved as seeds, about 560 accessions (29.6%) of the collections in Latin America, specifically ARG1347, CUB005, ECU023, GTM001, and 650 accessions (25%) at PER001 need seed regeneration. In Europe and Asia, only 20 accessions would seem to require regeneration. In the last survey (van Soest, 2006), more than 3,600 accessions were classified as in urgent need of regeneration. Although the recent survey indicates an improvement, the collections of wild species in RUS001, NLD037, GBR251, CZE027 have decreased significantly and it should be assumed that the remaining material will likely lose viability over time. In any case, van Soest (2006) stated that although three holders used 20–30 plants for regeneration of seed, most genebanks used between 10–20 plants and two genebanks used fewer than 10 plants for seed multiplication. Unfortunately, this aspect of seed multiplication was not included in the recent survey. However, the situation is not expected to be very different. If a small number of plants is used for seed multiplication, challenges due to genetic drift are higher, increasing the likelihood of alleles being lost. Additionally, self-incompatibility can lead to problems with seed sterility during reproduction.

**Landraces.** Of the total collection of 15,744 landraces accessions, about 1,900 accessions (12.1%) need to be regenerated. Most accessions are maintained as clonal plants in *in vitro* slow growth storage or in the field. In Latin America, field maintenance predominates, and about 1,600 accessions, 53.0% of the Latin American landrace collections, specifically COL017, ECU023, GTM001, PER860, need to be regenerated. Several Latin American genebanks reported sub-optimum storage condition due to defective and missing cold, tuber and *in vitro* storage facilities. As a consequence, a high percentage of material requires urgent regeneration. In Europe, three genebanks (BEL023, BGR001, GBR251) have predominantly field maintenance, with 4.6% of the collections (320 accessions) requiring urgent regeneration. In comparison to the previous survey, the number of accessions of landraces that need urgent regeneration has decreased from 6,000 (van Soest, 2006) to 1,900. For reproduction in the field, 15–30 tubers are used (van Soest, 2006), while

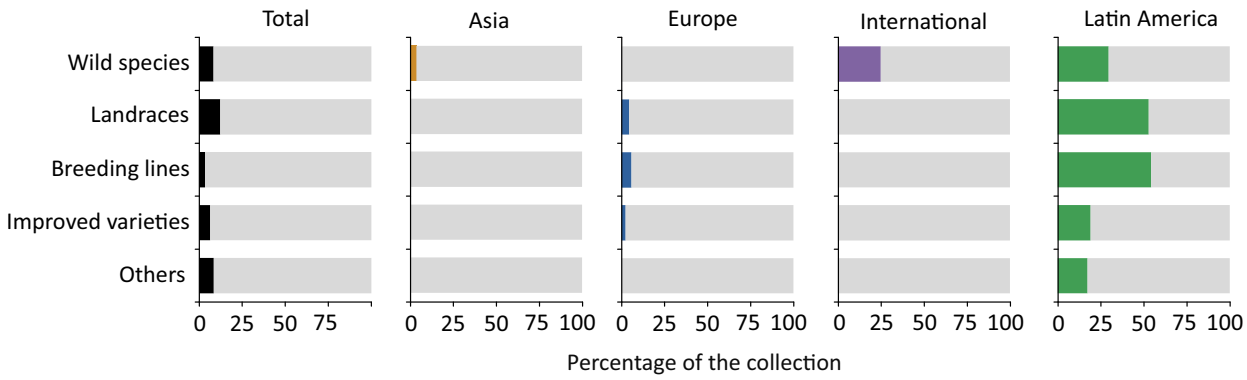



**Figure 8.2.1.** Percentage of accessions of wild species, landraces, improved varieties and breeding lines which requires urgent regeneration. Data of genebanks contributing to the survey (see chapter 6.3) are shown for all collections (total) and by region. North American genebanks (USA004 and CAN064) do not indicate having urgent regeneration needs.

for *in vitro* slow growth storage about 10 plantlets are used. Since specific allelic combinations are maintained, a higher number of plants is only necessary to assure that the material is not lost due to environmental risks. However, a backup *in vitro* or cryopreservation is strongly recommended.

**Improved varieties and breeding lines.** Comparable to landraces, the collections of improved varieties (16,147 accessions) and breeding lines (19,932 accessions) can be maintained in the field but are mostly stored in *in vitro* slow growth conditions. About 1,000 accessions (6.4%) of improved varieties and 700 accessions (3.4%) of breeding lines are in urgent need of regeneration. Again, Latin American genebanks, specifically BRA020, CUB005, COL017, GTM001, reported serious problems in regenerating improved varieties and BRA020 and CUB005 in regenerating breeding lines. In Europe, the high interest of breeders in this material ensures appropriate storage conditions for most of the material kept *in vitro*. However, urgent regeneration is also needed for accessions of improved varieties in IRL012, GBR0165 and specifically for breeding lines in BGR001. In the last survey, no need for regeneration was reported (van Soest, 2006). However, as the number of accessions has increased significantly in the last years (+5,000 accessions of improved varieties and +7,000 accessions of breeding lines), the regeneration capacities may not be sufficient to maintain all new lines.

## 8.3 Duplication status and security backups

The viability of plant genetic resources can be rapidly lost when environmental conditions are not adequate for growth. Biotic and abiotic stresses caused by fluctuations in growth conditions, pests, diseases and handling errors affect reproduction capacity, genetic stability and, consequently the survival and quality of the resources. To minimize the risk of losing valuable accessions during conservation, duplication and security backups of the material is common practice in genebanks. The Genebanks Standards for Plant Genetic Resources for Food and Agriculture (FAO, 2014) provide guidelines to back up collections (seed, field and *in vitro*).

**Duplication status.** Seventeen survey participants indicated that the germplasm is partially (ARG1347, BRA020, CZE027, COL017, ESP016, FRA010, JPN183, LVA006, PER860) or fully genetically unique (COL017) and is not maintained in another potato collection (Figure 8.3.1). Although genebanks are very efficient when the material is unique and not duplicated elsewhere, the risk of losing unique genotypes is high and the availability for distribution is hampered. Therefore, it has been common to duplicate and exchange the material among genebanks.

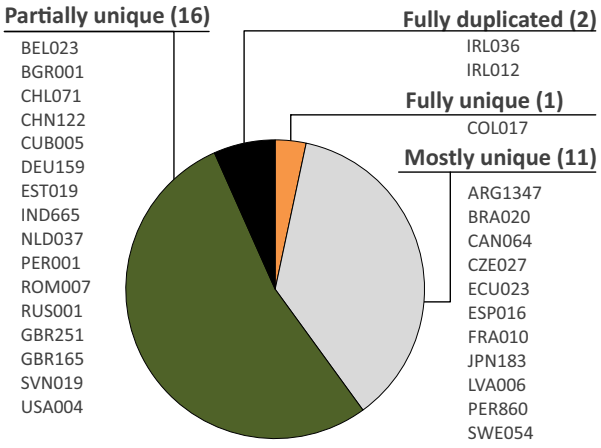



**Figure 8.3.1.** Duplication status (excluding safety backup) and uniqueness of the 32 genebanks participating at the survey.

**Security backups**. About 47% of the survey participants indicated organizing an active safety back up system at an external location or at their own facility (25%) (Table 8.3.1). As reported in chapter 7 and briefly summarized here, this system is well developed for wild species maintained as orthodox seed and, except for COL017, ECU023 and GTM001, most seed accessions are also kept at the SGSV (Figure 7.1.1). Landraces, improved varieties and breeding lines maintained as clonal plants in the field or *in vitro* are backed up to a lesser extent (Figure 7.1.1). However, about 100% of the *in vitro* collections of CAN064, IND665, PER001, SWE054, USA004 are safety backed up via dormant mini tubers or *in vitro* plantlets at external locations and about 100% of the field collections of CAN064, IRL036 and PER001 are duplicated at different locations. Only a few institutions (PER001, DEU159, JPN183, CEZ027) have initiated the safety duplication through cryopreservation and only DEU159 has backed up the cryocollection at an external location.

Different survey participants reported challenges to safety backup the collections. In most cases, duplication is labor intensive (ARG1347, FRA010) and requires additional expense (GBR165) for multiplication of seed or clonal plants. The current COVID-19 situation has increased the challenges for multiplication in some institutions (PER001). In addition, extensive storage capacities of collaborators are required and often unavailable (PER860). Political and logistic hurdles (COL017), breeders' rights (JPN183) and phytosanitary certificates (GBR165) complicate the situation and 56% of respondents mentioned constraints to duplicating their material elsewhere (Table 8.3.1).

## 8.4 Distribution

**National and international distribution.** The value of germplasm can only be recognized and exploited by distributing the material to breeders, researchers, farmers and other potential users. Access to the ger-

mplasm is subject to both national and international regulations (see chapter 11) and approximately half of the conserved material (46.0%, 30,900 accessions) is available at the national level and one third (36.7%, 24,600 accessions) at the international level (Figure 8.4.1).

Overall, for regional, national and international distribution, most accessions are available in Europe, in North America and at CIP (PER001, International) (Figure 8.4.1). In Europe, the survey participants estimated that about 14,000 accessions (20.8%) are available nationally and 11,000 accessions (16.7%) are available internationally. Most of them are internationally available from DEU159 (6,200 accessions), CZE027 (2,640 accessions) and NLD037 (1,450 accessions). RUS001 (1,200 accessions), IRL012 (600 accessions) and IRL036 (700 accessions) provide material only at the national level. Latin American countries can provide up to 4,100 accessions (6.1%) at the national level, most by ARG1347 (1,500 accessions), COL017 (1,600 accessions) and CUB005 (600 accessions). At the international level, material is only available from ARG1347 (1,500 accessions) and BRA020 (200 accessions). PER001, USA004 but also CAN064 can provide about 65% (4,900 accessions), 98% (5,800) and 100% (100), respectively, at national and international level. Although up to 46% of the material is available at the national level, only a small part (16%) has been requested (Figure 8.4.1). At the international level, the situation is worse. Here, only 2% of the material has been requested indicating some challenges in using the germplasm.

**Predictions about future distribution.** The delivery and request of genetic resources depends on political decisions, environmental changes and socio-economic factors. However, most genebank curators find it difficult to estimate whether this situation will change (28, or 47%) or predict "no change" (31) in the current situation (Table 8.4.1). However, curators of Latin American countries, especially BRA020, COL017, CHL071, GTM001, PER001 and PER860, expect an increase in demand for their germplasm in future.

**Type of material distributed.** Most potato collection holders are able to provide and distribute accessions of wild species (63%) and landraces (57%) (Figure 8.4.2). The number of available accessions of improved varieties and breeding lines is strongly limited and only 36% and 18% are available, respectively. European countries, PER001 and Latin and North American countries can provide the most wild species and landraces. Improved varieties and breeding lines are additionally available in Asian countries, in particular CHN116 and JPN183.

Due to political regulations, there are some discrepancies between the type of material and availability at national and international level. Most wild species can be supplied mainly as seeds by USA004 (4,000 accessions), DEU159 (1,200 accessions), NLD037 (1,200 accessions), PER001 (1,200 accessions) and ARG1347 (1,100 accessions). Landraces are usually available in the form of tubers or *in vitro* plantlets and can be delivered by PER001 (3,400 accessions), DEU159 (2,200 accessions), USA004 (1,200 accessions), ARG1347

**Table 8.3.1.** Duplication status and constraints of survey participants to duplicate potato germplasm elsewhere.

| | Yes | No | No answer | Total |
|---|---|---|---|---|
| Safety duplication in other institutions? | 47% (15) | 50% (16) | 3% (1) | (32) |
| Any safety duplicates in the own facilities? | 25% (8) | 63% (20) | 13% (4) | (32) |
| Constraints to duplicate elsewhere? | 34% (11) | 56% (18) | 9% (3) | (32) |

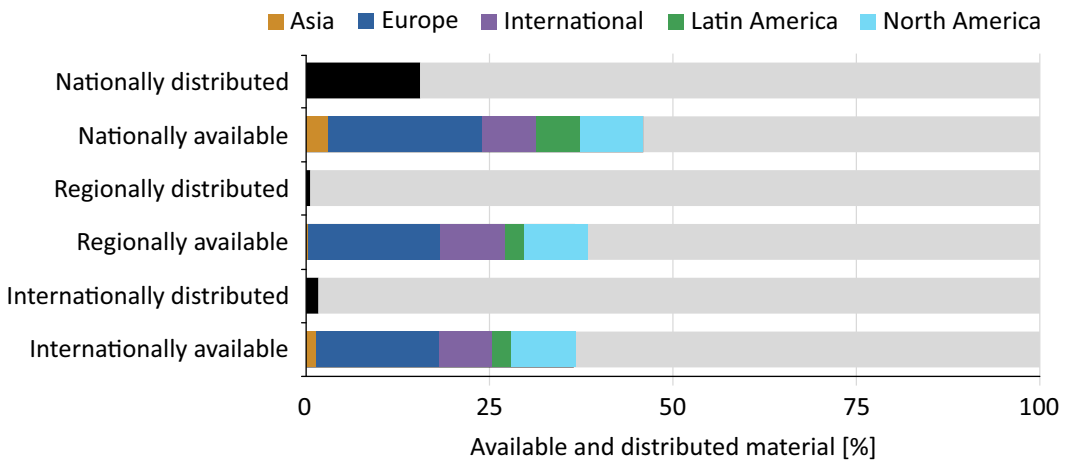



**Figure 8.4.1.** Availability and distribution of potato germplasm of genebanks participating in the survey. Black bars represent the total amount of distributed material.

(400 accessions) and COL017 (1,200 accessions). Most improved varieties are available from DEU159 (1,900 accessions), CHN116 (700 accessions), CZE027 (700 accessions) and IRL015 (500 accessions). Breeding lines can be requested from CHN116 (1,400 accessions), JPN183 (700 accessions) and DEU159 (600 accessions).

**Adequacy of distribution procedures.** One third of the genebanks (13) have the capacity to provide landraces, improved varieties and breeding lines as clonal *in vitro* plantlets (Figure 8.4.3). Most participants are able to provide between 1–6 *in vitro* plants or minitubers for a standard request. Depending on the type of user and the request, the curators of DEU159, EST019, FRA010, GBR165 and LVA006 can also provide between 2–6 tubers. In terms of seed, sufficient or partly sufficient amounts are available for distribution by nine and five potato collections, respectively, and often about 50 seeds are provided. Most genebanks have sufficient (23 participants) or partly sufficient (two participants) procedures for preparing phytosanitary certificates and 24 participants have at least partly sufficient procedures for healthy distribution. Procedures for packaging and shipping are less developed and only 15 genebanks have adequate procedures for this.

**Recipients of distributed material.** Based on the average of three years, 21 genebanks distributed approximately about 12,000 potato accessions (Figure 8.4.4). Eleven genebanks delivered more than 100 accessions, including USA004 (7,000 accessions), PER001 (1,900), DEU159 (830), FRA010 (500), SWE054 (380) and NLD037 (300). On average, about 66.4% of the material was requested by domestic users, 9.6% by academic researchers, 7.2% by foreign users, 5.6% by farmers and farmers' organization, 3.0% by private plant breeders and 1.1% by NGOs. However, the users of the delivered material differ between the countries and may reflect the different strategies of the genebanks. In AGR1347, CHN122, COL017, DEU159 and GBR251 most users were academic researchers. In CZE027, SWE054, PER001, USA004 and CAN064, domestic users requested most material. In FRA010 (500 accessions), private plant breeders are most interested in the accessions. Material was supplied to

**Table 8.4.1.** Expected changes in the distribution quantity of genebanks participating in the survey.

| | Increasing | Decreasing | No change | Don't know | No answer | Total |
|---|---|---|---|---|---|---|
| Nationally | 25% (8) | 3% (1) | 31% (10) | 28% (9) | 13% (4) | (32) |
| Regionally | 16% (5) | 3% (1) | 22% (7) | 38% (12) | 22% (7) | (32) |
| Internationally | 13% (4) | 3% (1) | 25% (8) | 47% (15) | 13% (4) | (32) |

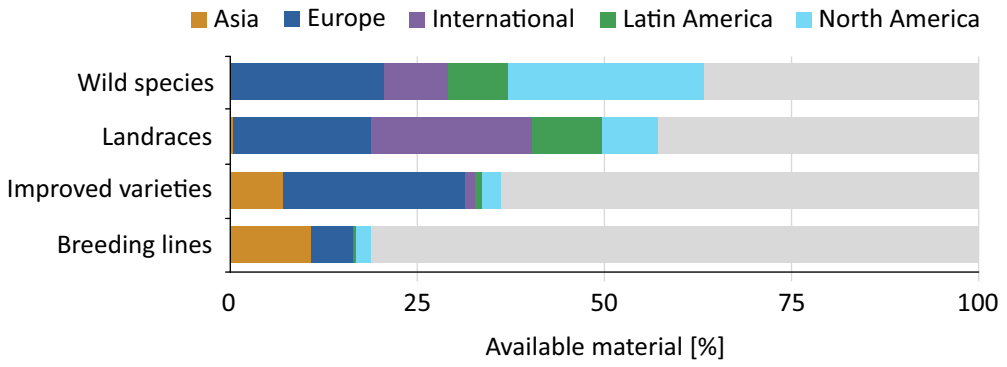



**Figure 8.4.2.** Type of available germplasm at different potato germplasm collections participating in the survey.

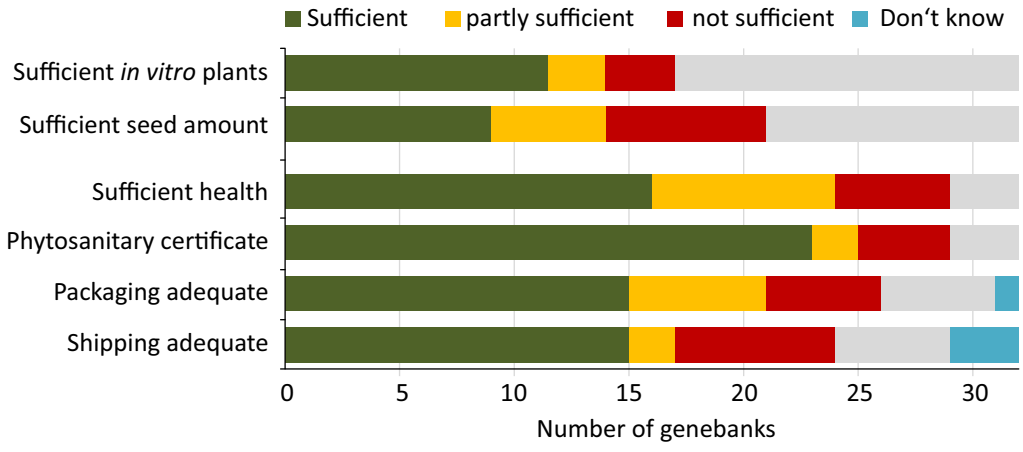



**Figure 8.4.3.** Availability of the germplasm and adequate procedures for distribution of genebanks participating in the survey.

NGOs from DEU159, SWE054 and CAN064. There are also some genebanks that reported not having distributed any material in the last three years (i.e. BGR001, GTM001, LVA006), or that do not keep records of distributions (i.e. PER860 and LVA006). When genebanks provided large amounts of material, it can be accessed through different websites, including GRIN-Global, Genesys, EURISCO and Europotato, or the institution-specific websites of DEU159, GBR251 and NLD037.

Most genebanks (20) have restrictions on the usage of the material and charge (12) for distribution (Figure 8.4.5). The restrictions are often based on legal aspects or agreements (e.g. ITPGRFA) and the material is usually only delivered after fulfilling country specific access laws and transfer agreements (BRA020, CAN064, COL017, ECU023, EST019, GBR251, GBR165, PER001). Other collections are reserved for researchers only (BGR001, PER860) or researchers and breeders (CZE027, FRA010) or to researchers, breeders and for educational programs (NLD037, SWE054, PER001) and depend on the availability of material (IRL012). When the material is released for distribution, most genebanks can cover the cost of the propagation and storage of the accession (19 genebanks) but only 14 and 12 genebanks are able to cover the costs for the shipment and phytosanitary inspections and certificates, respectively. When costs are incurred, some genebanks (DEU159, PER001) often differentiate between the type of users (i.e. users from developed or developing countries, hobby growers) or charge a general fee per accession (JPN183: Yen 570; PER001: USD 20; IND665: Rs 5000; DEU159: EUR 2). The shipment procedure is in most cases covered by the recipients and can range from the cost of postage to USD 500 (BRA020). Similarly, the costs for the phytosanitary inspections and certificates must also be paid by the recipients and can range from USD 75 (PER001), EUR 200 (LVA006) and shared costs for ELISA tests (FRA010).

## 8.5 Challenges and predictions for collection management

**Limitations.** Potato collections can be composed of wild species maintained and distributed as seeds, as well as landraces, improved varieties, breeding lines and research collections usually maintained and distributed as clonal plants in the form of tubers, *in vitro* plants or minitubers. The basic maintenance (Figure 6.1.1) of the different types of germplasm requires various basic equipment and facilities, including fields, greenhouses, growth cabinets with different temperatures, cold storage, tissue culture facilities, and facilities for cryopreservation. Additional staff, equipment, consumables and IT support are required when the collection is regenerated, duplicated, digitized, distributed, characterized and evaluated.

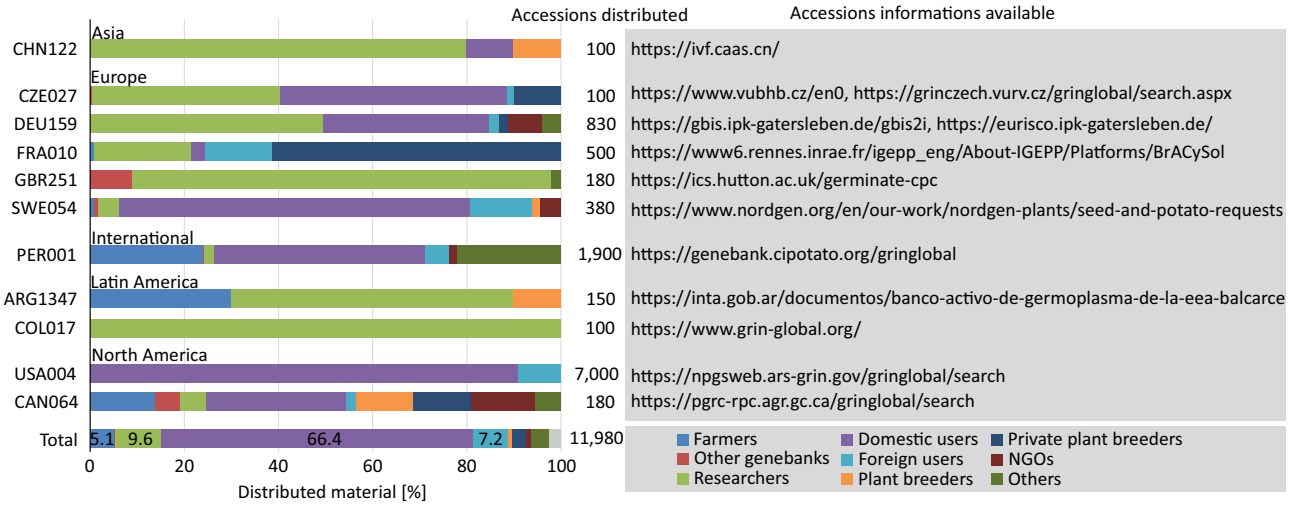



**Figure 8.4.4.** Recipients of the distributed material. Right, number of accessions distributed as an estimated average of three years.

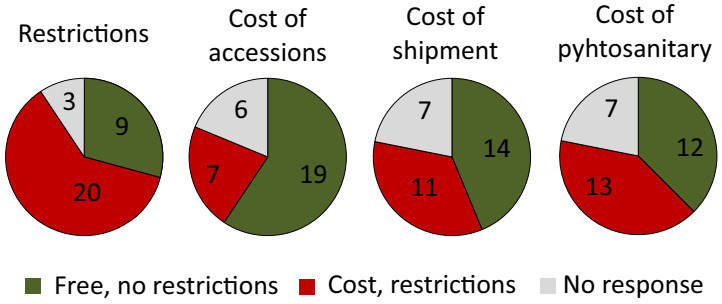



**Figure 8.4.5.** Restrictions and costs of distributions of genebanks participating in the survey.

Most curators consider staff shortages to be a major problem (Figure 8.5.1). In total, 15 potato collections have had to reduce staff in recent years. The technical support in BRA020, for example, has been halved, as between 2016–2021 the technicians in the *in vitro* laboratory were reduced from four to two and in the greenhouse and field from five to two (personal communications with Caroline Castro, 2021). Similarly, the limitation of funding reported by 14 curators increases the risk that equipment and facilities cannot be renewed and updated. As a consequence, most curators report a lack of, broken or old facilities and equipment (12), problems with plant health, virus testing and elimination (12) as well as limited capacities for hiring trained staff (10), for characterization and evaluation (8), digitalization of data (4), genotyping (4) and cryopreservation (3). As staff and funding are essential for the propagation of the material, a shortage forces the curators to focus on the most basic processes or to reduce the number of accessions within the collection to a manageable level and decrease the risk of losing valuable material.

Other constraints relate to a lack of research on potato genetic resources and their storage and propagation behavior. Low viability of the accessions, seed set and available quantities of seed are of concern for five curators. Two curators need improved protocols for pollination, seed germination and seed storage and two curators need improved procedures to eliminate duplicates. Other constraints may be difficult to change: limited access to germplasm collection due to legal regulations (5) and environmental stresses during reproduction in the field (5).

The survey participants were asked to predict the future situation for their collection management. Between 21–29 participants could forecast the situation in 2025 (Figure 8.5.2).

**Predictions on funding.** Funding is moderate in Asia with little change expected, although JPN183 expects some cut by 2025. In Europe, the situation of eight collections is good (DEU159, IRL036, ESP016, EST019) or moderate (four genebanks). Only two genebanks (NLD037, BGR001) suffer from a lack of funding and most expect this situation to change. Most collection curators in Latin America (ARG1347, BRA020, CUB005, PER860) confront serious funding problems, but some expect the situation to improve (ARG1347, COL017,


**Figure 8.5.1.** Constraints faced by the 32 genebank curators in the last years. The numbers in brackets indicate the number of genebank curators that have been confronted with these specific problems.

PER860). The curators of PER001 expect a further cut in basic funding.

**Predictions on staff retention.** The situation regarding the retention of staff is comparable to funding. Here, CHN122 and Latin American collections (CUB001, PER860) expect the situation to improve. Depending on the country, the situation in Europe is very different. A good to moderate situation is reported by BEL023, CZE027, DEU159, ESP016, EST019, FRA010, GBR165, IRL036, LVA006, NLD037, ROM007, SVN019 and SWE054, whereas GBR251 faces some problems. FRA010, GBR165, GBR251, LVA006, expect more challenges in this area by 2025. The situation for USA004 is moderate.

**Predictions on genetic variation in the collections.** Most participants assume that genetic variation in the collections is sufficient to good and expect it to remain sufficient in future. Overall, the curators of BEL023, COL017, IRL012 and JPN183 assume that genetic variability in the collection is not adequate but do not expect this to change in the future.

**Predictions on access to information about the germplasm.** Based on improved digitalization, network activities and various global initiatives, most participants predict a significantly improved access to information. Although access is currently not at the level desired for some collections, Asian (CHN122), Latin American (ARG1347, BRA020, CHL071, PER860) and European genebanks (BEL023, FRA010, IRL012, SVN019, SWE064) expect a substantial change. Only CHL071, FRA010, IRL012, GBR165, CUB005 predict that the situation will remain unsatisfactory or expect it to worsen.

**Predictions about user support.** Most curators do not expect strong support or feedback by users. Only few curators (GBR251, USA004, BRA020) report good feedback and expect this situation to continue. PER860 and BGR001 predict strong change and improvement.

**Predictions about donor interest.** Of the 21 genebanks able to assess this situation, Latin American genebanks (CHL071, COL017, ECU023, PER860) indicated that donor awareness of the need for conservation is poor. An improvement of the situation is only seen by PER860, LVA006, ESP016.

**Predictions about the level of use by breeders.** Most genebanks expect a positive change in the use of the collections by breeders. Currently, some Latin American (CHL071) and European (FRA010, IRL012, LVA006, USA004) collections are frequently used by breeders, while other European (BEL023, BGR001, CZE027) and Latin American genebanks (ARG1347, COL017, BRA020, PER860) anticipate an increased use of the collections for breeding in the future.

**Prediction on the level of use by researchers.** Most Latin American (ARG1347, BRA020, COL017, CUB005), European (BEL023, BGR001; CZE027, DEU159, FRA010, EST019, ESP016, GBR251, GIRL012, NLD 037, IRL036,

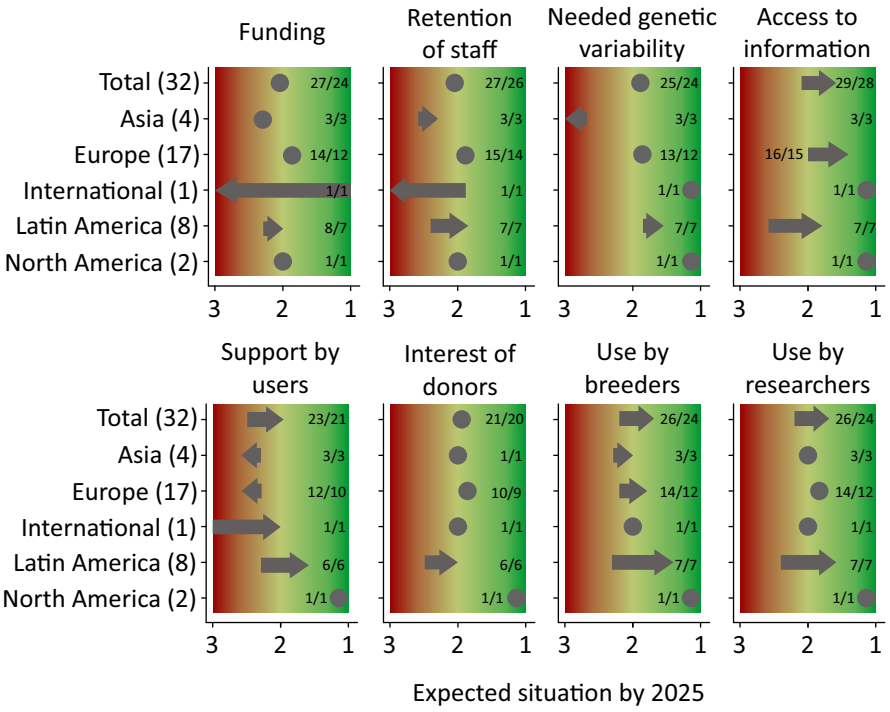



Figure 8.5.2. Current and expected situations in the collection management of 32 participating genebanks by 2025. The numbers at the end of each line indicate the current/ expected situation indicated by the respondents. 1 = high/good, 2 = adequate/moderate, 3 = not sufficient/bad.

LVA006, SWE064, USA004) and Asian (CHN122, IND665) genebanks consider that they are already moderately or well used by researchers and most expect this situation to improve. CHL071, ECU023, SVN019, JPN183, however, predicted no change in this area.

Overall, except for funding, staff retention and user support, most aspects are projected to slightly improve. Most improvements were seen in the area of accessibility of accession information and use by breeders, which may in turn improve the funding situation in the future.

## 8.6 Recommendations to improve collection management

**Protocols.** Only nine genebanks (DEU159, ESP016, EST019, NLD037, PER001, RUS001, SVN019, SWE054, USA004) keep protocols for all procedures and two (DEU159, NLD037) are certified by ISO 9001/2015. In summary, fundamental aspects of potato maintenance are documented by most genebanks. However, most genebanks participating in the survey cannot provide protocols for all procedures. To ensure high quality of the seed and clonal material and an appropriate guidance for technical staff, it is highly recommended that all procedures are fully documented.

**Regeneration.** Regeneration capacity needs to be improved, especially in Latin American countries. About 8.3% of wild species accessions maintained require urgent regeneration. In particular, the need to regenerate a total of 1,210 accessions is high in ARG1347, CUB005, ECU023, GTM001 and PER001. To avoid the risk of genetic drift and reduced seed set, plant propagation with a higher number of individuals in the population is required for seed production from wild species. About 12.1% of landraces, 6.4% of improved varieties and 3.4% of breeding lines are maintained as clonal plants in *in vitro* or in the field and require regeneration. In particular, landrace accessions (1,600 accessions) in Latin America genebanks (COL017, ECU023, GTM001, PER860) are challenged by continuing plant propagation in the field and require urgent regeneration. Serious problems are also reported for improved varieties and breeding lines in BRA020, CUB005, COL017 and GTM001. In Europe, Asia and North America, only a small portion of the collections are in urgent need of regeneration, and thus the situation is less critical compared to genebanks in Latin American.

**Plant health.** Plant health and the possibilities of virus testing and elimination are major constraints for managing and distribution of the collections. Therefore, funding has to be improved for plant health testing and virus elimination to make collections available for use.

**Safety duplication.** Some of the clonal collections considered as fully (COL017) or mostly unique germplasm (ARG1347, BRA020, CZE027, COL017, ESP016, FRA010, JPN183, LVA006, PER860) have not been duplicated elsewhere. Therefore, there is an urgent need to support duplication activities and to overcome hurdles such as national regulations, intellectual property protection and phytosanitary issues to ensure the safety duplicated storage of plant genetic resources.

**Distribution.** Although about 30,900 accessions are available for distribution, only 12,000 distributed accessions were finally delivered, most by the largest collections (DEU159, USA004, PER001) or other European genebanks. However, to stimulate the use of the germplasm, the accessibility of the material based on legal regulations and accession information (digitized passport, characterization and evaluation, and genotyping data) has to be improved, in addition to better health conditions including virus elimination and phytosanitary certification.

**Staff training programs**. About 10 curators were concerned about the retention and the training possibilities of genebank staff. International online training programs could help to support adequate training.

Digital entry of herbarium information at CIP.
Photo: Michael Major/Crop Trust

# 9 DATA MANAGEMENT

## 9.1 Management and types of genebank data

Genebanks generate a large amount of information during acquisition, registration, storage, monitoring, regeneration, characterization, evaluation and distribution. This data (Figure 9.1.1) can be fairly static with a high degree of use and low frequency of updating, such as passport data, characterization data and protocols or standard operating procedures. Other information, such as phytosanitary certificates, inventory and evaluation data need to be updated more frequently. For short term and internal collection management, field books and specific lists are used. All these data have different formats and relevance. To ensure transfer of knowledge, and thus the efficient conservation and utilization of germplasm, these data must be stored and maintained adequately.

Genebank data was for a long time managed using paper index card systems and registers, and documentation focused mainly on the origin of the material and taxonomic classification (Weise et al., 2020). To make the material more accessible for outside use,

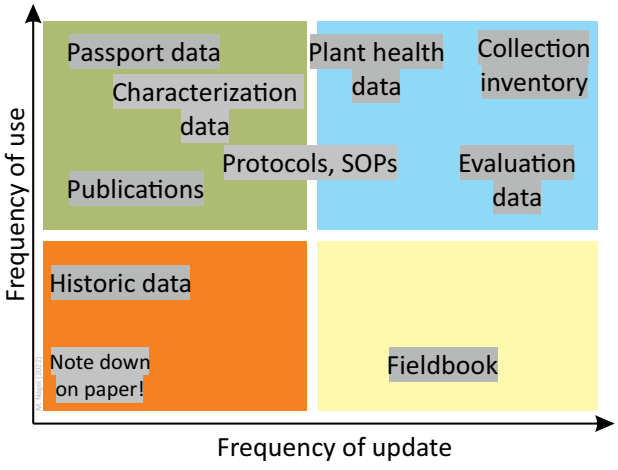



**Figure 9.1.1.** Degree of use and required update frequency of genebank data (personal communication with Matija Obreza, 2022).

most genebanks compiled a catalogue, the so-called 'Index Seminum'. Due to the complexity of the genebank processes, the first data management software was introduced to genebanks in the late 1960s and in DEU159 in the early 1980s (Knüpffer, 1989; Menting et al., 2007). The largest genebanks were able to implement their own in-house systems, such as GBIS

at DEU159 (Oppermann et al., 2015), GENIS at NLD037 (Menting et al., 2007) or Alelo at BRA020 (Alves and Azevedo, 2018). Some countries also developed transboundary cooperation networks such as the SESTO management system of the Nordic and Baltic countries or the Intergenebank Potato Database (Huamán et al., 2000). SESTO was replaced by GRIN-Global in 2020. The Germplasm Resource Information Network (GRIN) was initially developed by the United States Department of Agriculture (USDA). Thanks to joint efforts of the Global Crop Diversity Trust, Bioversity International and the USDA's Agricultural Research Service, GRIN-Global has been an open access tool since 2011 and provides a well-developed platform to manage genebank data, including inventory management. Since 2021, the new GRIN-Global Community Edition (GG-CE) offers a user-friendly interface for using and capturing data on mobiles, tablets and desktops, improved taxonomy search pages and enhanced access for public websites. As a result, the number of genebanks, here specifically potato collections, evaluating and adopting GRIN-Global is increasing (Figure 9.1.2).

To ensure long-term knowledge transfer and efficient management, high priority should be given by genebanks to the development and implementation of an effective information system. Figure 9.1.3 clearly shows that paper and spreadsheet tools are an intermediate solution and have their own advantages. For long-term reliability, consistency and accessibility, however, only databases and trained staff can ensure sustainable genebank management. Unfortunately, due to lack of funding and IT support, some genebanks are hardly able to use databases or to generate or transfer data to an appropriate system.

Genebank information management systems typically comprise three to four layers, including basic information, so-called passport data, conservation management data, characterization and evaluation data,

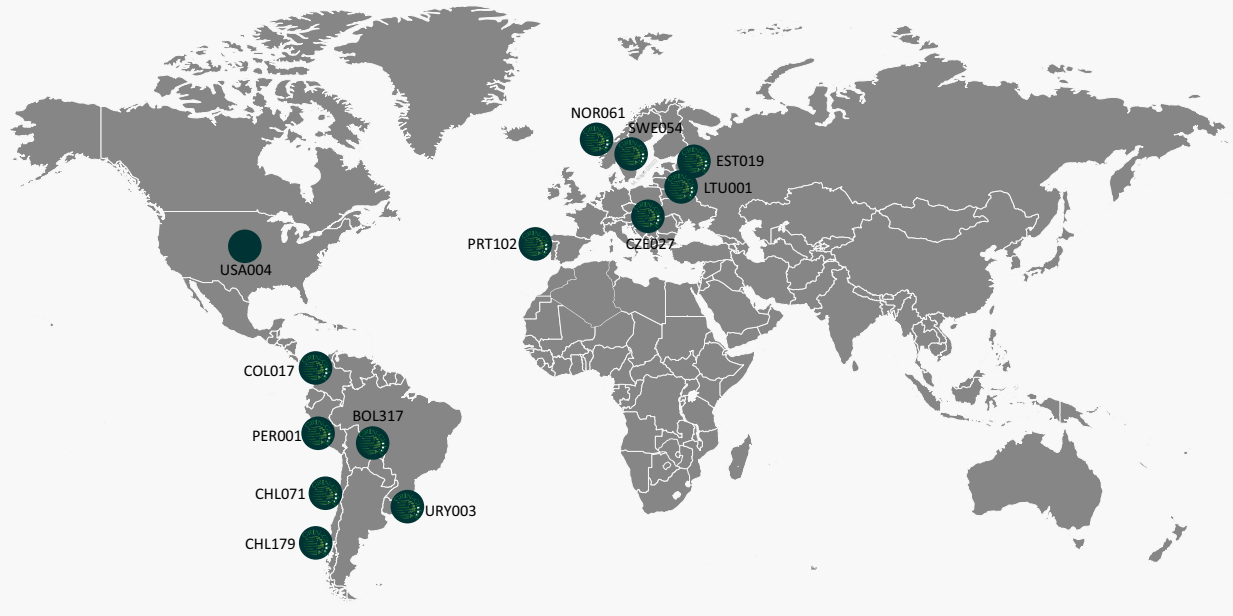



**Figure 9.1.2.** Potato germplasm collections that have already implemented (green) GRIN-Global (Source: personal communications Juan Carlos Alarcon Maldonado, CropTrust, 2022)

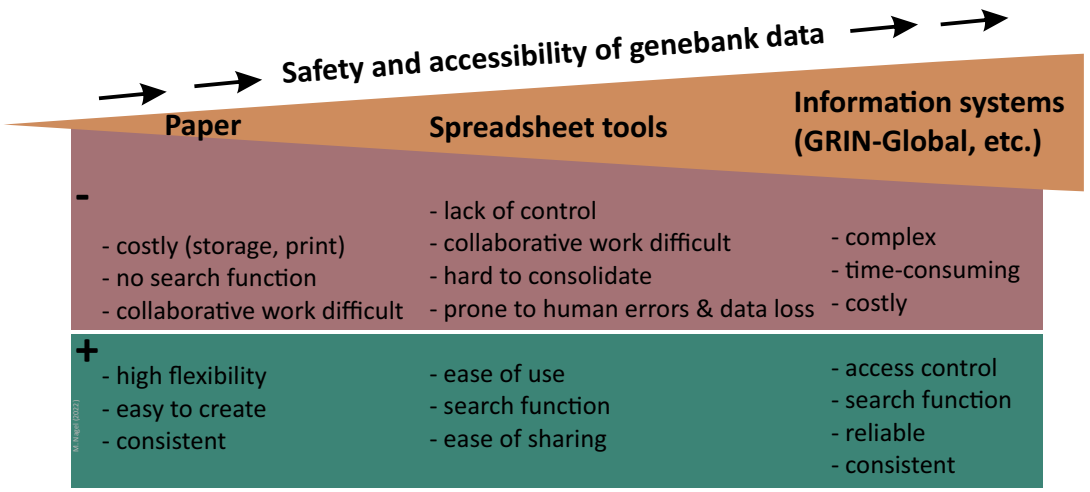



**Figure 9.1.3.** Pros and cons of the different tools used for the management of genebank data.

and in few cases genomic data (Figure 9.1.4) (Weise et al., 2020). The FAO Commission on Genetic Resources for Food and Agriculture (FAO, 2014) has developed recommendations on data standardization in the Genebank Standards and has also included standards for passport data (Alercia et al., 2015). In addition, other international initiatives such as the International DivSeek Network are elaborating standards and supporting the creation, integration and exchange of germplasm data. Furthermore, the Secretariat of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) has supported the introduction of Digital Object Identifiers (DOI) as unique and stable identifiers for genebank accessions (Alercia et al., 2018) which are easily accessible through the GLIS DOI portal. The DOI system allows genebank accessions to be linked to datasets, and enables publications and genomic data to be found automatically when DOIs are provided.

Managing of potato collections is particularly challenging due to the conservation of wild species through true potato seed and of landraces, improved varieties and breeding lines by clonal propagation (Figure 9.1.4). The crop therefore requires tools, protocols and operational procedures for the documentation of herbaria, field genebanks, seed storage, *in vitro* banks, dry (lyophilized) leaf banks, cryopreservation, plant health status, safety backup and distribution. Smaller genebanks in particular struggle to

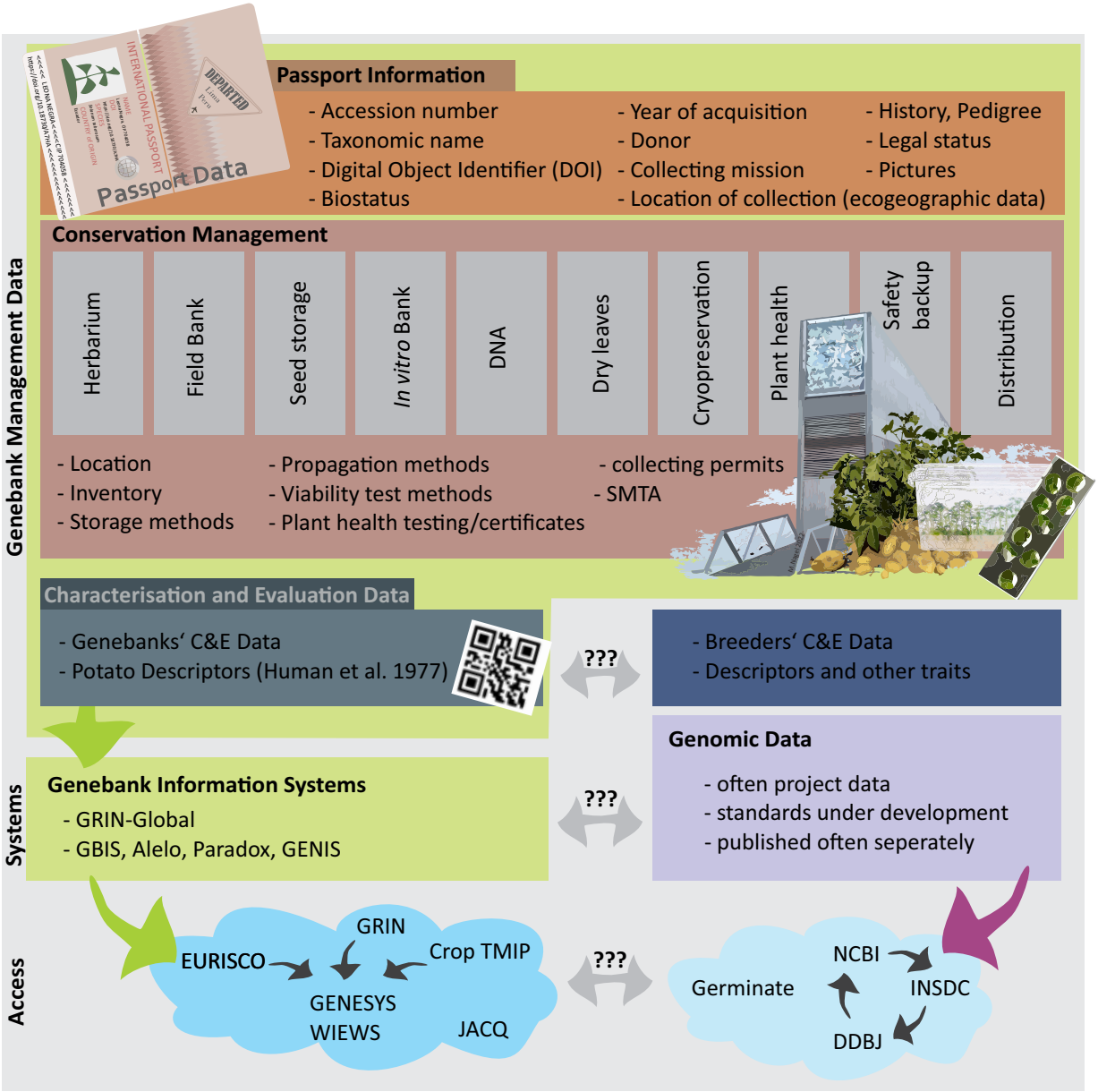



**Figure 9.1.4.** Consolidation and transfer of data through genebank information systems and web portals. EURISCO, European Search Catalogue for Plant Genetic Resources; Crop TMIP, Crop Trait Mining Informatics Platform; C&E, characterization and evaluation data; DDBJ, DNA Data Bank of Japan; INSDC, International Nucleotide Sequence Database Collaboration; GBIS, Genebank Information System; Genesys; Global Portal on Plant Genetic Resources; GENIS, Germplasm Resource Information Network; GRIN, Germplasm Resource Information Network; JACQ, jointly administered herbarium management system; NCBI, National Center for Biotechnology Information; SMTA, standard material transfer agreement; WIEWS, World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture.

implement the various tools needed to manage their collections. In addition, genebanks generate characterization and evaluation data based on descriptors for "Utilization of the genetic resources of the potato II" (Huaman et al., 1977; Gomez, 2000). This data can also be transmitted to aggregator systems such as EURISCO and Genesys. Although many collections are currently phenotyped and genotyped by breeders and third-party projects, the link between these and the genebank is poor. The DOI could support the traceability of these accessions. However, standards need to be developed and the links improved for the extended usability of all these data.

## 9.2 Accessibility of potato germplasm data

Most genebanks holding potato germplasm use electronic information systems to manage data on their collection. However, only 13 of these genebanks have fully implemented genebank information systems, of which seven (CAN064, COL017, CZE027, EST019, PER001, SWE054, USA004) use GRIN-Global (Figure 9.2.1). Other genebanks have developed in-house systems such as GBIS (DEU159), Paradox (RUS001), Germinate (GBR251), GENIS (NLD037), Alelo (BRA020), SIRGE (PER860) and three genebanks use other solutions (GBR165, ESP016) such as MS Access (IRL036). Although two collection holders (BEL023, CHN122) indicated that they do not use electronic systems and two genebanks did not respond, spreadsheets (i.e. MS Excel) are commonly used for data storage. As mentioned above, spreadsheet tools are advantageous intermediate solutions and can be structured in a way that facilitates the uploading of data into genebank information systems. To ensure long-term safety, reliability, consistency and accessibility of data, the implementation of genebank information systems is strongly recommended.

Similar to the previous survey (van Soest, 2006), and as an average across the 32 survey participants, passport data (61%) is the most frequently digitalized followed by the characterization (33%) and evaluation data (32%) (Figure 9.2.2). About 15 curators indicated that they organize some of their data in paper. About 100% of the passport data is available electronically for ARG1347, BRA020, BGR001, CHL071, CZE027, CUB005, DEU159, ECU023, ESP016, EST019, JPN183, LVA006, NLD037, PER001, ROM007, GBR251, SVN019 and SWE054 and USA004. For characterization and evaluation data, only ECU023, EST019, JPN183, SVN019 and USA004 reported to have 100% of their data available electronically. Although digitalization of data seems to have improved in recent years, it is strongly recommended that 100% of passport data and much more characterization and evaluation data be made electronically available.

In total, 19 genebanks provide direct access to a data subset through their own or other websites (Table 9.2.1), with one third of the collections nationally (BGR001, CAN064, ECU023, ESP016, DEU159, IRL036, RUS001, SVN019, SWE054) and internationally (CZE027, BGR001, DEU159, EST019, GBR251, IRL012, IRL036, LVA006, NLD037, PER001, RUS001, SWE054, USA004) available (Figure 9.2.3). The curators of 10 collections reported that the material is not accessible via internet (Figure 9.2.4). However, the European genebanks often use EURISCO and the European cultivated potato database as web portals, PER001 and USA004 uploading data to Genesys.

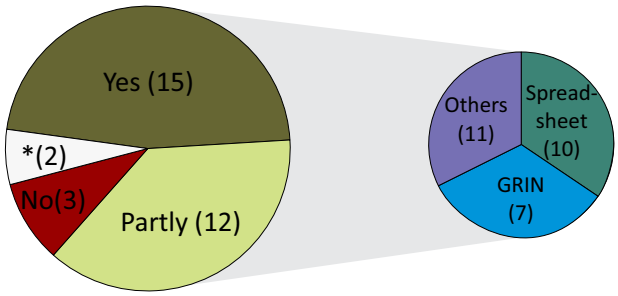



**Figure 9.2.1.** Potato collections using electronic information systems fully or partially. Among them, seven genebanks use the genebank information system Germplasm Resource Information Network (GRIN). The number in brackets indicates the number of responses. *no response; others indicate the usage of information systems such GBIS, Paradox, Germinate, GENIS Alelo or Sirge or other laboratory information systems (LIMS) or a combination of different systems.

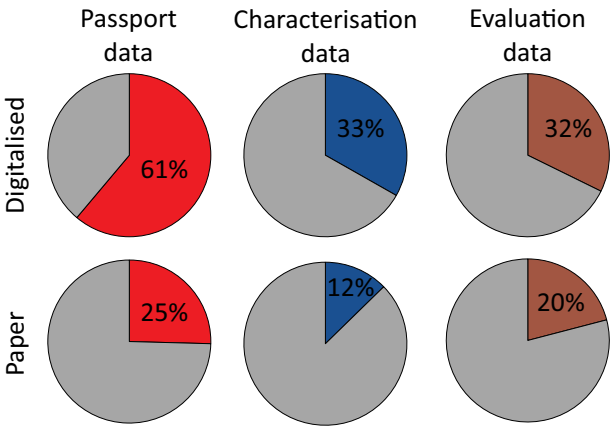



**Figure 9.2.2.** Digitalization and availability of passport, characterization and evaluation data in potato germplasm collections. Responses of 32 survey participants.

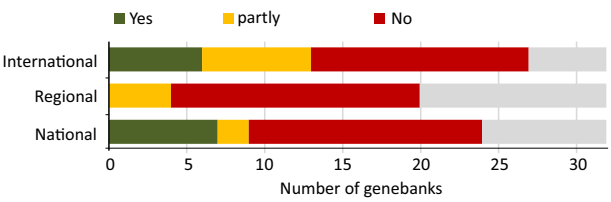



**Figure 9.2.3.** Number of potato germplasm collections that provide data in national, regional and international databases. Green, data are included; yellow, data partly included; red, data are not included in external databases; grey, no response. Responses of 32 survey participants.

The **EURISCO** catalogue stores passport and phenotypic information on plant genetic resources from about 400 European institutes and 2 million accessions. It is hosted and maintained at the Leibniz Institute of Plant Genetics and Crop Plant Research (DEU159) on behalf of the European Cooperative Program for Plant Genetic Resources (ECPGR). Data collected are based on the National Inventories of 43 member countries (Weise et al., 2017). Currently, data on about 15,000 accessions of *S. tuberosum* (19,000 accessions including synonyms) is accessible; including 4,200 accessions from DEU159, 2,400 accessions from CZE027 and 800 accessions from EST019.

**Genesys** is hosted by the Crop Trust and provides global access to information on plant genetic resources. It includes about four million accessions from 450 institutions around the globe including data from EURISCO and CGIAR genebanks. Genesys supports passport and phenotype data and can identify potential replicates/duplicates in the database based on available passport information. Genesys contains information on about 28,000 active potato accessions, including 25,000 accessions of *S. tuberosum*, 1,400 accessions of *S. acaule* and 1,200 accessions of *S. stoloniferum*. PER001, DEU159, USA004, UKR026, CZE027 and NLD037 hold the largest collections according to Genesys, as also identified by WIEWS (2021).

Beside the national and international databases, since 1990 the so-called **Inter-genebank Potato Database (IPD)** has comprised accessions of wild species from the Association of Potato Inter-genebank Collaborators involving CIP (PER001), US Potato Genebank (USA004), Groß Lüsewitz Potato Collection/IPK (GLKS, DEU159), Commmonwealth Potato Collection (CPC, GBR251), Center for Genetic Resources Netherland (CGN, NLD037), N. I. Vavilov Institute of Plant Industry (VIR, RUS001) and INTA, Balcarce (ARG1347) (Huamán et al., 2000). The IPD shows a global inventory of wild potato germplasm and matches accessions, thus duplicates that have been collected during the same mission but stored in different genebanks using different identifiers. Data from USA004 and NLD037 has been recently updated and the database, basically an Excel sheet, is still maintained by CIP and is accessible online. Over decades, IPD has supported collecting missions, research, collection management and can be the basis for the identification of core collections (personal communications John Bamberg, 2022). However, it would be helpful if this database is combined with data accessible through EURISCO or Genesys.

Genesys and EURISCO substantially support the conservation management, and hence the maintenance of the diversity of plant genetic resources, including duplicate finding, gap analysis and providing a link between passport, phenotypic and genomic data. However, it is a prerequisite that IT infrastructure and trained and qualified staff are available to create, curate and upload appropriate passport and phenotype data. In particular, for the effective use and reuse of phenotypic data, the FAIR (Findable-Accessible-Interoperable-Reusable) guidelines are an essential element for

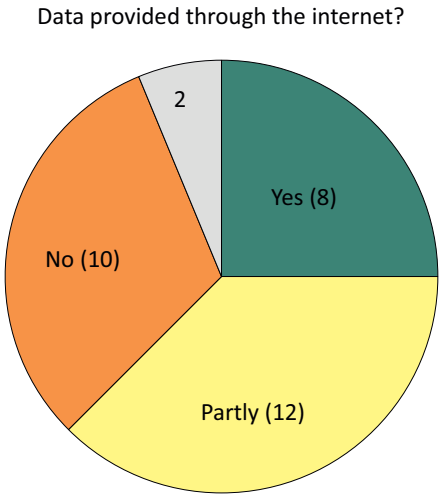



**Figure 9.2.4.** Number of potato germplasm collections that provide data through the internet. Responses of 32 survey participants.

**Table 9.2.1.** Accessibility of potato collections through following links.

| | Institution | Collection accessible |
|---|---|---|
| **Asia** | JPN183 | Link |
| | BGR001 | Link |
| **Europe** | CZE027 | Link |
| | DEU159 | Link |
| | ESP016 | Link |
| | EST019 | Link |
| | FRA010 | Link |
| | GBR251 | Link |
| | GBR165 | Link |
| | IRL012 | Link |
| | NLD037 | Link |
| | SWE054 | Link |
| **International** | PER001 | Link |
| **Latin America** | ARG1347 | Link |
| | BRA020 | Link |
| | COL017 | Link |
| | CHL071 | Link |
| **North America** | CAN064 | Link |
| | USA004 | Link |

future data use (Ghaffar et al., 2020). Genomic data are not held by these systems but are accessible via other platforms such as Germinate, Solgenomics, the Spud DB or through common platforms such as the National Center for Biotechnology Information (NCBI). However, the storage of genomic data and linkage to the passport data are not satisfactorily solved and the potato community urgently calls for better solutions. The DOIs assigned to samples and linked to source material in genebanks could be one of the options.

## 9.3 Required improvements for data management

**Implementation of genebank information systems.** The quality of genebank management is substantially linked to the quality of data management, as knowledge and information can be best transferred via standardized and high-quality data and workflows. Top priority should, therefore, be given to the implementation of a genebank information systems at every organization conserving potato germplasm, with the electronic recording of all data, including the electronic availability of passport, characterization and evaluation data and digitalization of voucher specimens. In addition, links need to be elaborated between accession IDs in different genebanks available in IPD and should be integrated in genebank data management systems and data transferred to the public domain. Public availability of data is a prerequisite for identification of unique accessions and duplicates, the analysis of gaps and the use of potato genetic resources.

**Implementation of FAIR data policy.** To enable a wide use of plant genetic resources data, the publication of phenotypic data should follow FAIR data principles and involve specialized platforms. Standards for the evaluation of phenotypic data (descriptors) need to be implemented in the system and used consistently to ensure a comparability of data in the future.

**Digital Object Identifiers (DOI)**. Consistent use of DOIs for all genebank accessions, which are freely available to PGR collections through the GLIS DOI portal, should be a requirement. The DOIs allow linking of material across genebanks, between passport, phenotypic and genomic data, and enable direct linkage to herbarium sheets that are often accessible via other platforms such as JACQ, a jointly administered herbarium management system.

**Staff training programs.** In order to implement standards and to create and digitalize phenotypic data, staff must be qualified. Therefore, specific training programs for data management must be implemented.

**Genomic data.** The current link between accessions and genomic data is unsatisfactory. Therefore, standards need to be further developed and the access clearly described and linked.

**Identification of duplicates.** To rationalize genebank collections, duplicates and unique accessions must be clearly identified via all available data (passport, characterization and evaluation, genomic data). Guidelines for the identification of duplicates and recommendation about the handling of duplicates must be developed.

Potato diversity. . Photo: Michael Major/Crop Trust

# 10 COLLECTION GAPS

Climate change and the growing world population are having a devastating impact on plant genetic resources, in particular on crop wild relatives and their habitats. In the US, about 7.1% of taxa of crop wild relatives are considered as critically endangered and 58.8% require urgent conservation (Khoury et al., 2020). In addition, in South America, about 90% of the original Atlantic rainforest is estimated to have been converted to farmland and urban territories, resulting in a threat to one third of the world's plant species (León-Lobos et al., 2012). Some potato crop wild relatives distributed between the southern USA to Chile and Argentina, an area where a quarter of all world's plant species are found, are critically endangered in their habitats (Castañeda-Álvarez et al., 2016). Therefore, due to the great potential of crop wild relatives to contribute traits for crop improvement (Vincent et al., 2013) and thus for food security, there is an urgent need to identify underrepresented taxa and to fill these gaps in *ex situ* collections before it is too late.

## 10.1 Gap analysis – a tool to aid conservation of plant genetic resources

In general, specific targets for the conservation of plants genetic resources include, for example, that 95% of all alleles of a random locus present in a target population at a frequency of over 5% are conserved. Marshall and Brown (1975) estimated that this could be achieved by collecting 50 individual plants from 50 populations/sites, although another estimate was by collecting 172 individual plants at random (Lawrence et al., 1995). However, the critical minimum sizes of populations to be collected is highly debatable because population size in natural habitats, demographic parameters and levels of genetic diversity vary and 50 or 172 accessions may not be sufficient (Maxted et al., 2008). Moreover, Vincent et al. (2013) showed that out of 1,667 crop wild relatives, about 1,250 taxa are present in genebanks with fewer than 50 accessions and 939 have fewer than 10 accessions. Although genetic diversity in the collections has not

been systematically assessed by genome sequencing, it could be speculated that there are considerable under-representations of taxa and of genetic diversity in *ex situ* genebanks. To identify so-called 'gaps' in the collections, comparisons between the actual distribution pattern of the species and the representation of these species in the collections, a so-called 'gap analysis' are performed (Margules, 1989; Maxted et al., 2008). This concept has recently been applied to a number of collections to improve our understanding of the representation of genetic diversity stored in our genebanks.

In principle, four steps were summarized by Burley (1988) and involve parameters at different levels (Figure 10.1.1). The first step (**1**) involves the identification of the specific biodiversity to be studied, e.g. site, taxa or landrace group. The second step (**2**) involves describing the biodiversity including the search for taxonomic details such as genus, species, accepted classification systems and consultation with taxon experts. To determine genetic diversity in genebanks, the parameter 'richness', the total number of genotypes or alleles present, or 'evenness', the frequency of different alleles, is usually calculated. Although, genetic diversity may not necessarily be related to ecogeographical differences (Del Rio and Bamberg, 2002), wide geographic or ecological amplitude is often taken as a proxy for genetic diversity (Maxted et al., 2008). In any case, environmental niche modelling techniques and geographic information systems (GIS) are often used to determine whether taxa are threatened. Maxted et al. (2008) suggested including the representation of taxa in herbarium and *ex situ* collections, their geographical distribution and coverage, intraspecific coverage, and potential for use in a threat assessment. The third step (**3**) is to revise current conservation strategies based on the results. This could include both *ex situ* and *in situ* interventions. In the fourth step (**4**), the effectiveness of conservation needs to be assessed and priorities continuously reviewed for both *in situ* and *ex situ* conservation *(Maxted et al., 2008)*.

## 10.2 Origin of the potato collections assessed by the survey

In order to determine the uniqueness of the collection in each country and to search for potential gaps, the participants were asked to estimate the proportion of accessions of national, regional and global origin. On average, 32% of all accessions are considered to be of national origin (17,300 accessions), 13% are of regional origin (6,080) and 55% are of international origin (32,000) (Figure 10.2.1). Most accessions maintained in Latin America and CIP (PER001) are of

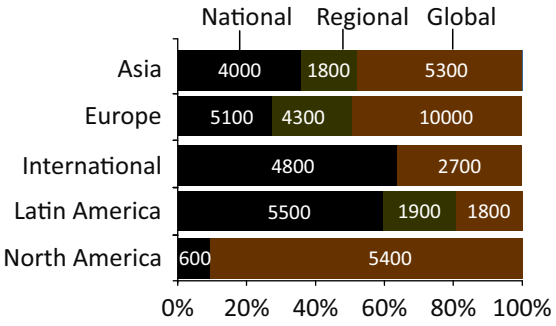



**Figure 10.2.1.** Estimated number of accessions that are of national (black), regional (dark green) and global (brown) origin. Responses of 32 survey participants.

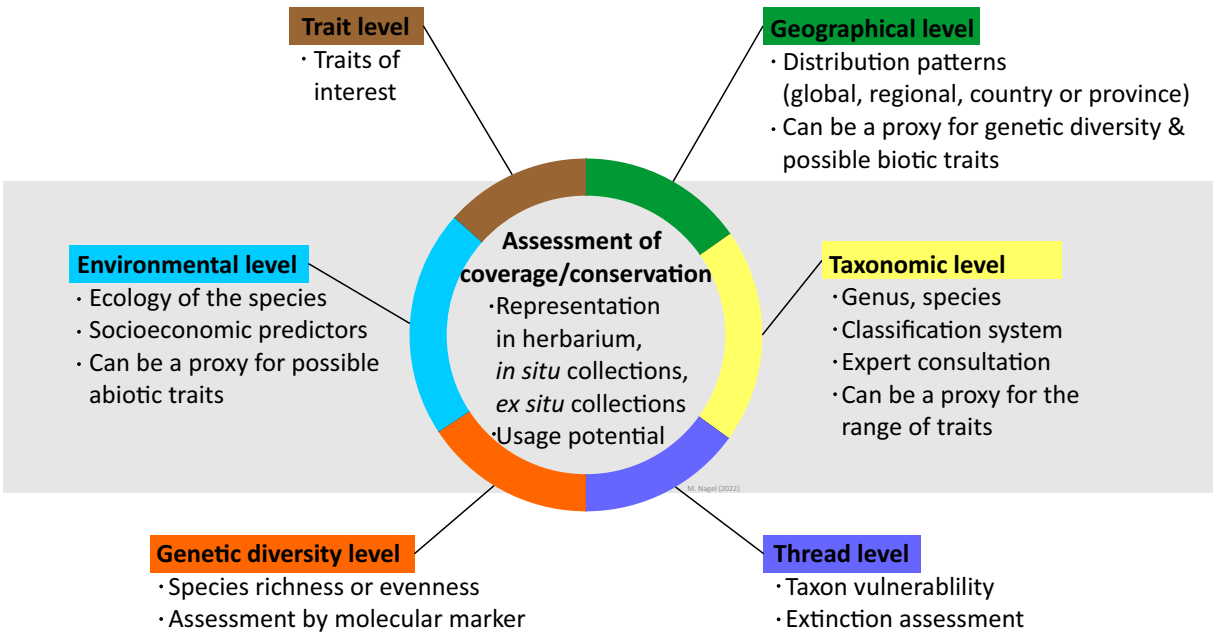



**Figure 10.1.1.** Parameters to be possibly included and considered in gap analysis of plant genetic resources. Based on description of Maxted et al. (2008).

national (about 60%) or regional origin (about 20%) and account for 12,200 accessions. ARG11347, CHL071, COL017, ECU023, PER860 consider that between 88% and 100% of their collections are national. In North America, most accessions were imported internationally and account for 90% (5,400). The collections in Europe and Asia come from different countries. About 30% (5,100) and 40% (4,000) of the accessions are from their own country, respectively. In Asia, CHN122 and JPN183 and in Europe (IRL036, LVA006, ROM007, GBR165 and SVN019) curators estimated that 80% to 100% originate from their own country. About 25% are of regional origin, corresponding to 4,330 and 1,800 accessions for Europe and Asia, respectively. In Asia, about 35% (5,300 accessions) and in Europe, about 40% (10,000 accessions) are of international origin.

Most genebanks (20 out of 32) consider that they have good national/multinational coverage (Figure 10.2.2). Asian respondents answered that the coverage is good for their respective countries (China, Japan). As well, respondents from Latin Americans genebanks consider that they also have an adequate range of genetic diversity from Argentina, Brazil, Bolivia, Chile, Colombia, Ecuador, El Salvador, Guatemala, Mexico, Paraguay, Peru, Uruguay, USA and Venezuela. The collections in Europe represent accessions from Belgium, Czechia, Estonia, France, Germany, Netherlands, Nordic countries, Slovakia, Spain, UK, and certain regions as Suceava and Maramures. However, only six genebanks (BGR001, CHN116, GTM001, RUS001, IND665, USA004) consider that they have good global coverage, with some gaps in their collection. Overall, the respondents indicated that European and Asian genebanks conserve a combination of unique national varieties and landraces or heirloom varieties, and South American landraces whereas Latin American genebanks, CIP (PER001) and the USA004 preserve unique resources from Latin America.

## 10.3 Gaps considered by the survey participants

More than 50% of the survey participants (18) responded that they have gaps in species coverage (Table 10.3.1) and especially in the population representation per species (19 participants). However, the answer differed according to the location of the collections. The respondents from the Asian collections (CHN116, CHN122, IND665, JPN183) suggest that gaps exist at the species, population and ecological representation levels. To fill these gaps, CHN116, CHN122 and IND665 are interested in exchanging material through international collaborations and introducing specific diversity from abroad. Half of the respondents in the American genebanks (ARG1347, CHL028, CUB005, USA004) identify no gaps in the species coverage, while the other half recognize gaps (BRA020, COL017, ECU023, GTM001, PER001) and most refer to gaps in the population representation (ARG1347, COL017, GTM001, CUB005, PER001, PER860) and in the ecological representation (ARG1347, GTM001, CUB005, PER001, PER860). Therefore, collecting missions are planned by ARG1347 in areas not previously visited for sampling and that are represented by few accessions.

**Table 10.3.1.** Major gaps in the collections as identified by the survey participants.

| Are there major gaps in the collection? | Yes | No | Don't know | Total |
|---|---|---|---|---|
| Species coverage of the crop | 56% (18) | 28% (9) | 16% (5) | (32) |
| Population (sample) representation per species | 59% (19) | 28% (9) | 13% (4) | (32) |
| Ecological representation of the species | 44% (14) | 31% (10) | 25% (8) | (32) |

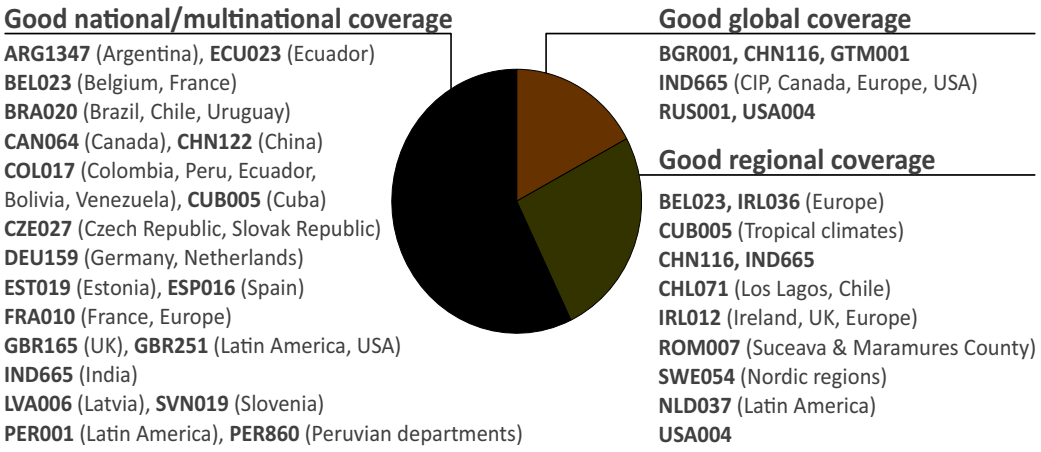



**Figure 10.2.2.** Global, regional or national/multinational coverage of potato collection including predominant countries (in brackets) estimated by 32 survey participants. Multiple answers possible.

PER001 is collaborating closely with Peruvian native communities to introduce and conserve new unique accessions. In 2017/18, a collecting mission was carried out and 330 unique accessions were added to the collection. PER860 promotes the recognition of "Zonas de Agrobiodiversidad" as a conservation strategy and strengthens *in situ* conservation in Peruvian indigenous territories, potentially involving the exchange of material. CUB005 and ECU023 are interested in filling gaps and ECU023 will focus on wild species. GTM001 reports that the collection is not sufficiently characterized to identify further gaps, and COL017 is interested in material from Colombian sites which not has been covered in previous collecting missions.

In Europe, survey participants consider that more than 50% of the originally collected material has good national and regional coverage, i.e., EST019, GBR165, IRL036, SVN019 and SWE054 see no gaps and have no plans for collecting missions. GBR165 and IRL036 regularly add new material from the Variety Catalogues. Respondents that maintain large collections and have introduced most of the material from abroad recognize gaps in their collections, i.e. CZE027, DEU159, FRA010, NLD037, RUS001, but have no plans to fill them due to legal and phytosanitary restrictions.

In the last survey (van Soest, 2006), the situation was comparable, with 21 out of 23 participants suggesting that there were gaps in the collections, i.e. 30 wild species according to Hawkes (1990) were not represented in the collections. However, the recent transfer of taxonomic names to the Spooner et al. (2014) taxonomic system showed that 105 of the 107 accepted wild species are listed in WIEWS (2021). When gaps are recognized, they can only be filled by collecting missions or international material exchange. Unfortunately, only a few collecting missions have been reported since 2006, e.g. four missions to collect *S. chacoense* and *S. commersonii* in Brazil between 2016 and 2018 (Medeiros et al., 2021). Although survey participants from Latin American countries indicated that they are highly motivated to conduct collecting missions, several curators mentioned that regional authorities are very restrictive when collecting missions are planned and require extensive documentation and lobbying. Overall, most genebanks have a large and balanced representation of national and international resources but gaps are still present (chapters 10.4 and 10.5). Survey participants of Latin American countries indicated a strong interest in identifying and filling the gaps through collecting missions and most are open to international collaboration to ensure that potato diversity can be safely preserved in genebanks. Therefore, awareness of the consequences of the loss of genetic diversity needs to be increased among policy makers and the public, especially in Latin American countries.

## 10.4 Identification of gaps in the representation of potato wild species

As a result of historic developments such as the Irish Potato Famine, potato crop wild relatives have been used extensively for germplasm improvement. Therefore, these resources had the benefit of being collected more frequently compared to other crop gene pools (Castañeda-Álvarez et al., 2016). Nevertheless, in order to identify gaps and priorities for further collecting mission, different types of analysis have been carried out. Vincent et al. (2013) analyzed crop wild relatives based on their social and economic importance, their potential use for crop improvement and their threat status, and found that 55% of wild potato species have fewer than 50 accessions in *ex situ* collections. Due to the high importance of potato as a

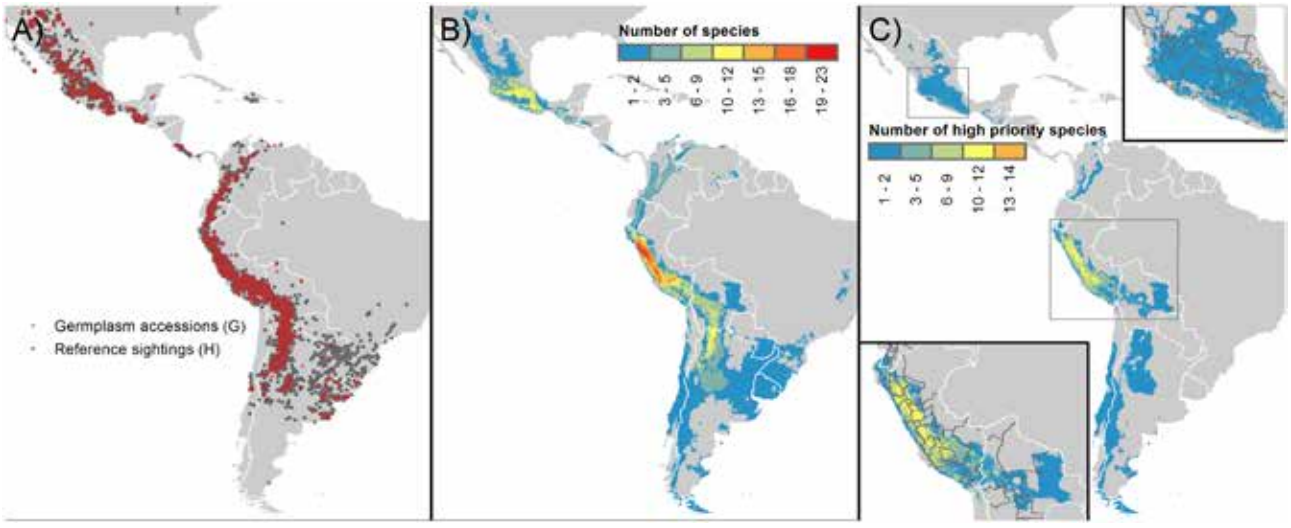



**Figure 10.4.1.** Distribution of potato wild species and priority species for collecting. (a) Herbarium records (grey) and germplasm accessions (red) included in the analysis. (b) Species richness calculated on basis of environment niche models. Further information is available on the project website: http://www.cwrdiversity.org/ and in Castañeda-Álvarez et al. (2015).

staple food, Castañeda-Álvarez et al. (2016) assigned a high priority to the further collecting of potato crop wild relatives and recommended gaps in potato collections be a priority focus before considering other crops.

In a more detailed study, seven species of the primary gene pool, 63 species of the secondary and three distant relatives of the tertiary gene pool were analyzed (Castañeda-Álvarez et al., 2015). In particular, scores for sampling representativeness, geographic representativeness and ecosystem representativeness were analyzed on the basis of 49,164 records and revealed that 32 species had large gaps in *ex situ* collections (Castañeda-Álvarez et al., 2016) (Figure 10.4.1). Of these, four are endemic in Mexico, three in Bolivia, two in Colombia, two in Ecuador and 21 in Peru, particularly in the departments of Cajamarca, La Libertad, Ancash and Huánuco. Some of the high priority species occur in habitats that are highly threatened, such *Solanum rhomboideilanceolatum* Ochoa and *Solanum piurae* Bitter. A further combined analysis of future climate in production areas as well as climates in the native habitats of 72 wild potato species revealed that the future climate scenarios for 26 species may be beneficial for future adaptation of potato varieties (Fumia et al., 2021). Overall, priorities should be assigned to those species that are not yet present in *ex situ* collections, have a geographic importance in the center of diversity and are of importance for breeding.

## 10.5 Gap analysis for potato landraces of the 'Andigenum group'

### Predicted gaps for *Solanum tuberosum* 'Andigenum group'

Potato landraces have an estimated conservation gap of about 50% (Ramirez-Villegas et al., 2022). To assess gaps in the geographical coverage of potato landraces conserved *ex situ,* the gap analysis of Ramirez-Villegas et al. (2020) was used as part of the work conducted by the CGIAR Genebank Platform (CGIAR Genebank Platform, 2020). The potential geographic distribution of landraces was modeled and compared with the geographical coverage of the accessions conserved *ex situ*. For the spatial analysis of potato landraces in the Americas, landraces of the 'Andigenum group' with accessible and georeferenced data (Table 10.5.1.1) were analyzed from different collections (Figure 10.5.1.1a). Following the approach of Ramirez-Villegas et al. (2020), gaps were categorized as low-probability (gap found with one approach), medium-probability (gap found with two approaches) and high-probability (gaps found with three approaches). The final results showed that the potato landraces in collections cover about 73% of the geographic area where potato landraces are grown (Figure 10.5.1.1). Further analysis of the gaps in the countries of distribution revealed that most landraces distributed in Guatemala (98%) were safely stored *ex*

(a) Predicted distribution (b) Predicted gaps

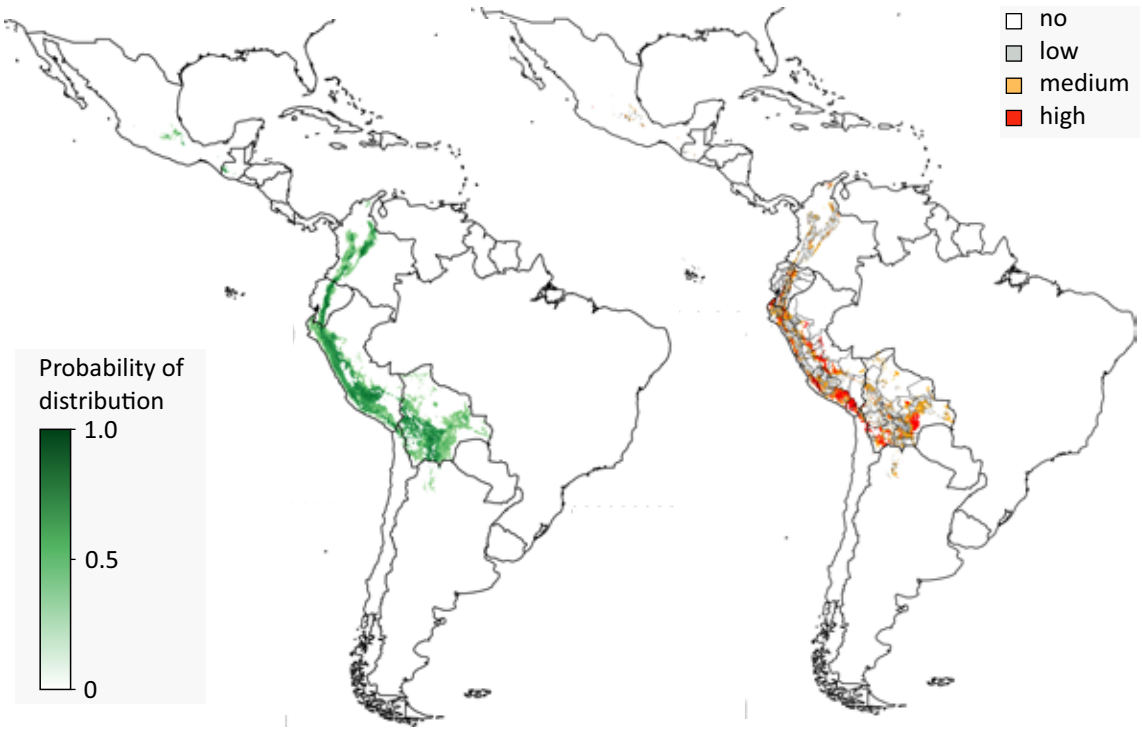



**Figure 10.5.1.1.** Predicted distribution and gaps of landraces of *Solanum tuberosum* 'Andigenum group'. (a) Probability of distribution of landraces of *S. tuberosum* 'Andigenum group' according to the distribution model. (b) Location of the gaps found by this analysis. Probability gaps are colored in grey for low-probability gaps found with one approach, in orange for medium-probability gaps found with two approaches and red for high-probability gaps found with three approaches. Color code is given in the figures.

*situ*. In contrast, it was estimated that only 69%, 67%, 63%, 40% and 0% of the area where landraces are expected to occur in Ecuador, Paraguay, Peru, Chile and Haiti, respectively, are covered by *ex situ* collections (Table 10.5.1.2)

### Composition and gaps of the CIP collection

The composition of the CIP (PER001) collections was analyzed by assigning the accessions of the *S. tuberosum* 'Andigenum group' to the groups in a potato diversity tree, a hierarchical stratification of the potato gene pool into groups and subgroups based on information from published literature and expert opinion. The concept of the diversity tree was initially proposed by van Treuren et al. (2009). Based on this concept, each row in Table 10.5.2.1 is a group in the potato diversity tree and is expected to be represented in a global *ex situ* collection of potato genetic resources, such as PER001. Groups with no accessions at PER001 are gaps in the representation of the potato genepool conserved *ex situ* at PER001. We also considered groups with fewer than 10 accessions to be poorly represented.

According to these results, gaps of the tetraploid (4x) landraces were found in Bolivia, in particular in the Tarija and Santa Cruz departments. For the same taxa, gaps were found in Ecuador, in the provinces of Pichincha, Napo, Tungurahua, Zamora-Chinchipe, and in Peru, in the departments of Arequipa, Moquegua, Piura, San Martin, and Tacna. However, in some accessions, i.e. for 520 accessions of *S. tuberosum* 'Andigenum group' from Peru, the ploidy is unknown, so the analysis is incomplete.

## 10.6 Challenges and steps towards gap filling

Most European and Asian genebanks have a combination of national, regional and international material in *ex situ* conservation. Those that keep national varieties and heirloom varieties consider that there are no or only a few gaps in the population representation in their collections. In all genebanks, gaps were identified in the *ex situ* collections for South American landraces and wild species.

Collection gaps might be filled by (1) exchanging and, (2) developing germplasm or (3) collecting missions (Bamberg et al., 2018). For material that is not yet present in genebanks, missions for collecting unique material need to be carried out. This raises the question what to collect first and where to go. As discussed in chapter 10.1, Marshall and Brown (1975) and Lawrence et al. (1995) suggested that 50 or 172 accessions, respectively, may be generally sufficient to cover 95% of the alleles that occurs at frequencies higher than 0.05 (i.e. 5%) within a target ecogeographic region without considering population genetics and demographic parameters (Maxted et al., 2008). Alternatively, allelic diversity can be estimated by DNA sequencing of the collections, and thus missing combinations and other gaps identified. Based on AFLP markers, Bamberg and Del Rio (2016) found that about 100 populations captured 95% of polymorphic loci for wild potato species and provide a reasonable threshold for the number of potato accessions needed for each species. However, although DNA sequencing technologies are becoming cheaper, it is unlikely that 16,500 accessions of wild species and 18,500 accessions of landraces can be sequenced and data comprehensively analyzed in the next few years. Due to habitat destruction and changes in land use, the likelihood of unique and important genotypes disappearing increases daily and collecting missions are urgently needed now.

**Table 10.5.1.1**. Accessions used for the spatial analysis. When multiple accessions had the same coordinate data only one was used for the analysis.

| Institute code | Accessions of *Solanum tuberosum* ('Andigenum group' and 'Chilotanum group') |
|---|---|
| PER001 | 4069 |
| BOL317 | 1566 |
| ITA406 | 1015 |
| COL017 | 948 |
| PER867 | 785 |
| USA004 | 647 |
| ROM007 | 321 |
| CHL071 | 242 |
| ESP172 | 75 |
| NLD037 | 65 |
| Other genebanks | 426 |

**Table 10.5.1.2**. Metrics of the *Solanum tuberosum* 'Andigenum group' gap analysis. Analysis by country conducted by CIAT (2021).

| Country | Average estimated gap area [km²] | Coverage of area where landraces are predicted to be found |
|---|---|---|
| Peru | 161000.5469 | 63% |
| Bolivia | 107303.8418 | 76% |
| Ecuador | 19634.63501 | 69% |
| Colombia | 15846.59253 | 91% |
| Chile | 8195.315186 | 40% |
| Argentina | 2567.720459 | 84% |
| Mexico | 1915.925018 | 91% |
| Brazil | 259.2323303 | 74% |
| Guatemala | 123.0456352 | 98% |
| Haiti | 60.86857605 | 0% |
| Venezuela | 23.94531083 | 74% |
| Paraguay | 12.03267717 | 67% |

**Table 10.5.2.1**. Number of *Solanum tuberosum* 'Andigenum group' accessions represented at PER001 in different groups of the diversity tree.

| Level of ploidy | County | Region | Number of accessions at PER001 |
|---|---|---|---|
| Andigenum group 4x | Bolivia | Chuquisaca | 6 |
| Andigenum group 4x | | Cochabamba | 117 |
| Andigenum group 4x | | La Paz | 33 |
| Andigenum group 4x | | Oruro | 46 |
| Andigenum group 4x | | Potosi | 61 |
| Andigenum group 4x | | Tarija | 1 |
| Andigenum group 4x | | Santa Cruz | 0 |
| Andigenum group 4x | Argentina | all | 148 |
| Andigenum group 4x | Colombia | all | 118 |
| Andigenum group 4x | Ecuador | Azuay | 17 |
| Andigenum group 4x | | Bolivar | 15 |
| Andigenum group 4x | | Carchi | 28 |
| Andigenum group 4x | | Canar | 11 |
| Andigenum group 4x | | Chimborazo | 40 |
| Andigenum group 4x | | Cotopaxi | 28 |
| Andigenum group 4x | | Imbabura | 25 |
| Andigenum group 4x | | Loja | 25 |
| Andigenum group 4x | | Napo | 0 |
| Andigenum group 4x | | Pichincha | 5 |
| Andigenum group 4x | | Tungurahua | 3 |
| Andigenum group 4x | | Zamora-Chinchipe | 0 |
| Andigenum group 4x | Peru | Amazonas | 18 |
| Andigenum group 4x | | Ancash | 129 |
| Andigenum group 4x | | Apurimac | 91 |
| Andigenum group 4x | | Arequipa | 0 |
| Andigenum group 4x | | Ayacucho | 136 |
| Andigenum group 4x | | Cajamarca | 89 |
| Andigenum group 4x | | Cusco | 380 |
| Andigenum group 4x | | Huancavelica | 75 |
| Andigenum group 4x | | Huánuco | 78 |
| Andigenum group 4x | | Junín | 426 |
| Andigenum group 4x | | La Libertad | 29 |
| Andigenum group 4x | | Lima | 44 |
| Andigenum group 4x | | Moquegua | 0 |
| Andigenum group 4x | | Pasco | 57 |
| Andigenum group 4x | | Piura | 4 |
| Andigenum group 4x | | Puno | 121 |
| Andigenum group 4x | | San Martin | 0 |
| Andigenum group 4x | | Tacna | 0 |
| Andigenum group 4x | Venezuela | | 28 |
| Andigenum group 4x | Mexico | | 27 |
| Andigenum group 2x | Peru | | 247 |
| Andigenum group 2x | Bolivia | | 67 |
| Andigenum group 2x | Colombia | | 92 |
| Andigenum group 2x | Ecuador | | 65 |
| Andigenum group 3x | Peru | | 140 |
| Andigenum group 3x | Bolivia | | 26 |
| Andigenum group 3x | Colombia | | 18 |
| Andigenum group 3x | Ecuador | | 8 |

Gap analysis is a tool that combines taxonomic, geographic, and ecological data and may also include information on genetic diversity, traits and threats and is used to compare the potential distribution of species with available accessions conserved *ex situ*. Based on this approach Castañeda-Álvarez et al. (2015) assigned a high priority to 32 wild species to be collected in Peru, Mexico, Bolivia, Colombia and Ecuador (Table 3.2.1). In addition, by adopting the modified approach of Ramirez-Villegas et al. (2020), gaps in landraces of the *S. tuberosum* 'Andigenum group' were identified after the analysis of about 10,000 potato landraces from 10 different genebanks. Based on a further comparison with the potato diversity tree, collection missions for tetraploid landraces are recommended in: Bolivia, in particular in the Tarija and Santa Cruz departments; Ecuador, in the provinces of Pichincha, Napo, Tungurahua, Zamora-Chinchipe; and Peru, in the departments of Arequipa, Moquegua, Piura, San Martin, and Tacna. In addition, landraces from Paraguay and Chile must also be considered.

Although gap analysis is of great value, it assumes that the eco-geographic pattern can predict genetic diversity, and, therefore, that accessions from different sites will increase the allelic diversity in the collection. Del Rio and Bamberg (2002) investigated the genetic distance among populations and compared it with geographical parameters such as latitude, longitude, elevation and distance. Unfortunately, no significant correlations were found for the populations of *S. sucrense, S. fendleri* and *Solanum jamesii* Torr. In another study, 152 RAPD markers were used to investigate the genetic distance of *S. verrucosum* populations. The genetic distance was found to be significantly correlated with spatial separation (r = 0.4*), longitude (r = 0.5**) and latitude (r = 0.7). In addition, significant correlations were also identified with the closely related species *S. hjertingii, Solanum hougasii* Correll and *S. demissum*. Del Rio and Bamberg (2004) speculated whether the significant associations are based on introgressions from other species, which would affect the conservation value, or whether they are coincidentally related to geographic determinants. However, gap analyses are limited because they depend on the availability of correct and comprehensive data (Ramírez-Villegas et al., 2010), i.e. geographic, taxonomic, ecological, trait and threat information. For crop wild relatives, this type of information may be insufficient. Voucher specimen in herbaria and other biological resources inventories play an important role in quantifying the completeness of *in situ* and *ex situ* collections but may be scarce (Maxted et al., 2008). In addition, the methodology is also limited by the models used and important information such as habitat quality and history are not integrated and can hardly predict variability of biotic elements. In any case, these studies and various considerations show that gap analysis should be complemented by other approaches to identify valuable genetic resources.

Overall, the following steps should be considered to successfully fill gaps in *ex situ* collections before populations disappear in the wild.

**Taxonomy**. Use of an appropriate and universal taxonomy that can be applied uniformly in the potato collections. The identification of gaps is essentially based on taxonomic classification and data correctness.

**Passport data.** Digitization and completion of passport data including GPS coordinates for the collection site(s) as a basis of further steps.

**Genetic information.** Genotyping is needed for the identification of unique genotypes and can assist gap analysis. Efforts should be made to collect sequence data and link it to passport information in order to identify priorities.

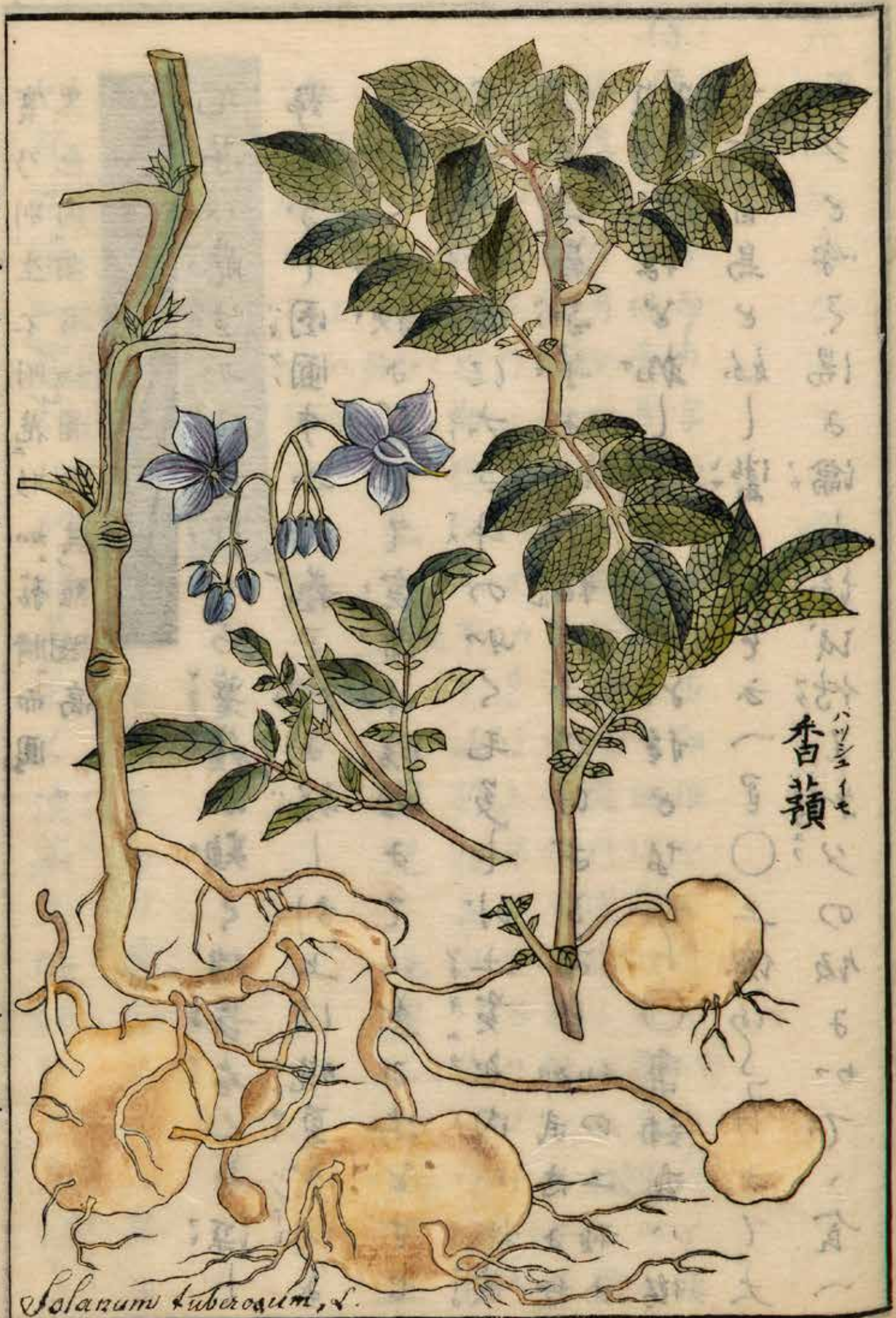
**Gap analysis** can help in setting priorities and identifying collection sites.

**Sites to collect**. Due to mutations, natural selection, genetic drift and gene flow, it is also important to re-collect populations from *in situ* sites which may already be in *ex situ* conservation. Cadima Fuentes et al. (2017) observed significant genetic differences on the basis of RFLP markers between *ex situ* and *in situ* conserved wild species. Further support from gap analysis and the experience of collectors is essential to identify hotspots and important habitats.

**Experts.** It is critical to identify and include the most knowledgeable expertise in collections and this includes crop curators with intimate knowledge of the species and crop as well as regional or local knowledge on where the material might be found.

**Financial resources.** Funding has been identified as a key limitation for many of the genebanks and funding for collecting missions is particularly scarce globally but most important for potato in South and central American countries. Therefore, the international community needs to support collecting missions through international collaborations.

**Local authorities.** Obtaining legal permission to collect has increasingly become a bottleneck. Thus, capacity building on Access and Benefit Sharing (ABS) needs to be strengthened for national authorities. Such training must provide clear and easy to understand concepts and clarify legal issues.



Potato cross pollination.
Photo: Michael Major/Crop Trust

# 11 POTATO BREEDING AND USAGE OF THE COLLECTION

The crops used for national food supplies have become increasingly similar among countries over the last 50 years (Khoury et al., 2014). At the same time, the genetic diversity within commercially grown potatoes dates back to a few founder lines from the 19th century, and has therefore not changed significantly in the last decades (Vos et al., 2015). Against the backdrop of global climate change, this could pose serious problems for the potato industry and was the cause of the devastation the industry faced in the 19th century. The integration of crop wild relatives and landraces into modern varieties is a well-known approach and it has been forecasted that potato will benefit most from the integration of crop wild relatives, especially in sub-Saharan Africa (Pironon et al., 2019). However, improved breeding strategies and technologies need to be used to overcome the current limitations in potato breeding. Overall, greater integration of potato genetic resources into breeding concepts will help diversify our food system, increases the crop's nutritional value and make the potato crop more tolerant toward environmental and other future challenges.

## 11.1 Historical aspects of potato breeding

Andean farmers were the first to domesticate and select potato genotypes for human consumption and they have continued to improve potato resources to the present time. Traditionally, the crop is planted in heterogenous fields that include various varieties, species and ploidy levels and may also be a mixture of tubers from both clones and seeds. The benefits of this well-established practice are that a) rejuvenation is integrated into the production system, b) a mixture of flavors, textures, shapes and colors can be produced for different kinds of specific dishes, and c) at least some plants are tolerant and can be harvested even after exposure to various environmental stresses. Under these conditions, very dynamic evolutionary processes have been supported, leading to new varieties and most likely new species (Quiros et al., 1992).

At the beginning of the 19th century, potato yields in most parts of the world were generally very low, and previous year's tubers were used for the next crop. The

British botanist Thomas Andrew Knight began with the first crossing trials in 1810 but targeted breeding was not considered until the late blight epidemics seriously damaged potato production in Europe and the USA. At this time, the US botanist Chauncey E. Goodrich imported plants from Chile and conducted the first undirected crossing trials. As a result, the newly selected lines, i.e. 'Garnet Chili', 'Purple Chile' and 'Early Rose', were superior to other US varieties and were released. The US botanist Luther Burbank continued to select from open-pollinated plants from 'Early Rose' and released the famous varieties 'Burbank' and 'Russet Burbank' in 1876, which became the most important varieties in the USA and Canada and are still grown today (Jansky and Spooner, 2018). In Europe, the Scottish botanist William Patterson and the Dutch Geert Veenhuizen initiated systematic crossing and breeding programs, releasing the first varieties 'Victoria' in 1856 (Stuart 1937) and 'Eigenheimer' in 1888 (De Haan, 1958). Although these systematic breeding approaches faced low male fertility in Europe and the USA, more than 350 varieties were released by the end of the 19th century (Hougas and Ross, 1956).

Through hybridising of inbred lines, further self-pollination and selection within the progeny, modern potato breeding began in the early 20th century (Jansky and Spooner, 2018). In particular, the use of exotic germplasm marked an important event in introducing resistance to viruses, bacteria and nematodes (Bradshaw et al., 2006). However, yield has not increased significantly over the last 100 years (Douches et al., 1996) and analysis of allele frequencies showed that most SNPs had hardly changed (Vos et al., 2015). Douches et al. (1996) speculated that this is due to the narrow genetic bases used, the inefficiency of breeding strategies and the diversity of quality traits needed to meet the requirements of the processing industry and consumers. Nevertheless, potato breeders managed to maintain a high degree of polymorphism and promote positive chromosomal rearrangements associated with resistance genes, e.g. resistances to *Globodera rostochiensis* (Vos et al., 2015). However, the limitations in fixing beneficial alleles due to the tetraploid nature of the crop need to be overcome in future.

## 11.2 Genetic hurdles in potato breeding

**Self-incompatibility** is common for most diploid tuber-bearing *Solanum* species (Spooner et al., 2014) and is controlled by the S-locus on chromosome 1 (Rivard et al., 1996). This polymorphic locus functions as a gatekeeper and produces an S-RNase (Luu et al., 2000). The S-RNase of the female- /pistil S-determinant encodes the primary amino-acid sequence of S—glycoproteins that is cytotoxic (McClure et al., 1989) and inhibits pollen tube growth in the upper first third of the style (Figure 11.2.1 b). In self-incompatible species, the RNase activity is 100 to 1,000-fold higher than in self-compatible genotypes of *Nicotiana tabacum* (McClure et al., 1989). The male/pollen S-determinant contains pollen-expressed F-box genes. The S haplotype-specific F-box proteins (SLFs) show sequence polymorphisms which were comparable to that of the S-RNAs. The SLFs encode F-box proteins that can, among other things, compose a class of ubiquitin ligase (Ushijima et al., 2003) that detoxify the non-self S-RNases, the allelic products of the pistil determinant, and allow compatible pollinations (Kubo et al., 2010). Overall, loss-of-function of S-RNAse is essential to introduce non-self SLFs and conferring self-compatibility in Solanaceae.

In the wild diploid *S. chacoense*, the dominant *S-locus inhibitor* (*Sli*) gene (Hosaka and Hanneman, 1998a) located on chromosome 12 controls self-compatibility and can be considered as a dominant gain of function (Hosaka and Hanneman, 1998b). Recent research has shown that *Sli* is able to interact with multiple allelic variants of the pistil-specific S-RNases and overcome self-incompatibilities (Eggers et al., 2021; Ma et al., 2021). Subsequently, several self-pollination events showed that vigorous, fertile clones with high homozygosity levels can be produced (Hirsch et al., 2013).

**Unilateral incompatibility and stylar barriers.** The second pre-zygotic hybridization barrier acting at the pollen-pistil level is cross-incompatibility (Maune et al., 2018). As hybrid zygote formation is possible after crossing fertile plants in one direction, it is termed unilateral. Commonly, the self-incompatible (SI) species can be used as a pollinator of the self-compatible (SC) species and produce fertile F1 plants but reciprocal crosses are usually not successful (Jansky and Hamernik, 2009). When the SI species is used as a female plant, the pollen tube growth is arrested in the upper, middle or bottom part of the style or even in the ovary (Figure 11.2.1 c-e). Due to the unilateral, but also in some cases bilateral, incompatibility with different reaction sites, cross-incompatibility cannot be completely explained by the S-locus or the S-haplotype (Maune et al., 2018). However, it is also possible for breeders to find exceptional plants that overcome the unilateral incompatibility crossing barrier and allow interspecific crosses as demonstrated by Eijlander et al. (2000) for *S. verrucosum*.

**Male sterility**. In contrast to most diploid wild potato species, tetraploids are self-compatible. However, due to the continuous selection pressure for tuber yield and quality, recessive sterility alleles can accumulate in cultivated potatoes (Jansky and Thompson, 1990). Cytoplasmic-genetic male sterility has frequently been detected in hybrid plants of crosses between

cultivated and wild potatoes (Larrosa et al., 2012). Interspecific crosses of haploid plants of the 'Chilotanum group' and clones of the 'Andigenum group' also produce sterile plants when haploids were the female parent (Carroll, 1975). Male sterility in di-haploids obtained from tetraploids is also a major barrier for use in breeding. However, in a few cases, when male-fertile diploids can be obtained, the generation of a higher frequency of male fertility is likely (De Maine, 1997) and breeding programs can be initiated.

**Endosperm Balance Numbers (EBN)**. Endosperm development is essential for production of viable and vigorous seed and partly explains the difficulties in crossing between species of the *Petota* section. Interspecific crosses and intraploidy can provoke endosperm failure. Thereby, the EBN hypothesis is based on the observation that endosperm develops normally when paternal:maternal gene ratio is 1:2 (Johnston et al., 1980) (Figure 11.2.2 a, b). EBNs for different species are assigned arbitrary values and are determined based on the crossing behavior of the species commonly with *S. chacoense* (Ortiz and Ehlenfeldt, 1992). Hanneman (1993) assigned tuber-bearing *Solanum* species and their close relatives to EBN numbers (Table 3.2.1) and revealed that most North American diploids, tetraploids and hexaploids are 1EBN, 2EBN and 4EBN, respectively. By contrast, South American diploids and tetraploids species are 2EBN and 4EBN but hexaploids are 4EBN. Therefore, species are isolated from each other due to the EBN differences, and this in part explains the challenges in crossing North and South American species. Similarly, the production of triploids via crossing of di- and tetraploid material

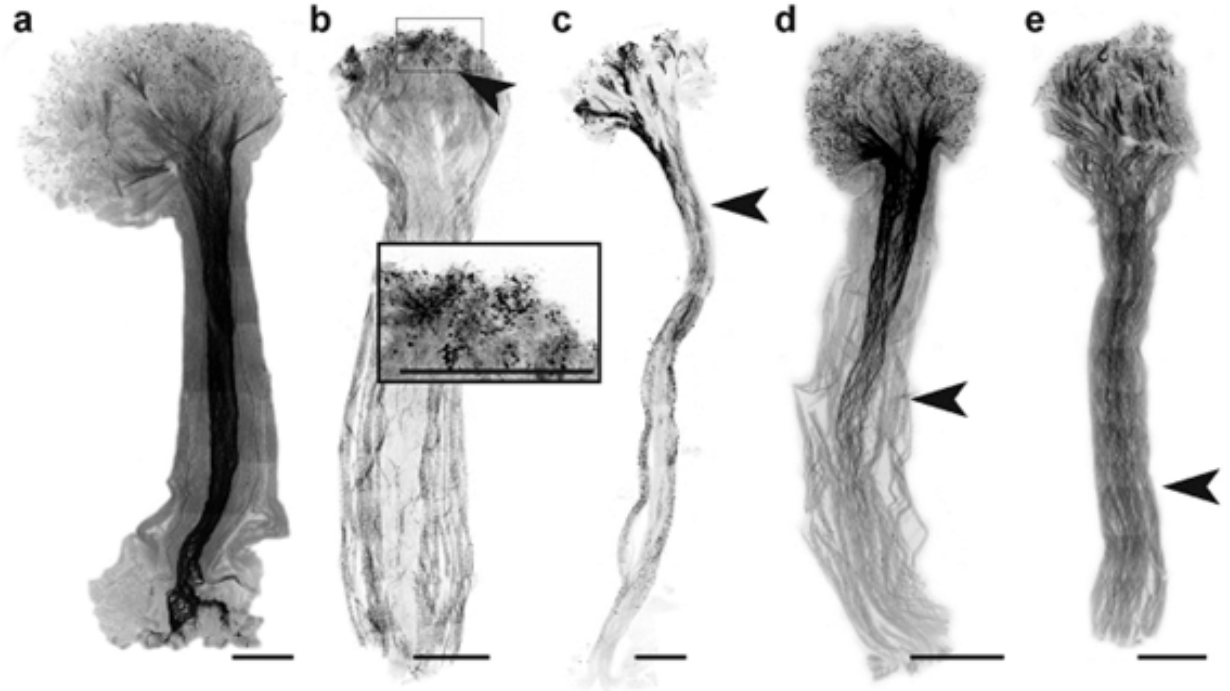



Figure 11.2.1. Pollen-tube growth after intra- and interspecific crossing events of accessions of the wild diploid potatoes *Solanum chacoense* Bitter, *Solanum gourlayi* Hawkes and *Solanum spegazzinii* Bitter and *Solanum tuberosum*. (a) Pollen-pistil compatibility was shown for most genotypic combinations. (b) Incompatibility at the top was present after selfing of the diploid genotypes. (c, d) Incompatibility at the middle and (e) bottom of the style was characteristic for cross-incompatibility. Scale bars = 0.1 cm. Source: Maune et al. (2018)

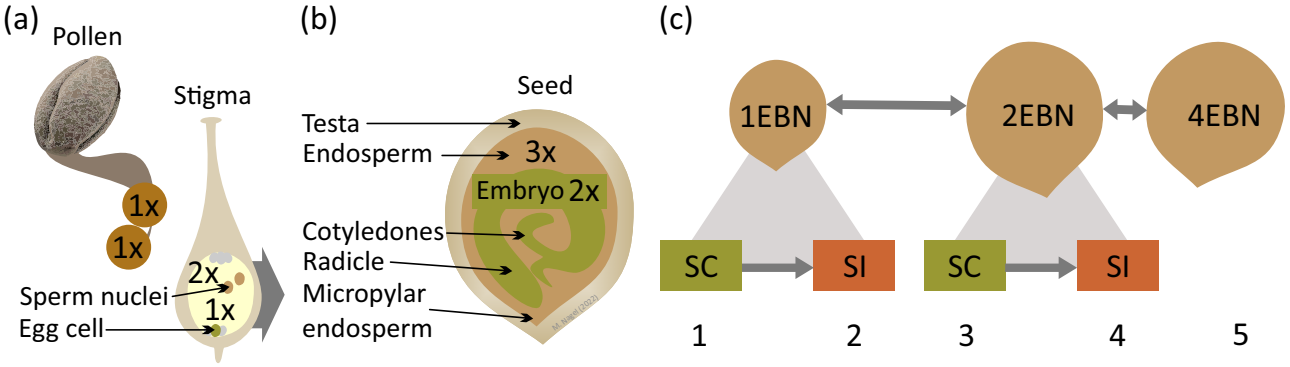



Figure 11.2.2. Endosperm Balance Number (EBN) and its implication for breeding. (a) Paternal:maternal gene ratio of 1:2 in the endosperm results in (b) successful hybridization and development of fertile seeds, adapted from Johnston et al. (1980). (c) Crossability groups based on the EBN and sexual compatibility (SC) or incompatibility (SI); based on Spooner et al. (2014).

results in an imbalance of the ratio (4:1) and, consequently, a failure in the endosperm development (Ortiz and Ehlenfeldt, 1992). Hence, these numbers have predictive power for the success or failure of interspecific crosses, the ploidy of the progeny and provide also implications for improvements in potato breeding.

## 11.3 Potato gene pools and use of wild species

The gene pool concept was established by Harlan and de Wet (1971) and describes the degree of relatedness between wild species and crops. Gene pools can be differentiated between primary, secondary and tertiary gene pool. Species of the primary gene pool are closely related and can generally be directly crossed to cultivated varieties. The hybrids produced from such crosses generally show normal meiotic chromosome pairing, are vigorous and fertile. To achieve hybrids by crossing wild relatives from the secondary gene pool, additional biotechnological techniques, e.g. embryo rescue, might be required and products may have reduced fertility. Species of the tertiary gene pool are generally not crossable and require additional technologies to enable gene transfer. For breeding and introgression of favourable alleles into the crop, species of the primary and secondary gene pool are mostly used (Maxted et al., 2012).

In potato, pre- and postzygotic barriers to hybridization are a challenge to categorize the gene pools. One determinant of success for interspecific hybridization is the EBN (Johnston et al., 1980). Based on EBN and degree of ploidy, Jansky et al. (2013) considered that hexaploid (6x, 4EBN), tetraploid (4x, 4EBN or 4x, EBN) and some diploid (2x, 2EBN) species can be categorized in the primary gene pool and most diploid species (2x, 1EBN) belong to the secondary gene pool. Spooner et al. (2014) proposed the inclusion of information about self-compatibility/incompatibility and the five crossability groups suggesting (Figure 11.2.2 c) where crossability between the groups is less likely. Based on this, Castañeda-Álvarez et al. (2015) assigned most wild species to the different gene pools (Table 3.2.1, Figure 11.3.1). Overall, seven species, including *S. acaule*, *S. berthaultii*, *S. brevicaule*, *S. candolleanum,* belong to the primary gene pool. In addition, 62 species were assigned to the secondary gene pool and 24 to the tertiary gene pool.

Vincent et al. (2013) applied the gene pool concept to potato and prioritized 88 wild relatives as requiring global conservation. About 43 of the 88 wild relatives are reported to have been either confirmed or of potential use in crop breeding and improvement (Table 11.3.1).

## 11.4 Breeding strategies and approaches

Most potato breeding programs use complementary parental lines of cultivated *S. tuberosum* for intermating and select best combinations based on the progeny. By further selection processes over several generations, phenotypes showing desirable traits and yields are released as varieties (Sood et al., 2017). However, the narrow genetic base of cultivated potato

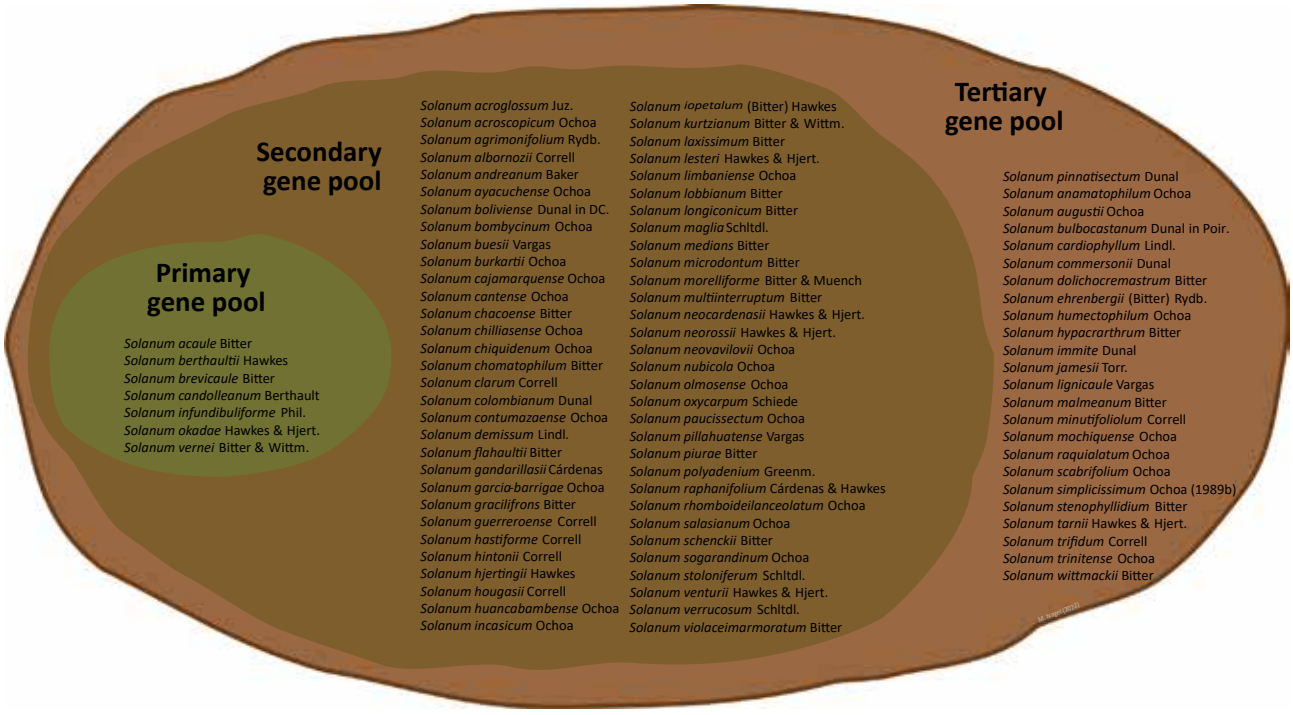



**Figure 11.3.1:** Species of the Petota group assigned to primary, secondary and tertiary gene pool. Based on data of Castañeda-Álvarez et al. (2015).

**Table 11.3.1.** Potential uses of wild potato species. Confirmed uses are in bold and potential are in regular text. Data source: Harlan and de Wet Inventory (https://www.cwrdiversity.org/checklist/ accessed on 05th November 2020).

| Scientific Name | Gene pool concept | Type of use | Confirmed or potential use |
|---|---|---|---|
| *Solanum acaule* | Primary | Abiotic stress | **Frost Tolerance;** Drought tolerance; Heat tolerance |
| | | Biotic stress | **Potato Virus X resistance;** Blackleg and soft rot resistance; Cyst Nematode Resistance; Early Blight resistance; *Fusarium* wilt resistance; Potato leaf roll virus resistance; Potato virus Y resistance; Spindle Tuber viroid resistance; Wart resistance |
| *Solanum ajanhhuiri* | | Abiotic stress | Frost tolerance |
| *Solanum berthaultii* | Primary | Biotic stress | **Blackleg and soft rot resistance; *Verticillium* resistance;** Aphid resistance; Colorado potato beetle resistance; Cyst nematode resistance; Early blight resistance; Late blight resistance; Potato virus X resistance; Potato virus Y resistance; Spindle Tuber viroid resistance; Wart resistance |
| | | Quality trait | **Cold induced sweetening resistance** |
| | | Abiotic stress | Drought tolerance; Frost tolerance; Heat tolerance |
| *Solanum boliviense* | Secondary | Abiotic stress | Drought tolerance; **Frost tolerance;** Heat tolerance |
| | | Biotic stress | **Blackleg and soft rot resistance;** Cyst nematode resistance; Wart resistance |
| *Solanum brevicaule* | Primary | Agronomic trait | **Percentage dry matter** |
| | | Biotic stress | **Cyst nematode resistance; *Globodera pallida* resistance;** Bacterial wilt; Blackleg and soft rot resistance; *Fusarium* wilt resistance; Potato virus X resistance; Potato virus Y resistance; Root knot nematode resistance; wart resistance |
| | | Abiotic stress | Drought tolerance; Frost tolerance; Heat tolerance |
| *Solanum bulbocastanum* | Tertiary | Biotic stress | **Late Blight resistance; Root knot nematode resistance;** Aphid resistance; Blackleg and soft rot resistance; Cyst nematode resistance; Early blight resistance |
| | | Abiotic stress | Drought tolerance; Heat tolerance |
| *Solanum candolleanum* | Primary | Abiotic stress | **Blackleg and soft rot resistance;** Drought tolerance; Frost tolerance; Heat tolerance |
| | | Biotic stress | Aphid resistance; *Verticillium* wilt resistance |
| *Solanum cardiophyllum* | Tertiary | Biotic stress | Cyst nematode resistance; Late blight resistance; Root knot nematode resistance |
| *Solanum chacoense* | Secondary | Agronomic trait | **Percentage dry matter** |
| | | Biotic stress | **Blackleg and soft rot resistance; *Verticillium* wilt resistance;** Bacterial wilt; Colorado potato beetle resistance; Common scab resistance; Early Blight resistance; Late Blight resistance; Potato leaf roll virus resistance; Potato virus X resistance; Potato virus Y resistance; Root Knot nematode resistance; tuber moth resistance |
| | | Quality trait | **Cold induced sweetening resistance** |
| | | Abiotic stress | **Drought tolerance; Heat tolerance** |
| *Solanum chomatophilum* | Secondary | Abiotic stress | Frost tolerance |
| | | Biotic stress | Aphid resistance |
| *Solanum circaeifolium* | Tertiary | Biotic stress | Cyst nematode; Late blight resistance |
| *Solanum commersonii* | Tertiary | Abiotic stress | Drought tolerance; Frost tolerance; Heat tolerance |
| | | Biotic stress | **Blackleg and soft rot resistance;** Colorado potato beetle resistance; Common Scab resistance; Potato virus X resistance |
| *Solanum curtilobum* | - | Abiotic stress | Frost tolerance |
| | | Biotic stress | Potato virus X resistance; Root knot nematode resistance |
| *Solanum demissum* | Secondary | Biotic stress | **Late blight resistance; Potato Leaf Roll virus resistance;** Blackleg and soft rot resistance; Colorado potato beetle resistance; Cyst nematode resistance; Late Blight resistance; Potato virus Y resistance; Wart resistance |
| | | Abiotic stress | Frost tolerance |
| *Solanum edinense* | - | Biotic stress | Late blight resistance |
| *Solanum etuberosum* | Tertiary | Abiotic stress | Frost tolerance |
| | | Biotic stress | Potato leaf roll virus resistance |
| *Solanum guerreroense* | Secondary | Biotic stress | Spindle Tuber viroid resistance |

| Scientific Name | Gene pool concept | Type of use | Confirmed or potential use |
|---|---|---|---|
| *Solanum hjertingii* | Secondary | Biotic stress | **Blackleg and soft rot resistance; Root knot nematode resistance;** Spindle tuber viroid resistance |
| *Solanum hougasii* | Secondary | Biotic stress | Late blight resistance; Root knot nematode resistance; Potato virus Y resistance |
| *Solanum infundibuliforme* | Primary | Biotic stress | Aphid resistance |
| *Solanum iopetalum* | Secondary | Biotic stress | Late blight resistance |
| *Solanum jamesii* | Tertiary | Biotic stress | Colorado potato beetle resistance; Common scab resistance |
| *Solanum juzepczukii* | – | Abiotic stress | **Frost Tolerance** |
| | | Biotic stress | Potato Virus X resistance |
| *Solanum kurtzianum* | Secondary | Biotic stress | Cyst nematode resistance; Fusarium wilt resistance; Root knot nematode resistance |
| *Solanum lignicaule* | Tertiary | Biotic stress | Aphid resistance |
| *Solanum marinasense* | Primary | Biotic stress | Aphid resistance |
| *Solanum medians* | Secondary | Biotic stress | Aphid resistance |
| | | Quality trait | Chip making from cold |
| *Solanum microdontum* | Secondary | Abiotic stress | Drought tolerance; Heat tolerance |
| | | Biotic stress | Bacterial wilt; Blackleg and soft rot resistance; Late blight resistance; Root knot nematode resistance |
| *Solanum mochiquense* | Tertiary | Biotic stress | Late Blight resistance |
| *Solanum multiinterruptum* | Secondary | Abiotic stress | Frost tolerance |
| | | Biotic stress | Aphid resistance; Cyst nematode resistance; Spindle tuber viroid resistance |
| *Solanum neocardenasii* | Secondary | Biotic stress | Aphid resistance |
| *Solanum okadae* | Primary | Quality trait | Chip making from cold |
| *Solanum palustre* | Tertiary | Biotic stress | **Potato leaf roll virus resistance;** Blackleg and soft rot resistance |
| | | Abiotic stress | Frost tolerance |
| *Solanum pinnatisectum* | Tertiary | Abiotic stress | Drought tolerance; Heat tolerance |
| | | Biotic stress | Blackleg and soft rot resistance; Colorado potato beetle resistance; Late blight resistance |
| | | Quality trait | Chip making from cold |
| *Solanum polyadenium* | Secondary | Biotic stress | Colorado potato beetle resistance; Late blight resistance |
| *Solanum raphanifolium* | Secondary | Quality trait | **Cold induced sweetening resistance;** Chip making from cold |
| | | Abiotic stress | Frost tolerance |
| | | Biotic stress | Potato leaf roll virus resistance; *Verticillium* wilt resistance |
| *Solanum sogarandinum* | Secondary | Quality trait | Chip making from cold |
| *Solanum stoloniferum* | Secondary | Biotic stress | **Late blight resistance; Potato virus Y resistance;** Aphid resistance; Potato leaf roll virus resistance |
| | | Abiotic stress | Drought tolerance; Heat tolerance |
| *Solanum tarnii* | Tertiary | Biotic stress | Late blight resistance; Potato virus X resistance; Colorado potato beetle resistance; |
| *Solanum tuberosum* subsp. *andigena* | - | Biotic stress | Bacterial wilt; Blackleg and soft rot resistance; Common scab resistance; Cyst nematode resistance; Late blight resistance; Potato leaf roll virus resistance; Potato virus X resistance; Potato virus Y resistance; Root knot nematode resistance; Tuber moth resistance; Wart resistance |
| | | Quality trait | Ascorbic acid content; Carotenoid content; Cold induced sweetening resistance; high starch content; protein content |
| *Solanum venturii* | Secondary | Biotic stress | **Late blight resistance** |
| *Solanum vernei* | Primary | Abiotic stress | Frost tolerance |
| | | Biotic stress | **Cyst nematode resistance; *Verticillium* wilt resistance;** Blackleg and soft rot resistance; Late Blight resistance; Potato virus Y resistance; Wart resistance |
| | | Quality trait | Cold induced sweetening resistance; high starch content; protein content |
| *Solanum verrucosum* | Secondary | Biotic stress | **Late blight resistance** |

has limited advancements in potato yield over the years (Douches et al., 1996). The different levels of genetic hurdles (see chapter 11.2), especially self-incompatibility within the diploids and inbreeding depression of the di- and tetraploids, are the major challenges in fixing favorable alleles in the next generations. When further wild species and landraces are crossed, many undesirable alleles, e.g. for deep eyes, small tuber size, short-day adaptation, and high glycol-alkaloid content, will need to be eliminated by backcrossing. This process can take decades. Newer technologies, i.e. CRISPR-Cas9 technologies or marker-assisted breeding, may speed up the processes (Bonierbale et al., 2020), but may still be hampered by the aforementioned problems, i.e. incompatibilities, infertility, differences in ploidy, and the acceptance of genetically modified organisms (GMOs). However, some current promising breeding strategies and approaches are listed below, following Bonierbale et al. (2020).

**Population improvement by open recurrent selection.** The basic idea is to improve the average performance of a population by retaining and enhancing genetic variation through systematic and regular introduction of new material. Therefore, pre-bred plants with desired traits are periodically intermated into a population. Plants produced are re-selected and used for recombinant populations for the next cycle. In polyploid potato, more than one allele per locus is usually transferred. However, over time, linkage blocks are commonly destroyed and desired traits maintained in the germplasm. Depending on the population stage, some of the selected material can be used as varieties.

**Crossing parents**. The result from crossing tetraploid parental potato lines is hardly predictable as dominance and epistatic effects determine the clonal performance. However, to increase the predictability of a cross and to select the best parents, parental values can be assigned. The parental value can be determined by progeny testing using suitable designs, by evaluating the pedigree or by observing selection ratios. Additional information about trait variance, covariance, heritability, and additive and dominance variation allows the estimation of genetic effects and parameters and increases the chance to select best parental lines.

**Mating designs**. To determine genetic parameters, parental values and to identify superior progenitors, systematic crosses of plants need to be carried out. Depending on the number of factors, parents and modalities, different designs can be applied. The most common designs are the diallel mating design, line x tester design, design II. Briefly, as described by Bonierbale et al. (2020) the diallel mating design refers, in principle, to all possible combinations of crosses. Since this is usually not feasible, a random combination of crosses is usually analyzed. In the line x tester design, different lines are crossed with one or more testers and the progeny of full siblings are further evaluated, e.g. in randomized block designs. Design II is comparable to the diallel mating design although it includes all possible combinations. All of the designs show advantages and disadvantages; and sterility barriers and incompatibilities during systematic matings can be a challenge.

**Estimated breeding values.** In contrast to the parental value, which predicts the ability of a parental line to transmit desired alleles to the offspring, the estimated breeding value allows the modeling of underlying random effects and error components of variance. By applying mixed models, i.e. best linear unbiased prediction (BLUP), the genetic gain can be increased for traits with low heritability. This concept has been successfully transferred from animal breeding to various crops and should be carefully examined in the future.

**Early versus late generation selection.** Comparison of breeding lines can be carried out at earlier breeding stages, i.e. phenotyping of a few plants for highly heritable traits, or at later breeding stages when more seeds/plants are available. Economically important traits in potato are commonly complex traits involving interplant competition, which may require block designs and homogenous field conditions. The trait of interest and the available number of plants determine the decision on early to later stages of selection, including the specific designs involving adequate number of blocks and replicates.

**Breeding using diploids.** Diploid potato varieties, especially those of the 'Phureja Group', have long been used by farmers in the Andes. For breeding tetraploids, desirable diploid clones are usually screened, tested, selected and vegetatively multiplied and by combining 2n gametes from the female and male parent important alleles are fixed faster. To avoid problems, the genetic loci of male- and female-derived clones must complement each other, so that deleterious recessive alleles are not harmful (Bradshaw, 2022). Compared to the F1 hybrids for TPS production, diploids lines can be still heterozygous. Recently, more and more potato breeding companies are investing time and efforts in developing diploids that use their advantageous alleles for further introgression (personal communication Richard Visser, 2022).

**True hybrid potato breeding.** The principal idea of hybrid potato breeding is more than 60 years old and aims at combining the advantages of true potato seed, diploid genetics and homogeneous parental lines. However, acceptable agronomic performance of homozygous potato have not been present for a

long time (Lindhout et al., 2011). The main problem is that about 20 of the 39,000 protein-encoding genes (Potato Genome Sequencing et al., 2011) have severe fitness effects. The odds of producing a vigorous diploid progeny that is heterozygous at these 20 loci is only 0.3%. Heterozygous tetraploid plant material has a higher chance of masking the effects of the unfavourable alleles (Lindhout et al., 2011). Although tetraploids usually have higher yields, some diploids are compatible with the tetraploid standards (Hutten et al., 1995).

A hybrid breeding system could allow systematic incorporation of new genes, traits and the possibility of substantial yield increases through crossing well-defined heterotic groups. In addition, low multiplication rates of clonally propagated tubers can be avoided by producing true seeds from uniform F1 hybrid plants, including further beneficial effects of true potato seeds, i.e. low pathogen accumulation and higher storability. Major challenges are self-incompatibility in inbred lines (Bonierbale et al., 2020) and inbreeding depression caused by recessive deleterious mutations (Charlesworth and Willis, 2009). However, Hosaka and Hanneman (1998a; 1998b) discovered that the introgression of the *Sli* gene from *S. chacoense* can alter self-incompatibility and allow the production of selfed diploid potato seed. The second obstacle was recently overcome by implementing a genome design involving sequencing, analysis of haplotype information and the assessment of genome homozygosity, the number of deleterious mutations and final selection of beneficial alleles. After analysing the genome complementary of inbred lines, the parental lines for vigorous F1 hybrids were selected. The end product was the production of F1 hybrid tubers showing strong heterosis and yield potential comparable to tetraploid varieties (Zhang et al., 2021).

Basic requirements for future developments, i.e. estimated breeding value, marker-assisted selection and true hybrid potato breeding, are a deeper understanding of the potato genome, including the availability of genetic resources and linked sequencing information.

## 11.5 Sequencing information

### The potato reference genome

**First potato genome.** Sequencing heterozygous tetraploid plant material such as cultivated potato has been a major challenge. Therefore, the potato germplasm DM BARD 1–3 516 R44 (DM) (Veilleux, 2017), homozygous for a single set of the 12 chromosomes was used to develop a reference genome. These monoploids were developed from heterozygous adapted *Solanum tuberosum* group *Phureja* clones that were subjected to chromosome doubling (Paz and Veilleux, 1997). After sequencing, the final assembly covered about 86% of the potato genome with 844 Mb and some 39,000 genes predicted. The sequence of DM was compared with the heterozygous diploid potato genome (RH89–039-16, short RH) that had a high degree of heterozygosity. Only 55% of the RH genome could be aligned to the DM genome and potentially deleterious mutations occur frequently and are a likely cause of inbreeding depression (Potato Genome Sequencing et al., 2011).

**Further genome developments**. To improve the genome assembly and its applicability for potato breeding, marker analysis of a backcross segregation population of DD x (DM x DD) and *in silico* anchoring approaches were used along with physical and genetic maps from RH and tomato. DD was a heterozygous clone of the *S. tuberosum* 'Andigenum Group' (Sharma et al., 2013). Based on the sequencing information, the Coordinated Agricultural Project (SolCAP) developed the Infinium 8303 Potato Array that allowed genetic mapping of numerous genotypes. Two mapping populations (DRH and D84) using DM as female parent showed that over 4,400 markers were mapped. The genetic maps covered 965 cM (DRH) and 792 cM (D84), respectively, and about 87% of the genome sequence length (Felcher et al., 2012). In 2015, based on the Infinium 8303 Potato Array and sequencing data of six varieties, the 20 K Infinium SNP array became available (Vos et al., 2015) and has been further developed into the Infinium 22K V3 Potato array (Pandey et al., 2021) by using additional SNP marker data of the three varieties (Hamilton et al., 2011). Furthermore, the draft genome of the wild species *S. commersonii,* which diverged from potato about 2.3 million years ago, was published. Compared to the potato genome, the draft assembly had a similar size (830 Mb) but showed significantly less heterozygosity and provided valuable insights into evolutionary changes and environmental adaptation (Aversano et al., 2015). Further sequencing efforts complement information about cultivated potato and wild species and are listed below:

1. DArT marker-based linkage map for the wild potato *Solanum bulbocastanum* Dunal in Poir. (Iorizzo et al., 2014)
2. Genome assembly of the diploid inbred clone (M6) of *S. chacoense,* with 882 Mb genome, 37,740 functionally annotated genes (Leisner et al., 2018)
3. Genome assembly and annotation of the heterozygous diploid potato RH89–039-16, 1.67 Gb haplotype- resolved assembly, 10,642 annotated genes (Zhou et al., 2020)
4. Long-read reference genome assembly for potato DM1–3 516 R44, the doubled monoploid clone of *S. tuberosum* 'Group Phureja', 742 Mb genome assembly, 44,851 functionally annotated genes

(Pham et al., 2020)

5. Bacterial artificial chromosome (BAC) libraries of the tetraploid potato varieties C88 was used to establish a physical map of target regions (Yang et al., 2020)
6. Assemblies of 12 potato landraces varying in ploidy levels (2x to 5x) (Kyriakidou et al., 2020)
7. Assemblies of the somatic hybrid P8 (J1), the wild species *Solanum pinnatisectum* Dunal (J2), progeny MSH/14–112 (P8 × cv. 'Kufri Jyoti') (J3), and *S. tuberosum* dihaploid C-13 (J4), assembly size between 725 (J1-J3) and 810 MB (J4) (Tiwari et al., 2021a)
8. Chromosome-scale assembly of the variety 'Otava', 3.1 Gb haplotype-resolved, 38,214 genes (Sun et al., 2021)
9. Pan genome assemblies of six varieties used for fresh ('Colomba', 'Spunta'), chip processing 'Atlantic'), frozen processing ('Castle Russet') and starch markets ('Altus', 'Avenger') were constructed, 3.1 Gb (Hoopes et al., 2022)

**Accessibility of genetic information.** The development of the various genetic resources including SolCAP Diversity Panel with phenotypic and genetic data from 250 potato clones (Hirsch et al., 2013), was accompanied by the need to improve the accessibility of complete information. In 2013, the following resources were available, and they still are:

1. the Solanaceae Source provides taxonomical information
2. SolEST provides EST marker information for Solanaceae species (D'Agostino et al., 2009)
3. PlantGDB includes transcript data (Duvick et al., 2007)
4. KaPPA-View4 SOL presents metabolic pathways ()
5. the PoMaMo database contains potato genetic maps and sequences
6. SolRgene provides information and search function on disease resistance genes in tuber-bearing *Solanum* species (Vleeshouwers et al., 2011)
7. the Potato Pedigree Database houses pedigree information for potato varieties

However, to centralise potato-specific information and to share genome sequence of the Potato Genome Sequencing Consortium (PGSC), the database **Spud DB** was established providing associated annotation data and linked large-scale potato datasets as well as powerful search tools to identify genes and regions of interests. In addition, a Breeder's Assistant was developed to provide genotypic and phenotypic data linked to the SolCAP potato 8303 Infinium SNP array (Hirsch et al., 2014). Altogether, the databases, including available sequencing, taxonomic and multiomic information, represent key sources for the characterization and genotyping of potato varieties and plant genetic resources.

## Genotyping of potato genetic resources

Genome sequencing and marker genotyping are the basis of emerging strategies in the molecular breeding of polyploid plants by identifying potential genes for resistance and tolerance against abiotic and biotic stresses, and can also assist in identifying unique accessions in potato collections. The analysis of genetic identity is an important tool to reveal the genetic diversity within collections and to identify duplicates and unique material at local and global levels.

Based on the survey data provided by 32 genebanks, only two collections (PER001; IRL036) have fully genotyped their potato germplasm, but 20 collections have been partly genotyped (Figure 11.5.2.1). Unfortunately, data are only publicly available from 10 genebanks so far. Simple sequence repeat (SSR) markers, also known as microsatellites, have been used most frequently in the past. More recently, single nucleotide polymorphisms (SNPs) using genotyping-by-sequencing (GBS) or the SolCAP 8K, 12K or 20K Infinium array have been adopted (Illumina Inc., San Diego, USA). Some eight genebanks have not yet genotyped their germplasm and two collections are in the planning stage. Therefore, the following information provides only a partial overview and cites important and recent peer-reviewed manuscripts. More detailed and up-to-date information can be obtained directly from the potato curators.

**Asia.** Japanese germplasm **(JPN183)** is specifically screened for the potato cyst nematode (Asano et al., 2012). The pale potato cyst nematode *Globodera pallida* (Stone) Behrens. was first found in Japan in 2015. Therefore, a screening of over 1,000 Japanese germplasm accessions was initiated and potential resistant varieties were identified (Asano et al., 2021). In China,

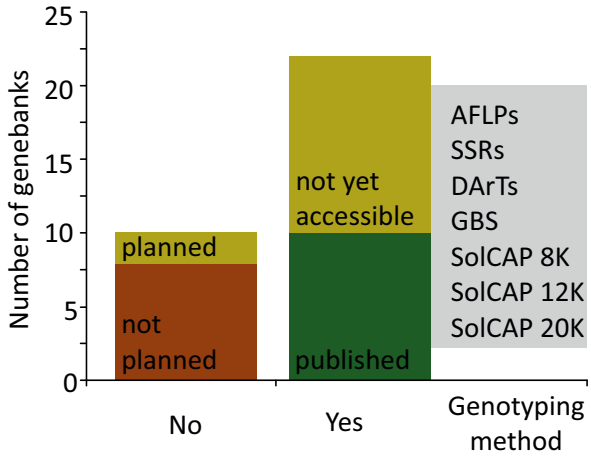



Figure 11.5.2.1. Status of genotyping in potato collections of the 32 genebanks participating in the survey. AFLP, Amplified Fragment-Length Polymorphism; DArT, Diversity Array Technology; SSR, Simple sequence repeat, SNPs, single nucleotide polymorphisms analyzed by genotyping-by-sequencing (GBS) or using different arrays (SolCAP 8K – 20K).

there is a common interest to improve the genepool for future breeding programs, therefore several research groups have initiated genotyping of local varieties and material from local genebank collections (Wang et al., 2019).

**Europe.** The European collections have different goals, i.e. conservation, breeding, working, reference collection (Figure 11.7.1). Therefore, genotyping of the collections is related to different topics. To assess genetic diversity in the Nordic potato collection **(SWE054)** and between breeding lines, 133 potato accessions, varieties and breeding clones typically grown under long daylength in Europe were genotyped using the Infinium Illumina 20K SNP array. The results indicated that the background of all genotyped material is very similar and new genetic material should be introduced for breeding Nordic varieties (Selga et al., 2022). In Estonia **(EST019)**, for validation of varieties and identification of the origin of the material, more than 450 potato varieties and landraces of the Estonian Crop Research institute were fingerprinted using 8 SSR markers and revealed unique accessions and duplicated varieties (Ivanova-Pozdejeva et al., 2021). The Latvian (**LAV006**) potato collection (83 accessions) and some additional varieties were genotyped using Diversity Array Technology (DArT) makers resulting in 1,482 polymorphic loci. Overall, the material was grouped in breeding lines, Latvian, Western European and Eastern varieties and showed that genetic diversity has increased in the modern varieties compared to varieties released prior to 1970 (Rungis et al., 2017).

To develop core collections and for marker-assisted selection about 2,000 accessions of the **FRA010** collection were fingerprinted. For further genotyping and genome-wide association (GWAS) studies, Cleaved Amplified Polymorphic Sequence (CAPS) markers and the SolCAP 8K array were used. The Commonwealth Potato Collection **(GBR251)** has been partly genotyped and used in numerous taxonomic (Hawkes, 1994; Spooner et al., 2005), breeding (Bradshaw and Ramsay, 2005) and screening studies including evaluation of various resistances and tolerances against biotic and abiotic stress, e.g. Potato Virus Y (Torrance et al., 2020). The collection of **NLD037** is similarly used and in particular accessions of *S. acaule* and *S. demissum* were genotyped. The results have been used to elucidate changes during *ex situ* and *in situ* conservation (Cadima Fuentes et al., 2017). In Russia (**RUS001**), 237 accessions of cultivated potato species, 155 accessions of closely related wild potato of the VIR collections (Gavrilenko et al., 2010; Gavrilenko et al., 2013) and 180 varieties were genotyped with SSR markers (Antonova et al., 2016; Antonova et al., 2020). In Germany (**DEU159**), the entire clonal collection was genotyped using SSR markers and **ESP016** used fingerprinting of local potato varieties from Tenerife Island, La Palma and Spain to identify unique alleles that they may date back to the first introduction of potato in Europe (de Galarreta et al., 2011).

**International collection (PER001).** The potato germplasm collection at CIP has been intensively genotyped over the years and some results are summarized in Ellis et al. (2020). The cultivated and wild potato collections have been partially genotyped with Amplified Fragment-Length Polymorphism (AFLP) and SSR markers, i.e 1,000 landrace accessions (Ghislain et al., 2004) or 742 landraces and some wild progenitors (Spooner et al., 2007). Furthermore, the entire cultivated collection has been genotyped with the SolCAP 12K array. Genotypic information from 250 accessions was compared between plants maintained in the field and as *in vitro* clones in slow-growth storage (Ellis et al., 2018). About 4.4% of these accessions were found to have mismatches, which is comparable with genetic mismatches found in other stock centers (Anastasio et al., 2011). Furthermore, around 25% of the cultivated collection was genotyped with DarTseq and about 2,000 accessions of cultivated and wild species were genotyped with GBS. It is interesting to note that use of the data from the SolCAP 12k array on its own can be used to predict the species based on Hawkes taxonomy with a high degree of accuracy.

**North America.** Many comprehensive genotyping studies have been carried out in the **USA004** collection on different topics. Recently, heterozygosity levels of three diploid wild species, *S. boliviense, S. amesii*, and *S. microdontum*, and the diploid cultivated species *S. phureja,* were studied (Bamberg et al., 2021) and a core set of 38 *S. demissum* accessions was established based on 1,403 AFLP markers (Del Rio and Bamberg, 2020). In Canada, about 90 current and heirloom Canadian garden potato varieties were genotyped with SSR markers to complement information from the Food Inspection Agency reference SSR profile collection for potato varieties. Overall, the SSR profiles of 68 varieties were unique. Although some morphological differences appeared between heirloom varieties, the genetic profiles clustered together (Marie-JoséCôté et al., 2018).

**South America.** Native potato germplasm has been genotyped in several studies. For example, by using SSR markers or the SolCAP array, 98 Argentinian potato landraces from **ARG1347** (Sucar et al., 2022), 809 accessions from the 'Andigenum group' (Berdugo-Cely et al., 2017) and 144 breeding lines from **COL017** (Berdugo-Cely et al., 2021) and 152 Ecuadorian **(ECU023)** landraces were genotyped (Monteros-Altamirano et al., 2017). To evaluate the Chilean landrace collection of *S. tuberosum* 'group Chilotanum', 589 accessions from **CHL071** and the Agricultural and Livestock Service of Chile (SAG)

were genotyped with SSR markers. It was found that **CHL071** maintained accessions not previously listed in SAG and more than 320 landraces were characterized as unique genotypes (Muñoz et al., 2016). By sequencing 155 genotypes from **BRA020** using SolCAP 8303 Potato Array, different subpopulations were identified. Among these were diploid genotypes from Phureja group, germplasm for chip processing market class and cultivars and advanced breeding clones from Europe and Embrapa, including genotypes for fresh market class and French fry processing (Castro et al., 2018).

Overall, genotyping studies have been initiated at various scales in the different collections. However, systematic overviews of these studies do not exist and data are only partly accessible. To support breeding programs in the future, recent technologies, i.e. SolCAP, DArTs or GBS approaches, should be applied to whole collections and emerging information needs to be strategically stored in suitable easily searchable databases.

## 11.6 Policies on access to collections

International agreements regulate the access and benefit sharing (ABS) of genetic resources and have adopted strategies for their conservation. In particular, the 'Convention on Biological Diversity' (CBD) entered into force in 1993 and in 2014 its supplement agreement the "The Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from Their Utilization to the CBD". In 2004, the 'International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) established a multilateral system (MLS) of access and benefit-sharing for contracting parties and international organizations. For the purposes of conservation, research, training and plant breeding, facilitated access to the genetic diversity of 64 crops (Annex I) has been provided (Halewood et al., 2018) and Standard Material Transfer Agreements (SMTA) are required to be used for the transfer of all material under the MLS. In accordance with all agreements, the origin of genebank accessions including date of access, legal permits and documentation of the collecting mission must be available for the international transfer, exchange and utilization of plant genetic resources (Weise et al., 2020).

The survey data demonstrates that most potato collections belong to governmental organizations (25 collections, Figure 6.3.1) that follow the terms and conditions of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA, 21 collections, Figure 11.6.1a). The other seven collections of the 32 survey participants belong to different types of organizations: PER001 (CIP) is an international research center and the potato collection is held in trust under the terms of the ITPGRFA and is available with the SMTA. NLD037, LVA006, BGR001 are research institutes, whereby NLD037 is also partly governmental. DEU159 is a non-university research institute, CZE027 a private organization, and COL017 a decentralized public entity. Most of the largest national potato collections, such as USA004 and DEU159, have also assigned their material to the MLS. As these holders distribute most of the accessions (Figure 8.4.4), about 88% (10,500 accessions) of the accessions distributed can be provided with an SMTA (Figure 11.6.1). Some Latin American (ARG1347, CHL028, COL017, GTM001), Asian (CHN116, CHN122, IND665) and European collections (BEL023, IRL012, LVA006, ROM007, RUS001) have not yet assigned their collections to the MLS and mostly distribute the material through institute-specific MTAs. Overall, about 8% (1,000 accessions) are distributed via institute-specific MTAs and for 4% of the material the legal basis was not stated. None of the institutions stated that they distribute their material under the regulations of the Nagoya protocol.

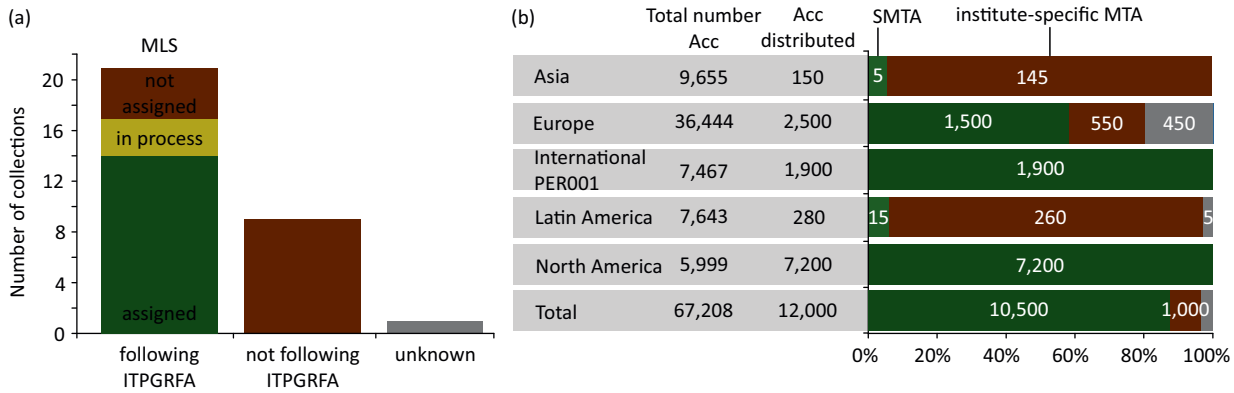



**Figure 11.6.1.** Policies for distribution and access to material of the 32 genebanks participating at the survey. a) Number of collections subject to the conditions of the International Treaty on Plant genetic Resources for Food and Agriculture (ITPGRFA) and assigned to its Multilateral System (MLS). b) Number of collections and percentage of distributed material via Standard Material Transfer Agreement (SMTA) or an institute-specific material transfer agreement (MTA).

In summary, the legal basis is fundamental for the use of genetic resources and progress in plant breeding. Therefore, efforts must continue to ensure legal transfer, exchange and use of potato resources for future improvements.

## 11.7 Type of collection and uniqueness

The type of collection is important for finding unique material to be used for breeding and development. Thereby, long-term conservation is the main objective of most potato collections, i.e. CHN116, CZE027, DEU159, IND665, PER001, RUS001, USA004 (Figure 11.7.1.). Nine collections are considered as working collections, including FRA010, with largest number of breeding lines (10,000 accessions). Four are breeding collections (CHL071, CHN122, CUB005, IRL012) and three are reference collections (ARG1347, GBR165, IRL036). Reference collections play an important role in accession identification and authentication (FAO, 2014) and are generally well studied. These include collections preserving unique Irish (IRL036) and Argentinian landraces (ARG1347) as well as the so-called 'Commonwealth potato collection' (CPC) preserving also 19th century British landraces (GBR165). Six collections (BEL023, ESP016, EST019, GTM001, IND665, USA004) have multiple objectives and function as breeding, working and long-term conservation collections.

Most of the unique material is expected to be held in South American collections, including native Chilean landraces of the *S. tuberosum* 'Chilotanum group' (CHL028), but also Colombian (COL017) and Peruvian (PER001, PER860) landraces of the *S. tuberosum* 'Andigenum group' and Brazilian (BRA020) and Ecuadorian (ECU023) wild species. Some of this material carries resistance genes against various pest and diseases, such as *Phytophthora* and *Globodera.* Most European potato collections preserve and develop national landraces and varieties, i.e. Bulgarian (BGR001), German (DEU159), Czech (CZE027), Irish (IRL012), Latvian (LVA006), Russian (RUS001), Romanian (ROM007) and Nordic (SWE054) landraces. Similarly, CHN116 and JPN183 preserve Chinese and Japanese landraces and adapted lines. As most of the material is distributed at the national level (Figure 8.4.1), the collections are an important source for new allelic diversity that can be introgressed in breeding programs.

## 11.8 Characterization and evaluation

Vegetative propagation is known to be associated with the spread of pathogens and pests. Clonal propagules carry and transmit viruses, bacteria, fungi and parasites, and healthy propagules can be easily infected. In the field, the older a clone is, the more pathogens are accumulated (McKey et al., 2010). Potato production is severely affected by several serious pests and diseases that can cause yield losses up to 100%. Some of these are particularly invasive and devastating. These are monitored and listed, for example by the European and Mediterranean Plant Protection Organization (EPPO) that follows the guidelines of the International Plant Protection Convention. Based on detailed documentation, the EPPO recommends pests be regulated as a quarantine pest in national phytosanitary regulations and discriminates between A1, a pest that is not yet present in the EPPO region and A2, a pest which is present in the EPPO region (Table 11.8.1).

Genebanks follow international rules and recom-

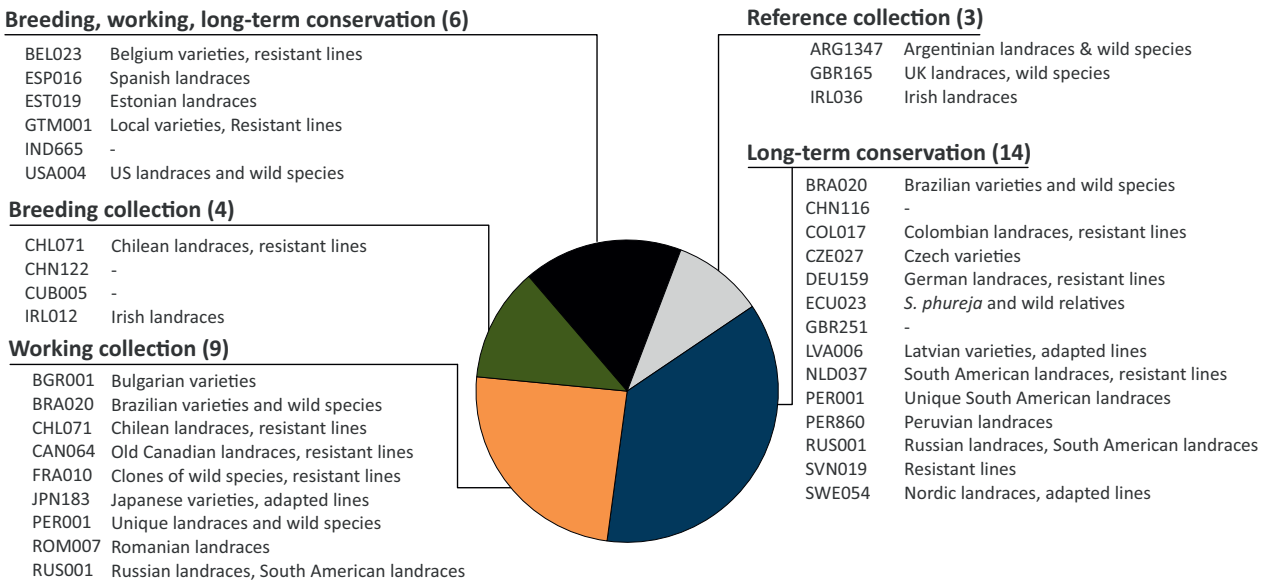



**Figure 11.7.1.** Main objectives of the potato collection of the 32 genebanks participating at the survey and the importance of their collection for use and breeding. Multiple answers allowed.

mendations, and screen material for specific pests and resistance genes. This information is particularly relevant for the international transfer and exchange of plant genetic resource and for the selection of parental lines in breeding programs. The most important pests and diseases phenotyped in 32 potato collections are listed below.

### Fungal and Late blight disease

The main biotic threat to potato production is **Late blight,** caused by the oomycete *Phytophthora infestans*. It causes light to dark brown spots on leaves, stems and tubers and diminishes tuber quality. Nowadays, effective pest management includes a combination of: (1) monitoring of *Phytophthora infestans* population, (2) monitoring environment and weather conditions, (3) molecular diagnostics kits and (4) smart-phone-based systems to support decisions on fungicide treatments (Adolf et al., 2020). Although there have been some resistance genes identified and introgressed from *S. berthaultii, S. bulbocastanum, S. demissum, S. microdontum, S. stoloniferum, S. venturi* and *S. chacoense* and markers are available, some races of the pathogen have overcome the resistance over time. To prevent rapid evolution of the oomycete races, strategies to combine different resistance genes involving different mechanisms seem to be promising. Currently, novel resistance genes detected via QTL mapping are evaluated and will be a great source for marker-assisted selection (Sood et al., 2017). Also, the functional stacking of resistance genes using *Agrobacterium tumefaciens*-mediated transformation has been proven to be successful (Zhu et al., 2012; Ghislain et al., 2019). However, further use of resistance genes also depends on evaluation of potato genetic resources, appropriate screening approaches and the availability of data. To date, potato collections in 27 genebanks have been screened for late blight resistances (Figure 11.8.1.1). Among some examples, Bachmann-Pfabe et al. (2019) examined the wild potato collection of DEU159 and found 68 highly resistant and 311 partially resistant accessions among 1,055 accessions of *S. acaule*, *S. fendleri*, *S. megistacrolobum*, *S. polytrichon*, *S. jamesii*, *Solanum trifidum* Correll, and *Solanum tarnii* Hawkes & Hjert. New blight resistant plants were also discovered in the wild potato collection of USA004; in *Solanum albornozii* Correll, *Solanum agrimonifolium* Rydb., *S. chomatophilum*, *S. ehrenbergii*, *S. hypacrarthrum*, *Solanum iopetalum* (Bitter) Hawkes, *Solanum palustre* Schltdl., *S. piurae*, *S. morelliforme*, *S. neocardenasii*, *S. trifidum*, and *Solanum stipuloideum* Rusby (Karki et al., 2021). Finally, in a screening of 79 accessions from 39 wild potato species and seven species of landraces (using the taxonomy of Hawkes 1990), novel late blight resistance was found in *S. albornozii*, *Solanum andreanum* Baker, *Solanum lesteri* Hawkes & Hjert, *Solanum lon-*

**Table 11.8.1.** List of potato pests recommended for regulation as quarantine pest (EPPO, 2021).

| Category | Common name | Latin/Full name | Category |
|---|---|---|---|
| **Fungus** | Potato wart | *Synchytrium endobioticum* | A2/82 SYNCEN |
| **Viruses and virus-** | APLV, Tymovirus | Andean potato latent virus | A1/244 APLV00 |
| **like organism** | APMMV, Mycovirus | Andean potato mild mosaic virus | A1/384 APMMV0 |
| | APMoV, Comovirus | Andean potato mottle virus | A1/245 APMOV0 |
| | Nepovirus | Potato black ringspot virus | A1/246 PBRSV0 |
| | PSTVd, Pospiviroid | Potato spindle tuber viroid | A2/97 PSTVD0 |
| | PVT | Potato virus T | A1/247 PVT000 |
| | PYDV, Crinivirus | Potato yellow dwarf virus nucleorhabdovirus | A1/29 PYDV00 |
| | PYVV | Potato yellow vein virus | A1/30 PYVV00 |
| | PYV | Potato yellowing virus | A1/220 PYV000 |
| **Bacteria & phytoplasm** | Potato purple top wilt | *Candidatus phytoplasma americanum* | A1/128 PHYPAE |
| | Bacterial wilt | *Ralstonia solanacearum* | A2/58 RALSSL |
| | Potato ring rot | *Clavibacter sepedonicus* | A2/51 CORBSE |
| **Insects** | Guatemalan potato tuber worm | *Tecia solanivora* | A2/310 TECASO |
| | Andean potato weevil | *Premnotrypes latithorax* | A1/143 PREMLA |
| | Andean potato weevil | *Premnotrypes suturicallus* | A1/143 PREMSU |
| | Andean potato weevil | *Premnotrypes vorax* | A1/143 PREMVO |
| | Colorado potato beetle | *Leptinotarsa decemlineata* | A2/113 LPTNDE |
| **Nematodes** | Potato cyst nematode | *Globodera rostochiensis* | A2/125 HETDRO |
| | Potato cyst nematode | *Globodera pallida* | A2/124 HETDPA |

*giconicum* Bitter, *S. morelliforme*, *Solanum stenophyllidium* Bitter, *Solanum mochiquense* Ochoa, *Solanum cajamarquense* Ochoa, and *Solanum huancabambense* Ochoa (Perez et al., 2022).

The fungal disease **Early blight** is caused by *Alternaria solani,* which infects leaves and causes dark brown to black spots with concentric rings, leading to considerable yield losses. The disease can be controlled by a combination of elimination of soil-born inoculum from the field, using tolerant varieties, and pesticides. However, loss of sensitivity towards specific pesticides, i.e. succinate dehydrogenase inhibitor (SDHI) and Quinone outside inhibitor (QoI), has been reported in many countries. Therefore, the importance of the disease will increase in the future (Adolf et al., 2020). So far, only PER001 and CUB005 have had the opportunity to screen their collection fully or partially for this disease (Figure 11.8.1.1). Screening 217 cultivated potato accessions of the USDA ARS-Beltsville breeding program revealed 28 resistant and 62 moderately resistant varieties (Xue et al., 2019), which could be useful in future breeding programs. Interestingly, Wolters et al. (2021) identified both quantitative and qualitative resistance against this disease. The cross between *S. berthaultii* and a susceptible diploid *S. tuberosum* showed that resistence was inherited quantitatively, whereas the cross between *S. commersonii* subsp. *malmeanum* with diploid S. *tuberosum* revealed that resistance was inherited qualitatively.

**Potato wart** is caused by the soil-born fungus *Synchytrium endobioticum,* which causes cauliflower-like galls that can grow in all meristematic tissues, except the roots. The fungus produces mobile zoospores that can survive more than 40 years without a host. Due to the serious losses in potato production and the long survival period, it has been listed on the EPPO A2 quarantine list (Table 11.8.1). Based on a GWAS approach, Prodhomme et al. (2020) identified SNP markers significantly associated with pathotype 1 resistance at the *Sen1* locus. As the locus only partly explains the resistance observed, the authors assumed that new and rare haplotypes were introduced by recombination and introgression breeding. Currently, the only strategy to control the disease is strict quarantine and phytosanitary measures and cultivation of resistant varieties (Adolf et al., 2020). Overall, eight (ARG1347, CAN064, DEU159, GBR165, NLD037, PER001, SWE054, USA004) out of 32 survey participants had the possibility of screening the collection fully or partly for potato wart resistances (Figure 11.8.1.1).

*Verticillium dahlia* is the most common pathogen of ***Verticillium* wilt**, a major threat for potato production, especially in cooler climates. After infection, it impairs the plant's water uptake, leading to leaf discoloration, necrosis, wilt and a yield loss up to 50%. The fungus can survive in the soil for more than 10 years (Jing et al., 2018). However, due to lower importance compared to the other diseases, resistances to this pathogen have only been assessed by PER001 and BRA020 (Figure 11.8.1.1).

**Fusarium dry rot** disease is caused by more than 13 *Fusarium* species and results in 25–60% tuber losses in storage (Tiwari et al., 2020; Tiwari et al., 2021b). Infected tubers have reduced dry matter, shrivelled flesh and necroses which mummify at the final stage. Pest control is largely through crop rotation, appropriate harvest and storage conditions, post-harvest fungicide application, however these are reported to become less effective. None of the potato varieties are resistant to the full range of *Fusarium* species, however resistant varieties may be an option when the strain is known (Bojanowski et al., 2013). In national and international genebanks, only four collections have been fully or partly investigated (Figure 11.8.1.1), thus resistant resources may still be hidden.

## Virus diseases

An overview of **virus diseases** and the **Potato Spindle Tuber Viroid** (**PSTVd**) is provided by Kreuze et al. (2020). The expansion of potato production to warmer climates, such as the tropics, and continuous cultivation throughout the year, are often associated with an increase in virus vectors, and hence an increase in potato virus diseases. Overall, more than 50 different viruses, including PSTVd, are known to infect potato (Kreuze et al., 2020). The most common viruses in potato are the potato virus Y (**PVY**), **PVX**, **PVS**, **PVA**, **PVM**, potato leaf roll virus (**PLRV**) and apical leaf curl virus (**PALCV**) (Sood et al., 2017). Single infections with PVM and PVS usually cause only minor tuber losses. In contrast, PVY and PLRV are the most damaging and widespread viruses and causes significant losses alone or in combination with other viruses. A combination of PVY, PVX and PVA can reduce potato yield by up

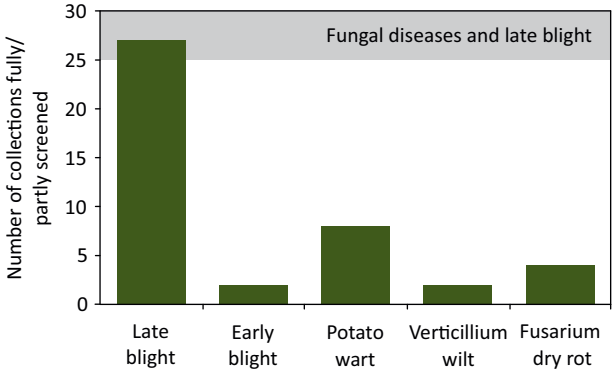



Figure 11.8.1.1. The number of collections partially or fully screened for resistances to selected fungal diseases and the oomycete late blight. Responses are provided from 32 participating genebanks.

to 80%. In addition, some recombinant strains of PVY, PLRV and the PSTVd compromise potato quality (Kreuze et al., 2020). PSTVd causes smaller leaves, spindle-shaped and/or multiple small tubers, and reduces yield up to 64%. Although the occurrence of PSTVd in potato has been reduced globally and largely eradicated in Europe and North America, it infects different hosts of the *Solanaceae* family. Currently, the most prevalent PSTVd strains in tomato can severely affect tomato fruit and potato tuber production and represent a threat to both markets (Mackie et al., 2019). So far, most viruses can be controlled via: (1) clean handling systems including virus testing, the utilization of disease-free material and sanitizing tools; (2) agronomic tools to prevent transmission through virus vectors or to eliminate virus infected plants at an early stage of cultivation (Polder et al., 2019); and (3) host plant resistances. Therefore, 15 collections have already been evaluated for different resistant accessions to PVY and PVY, to PLRV (CUB005, PER001, SWE054), PSTVd (IRL036) and PVS (PER001) (Figure 11.8.2.1). Another genebank, the Chilota potato genebank, studied the PVY resistance genes $Ry_{adg}$ and $Ry_{st}$ and identified 99 and 17, respectively, out of 271 accessions that possess resistance genes (López et al., 2015). Some of these resistance genes have already been introduced by breeding programs. Further resistance genes to PVA, PVV, PVS and PVM and to control PVY were also mapped. However, due to the complex genetics of potato, successful integration of resistances in combination with maintenance of tuber quality is challenging and may require the availability of acceptable additional tools in future (Kreuze et al., 2020).

## Bacterial diseases

Charkowski et al. (2020) studied in detail potato diseases caused by bacteria and the results are briefly summarized here. Bacteria cause severe damage to tubers and threaten potato production in warmer and cooler climates depending on the genus. Bacterial wilt and black leg are the most important diseases, followed by potato ring rot and common scab. **Bacterial wilt and brown rot** are caused by the bacteria strain *Ralstonia solanacearum*, especially the Phylotype IIB strain. It causes wilting of the leave,s and cut tubers and stems show a creamy, liquid exudate. Losses in potato production are estimated at USD 1 billion per year. Therefore, the organism has A2 quarantine status in some countries. So far, no new variety has shown resistance to the bacterium (Charkowski et al., 2020) although several collections (IRL036, IND665,PER001) have been screened for resistance genes (Figure 11.8.3.1).

The genera *Pectobacteria* and *Dickeya* cause the symptoms of the **black leg** disease and **tuber soft rot** in storage. The bacteria are transmitted via soil or through clonal material, though the role of insects is not fully understood at present. The development of the disease is highly dependent on the environment, and the use of micropropagated *Pectobacteria* and *Dickeya*-free plantlets and the application of hygiene standards are essential (Charkowski et al., 2020). Due to the importance of other diseases, only GBR165 was able to evaluate its collection for resistance plants to date (Figure 11.8.3.1).

*Clavibacter sepedonicus* causes **potato ring rot**, also termed bacterial ring rot (BRR), a quarantine disease that occurs in cooler climates and was first discovered in Germany in 1905. So far, only Irish collections (IRL036) have been evaluated for resistant genes (Figure 11.8.3.1). The bacteria is spread between infected tubers and causes tuber necrosis around a vascular ring and further wilting and leaf distortion. However, due to zero tolerance policies, outbreaks are rare and losses are limited to the loss of batch certification and restrictions in cropping (Charkowski et al., 2020).

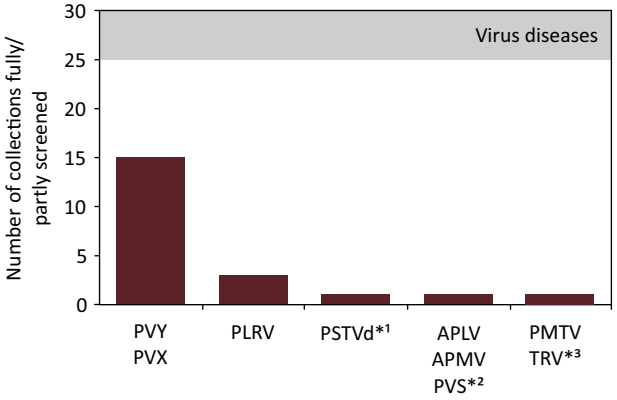



**Figure 11.8.2.1.** Number of collections partially/fully screened for resistances to Potato virus X (PVX) and Y (PVY), potato leaf role virus (PLRV), potato spindle tuber viroid (PSTVd), Andean potato latent virus (APLV), Andean potato mild mosaic virus (APMV), tobacco rattle virus (TRV). Responses are provided from 32 participating genebanks. *1 screening at IRL036, *2 screening at PER001, *3 screening at SWE054.

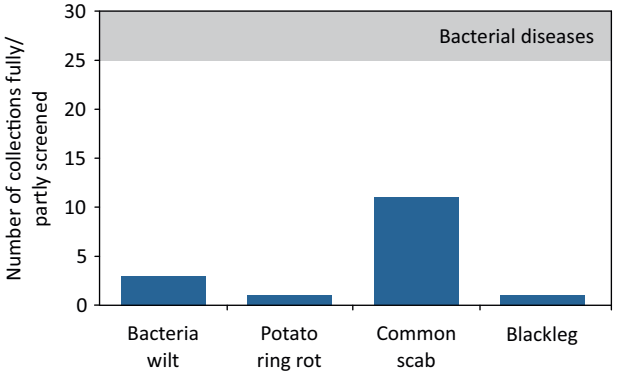



**Figure 11.8.3.1.** Number of collections partially/fully screened for resistances to important bacterial diseases. Responses are provided from 32 participating genebanks.

The bacterial disease most frequently assessed and investigated in 11 potato collections is **common scab** (Figure 11.8.3.1). It is one of the important potato diseases globally and is caused by *Streptomyces* species, with *Streptomyces scabiei, Streptomyces acidiscabiei* and *Streptomyces turgidiscabiei* being most common. The bacteria infect all underground parts including stems, roots, stolons and tubers, and cause necrosis and total loss. Quality and cropping regulations limit the spread. Overall, the introduction of resistance and increased tolerance in cultivated potato would be the most effective control for the bacterial disease. However, strict certification of clean material, cropping regulations and sanitization of tools are the only approaches currently used to combat the disease, which is a major challenge, in particular for developing countries (Charkowski et al., 2020).

### Insects and nematodes

Insect pests are commonly associated with potato production and most have evolved in the center of origin of the crop. Kroschel et al. (2020) gave a comprehensive overview of different insects and pointed out that seven main species (potato tuber moth, Andean potato tuber moth, Guatemalan potato tuber moth, Andean potato weevils, pea leaf miner fly, potato psyllid, bud midge) are most relevant in tropical and subtropical regions, two main species (European corn borer and Colorado potato beetle) affect potato production in temperate regions, and three species (aphids, whiteflies, ladybird beetles) can be considered as global pests.

The **potato tuber moth** (*Phthorimaea operculella*) is native to the tropical mountains of South America but has spread widely and is a serious pest in tropical and subtropical climates. The larvae of *Phthorimaea operculella* damage leaves and stems and feed on tubers, resulting in yield losses up to 70%. The **Andean potato tuber moth** (**APTM**, *Symmetrischema tangolias*) is native to Peru and Bolivia and has spread in recent decades. The larvae enter the stems through small holes and damage the plants by feeding until they wilt and collapse. Losses can be up to 30% in the field but increase when other tubers are re-infested in storage (Kroschel et al., 2020). **Guatemalan potato tuber moth** (**GPTM**, *Tecia solanivora*) originates from Guatemala and has been considered a major threat to southern Europe since 2000. So far, the evaluation of resistant plants could only be carried out in the collections of PER001, RUS001 and COL017 (Figure 11.8.4.1). However, the larvae feed exclusively on tubers and leave a visible hole when they leave. An infestation with GPTM can result in the complete loss of the harvest. In general, when tubers are infested by any of the larvae of the different moths, their taste becomes bitter and they are not suitable for human consumption.

About 14 species, most of which belong to *Premnotrypes*, are considered as **Andean potato weevils**, with *Premnotrypes vorax*, *Premnotrypes latithorax* and *Premnotrypes suturicallus* being particular damaging. These species are highly adapted to Andean climate and are restricted to the mountainous regions from Argentina to Venezuela and resistant genes were screened in the PER001 collection (Figure 11.8.4.1). The adult stages feed on leaves, even up to the central vein. The larvae seriously damage the crop by penetrating tubers and causing losses of between 16–45%. Crop rotation, early harvest, plastic barriers around plantings, and removal of crop residues are the best ways to control the weevil (Kroschel et al., 2020).

In the temperate zones, the **Colorado potato beetle** (*Leptinotarsa decemlineata* (Say)) is a major pest whose infestation can lead to a complete loss of potato yield. The beetle is native to Mexico and has spread globally once at the beginning of the 20th century. Larvae and adults are leaf feeders and completely defoliate plants. The beetles can be controlled at the cultural, biological and chemical level (Kroschel et al., 2020). Evaluation to screen for resistant and susceptible accessions were carried out in ECU023, ROM007 and RUS001 (Figure 11.8.4.1).

A common pest that has spread globally is the **Green peach aphid** (*Myzus persicae*), which is assumed to have originated in China. They damage potato production by sucking the plant sap and impairing plant development or by transmitting virus diseases, i.e. PLRV or PVY (Kroschel et al., 2020). Often, a combination of plant protection approaches is considered and the search for resistant accessions is currently underway at AGR1347, CUB005, GBR251 (Figure 11.8.4.1).

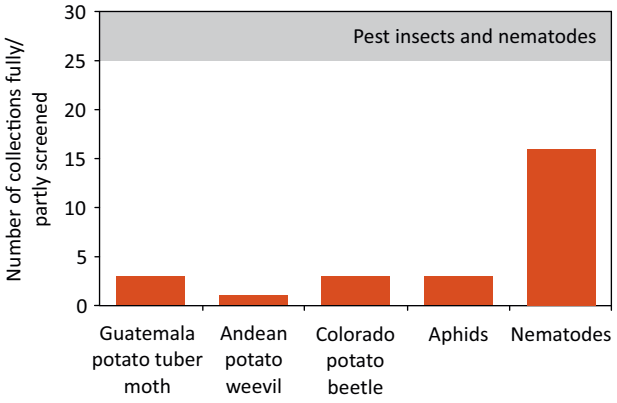



**Figure 11.8.4.1.** Number of collections partially/fully screened for resistances to important pest insects and nematodes. Responses are provided from 32 participating genebanks.

The **potato cyst nematodes** *Globodera rostochiensis* and *Globodera pallida* reproduce rapidly, are difficult to eradicate as cysts remain viable for about 20 years, causing severe yield loses after hatching (López-Lima et al., 2020). Therefore, they are quarantine pests and the identification of resistance genes is of major interest. Many of those genes encode for immune receptors that include a leucine-rich-repeat domain (NB-LRR) that have been analyzed using genetic mapping (Bakker et al., 2011). Furthermore, out of 32 survey participants, 16 collections have partially/fully screened their collections for resistant accessions (Figure 11.8.4.1). When the juvenile nematodes hatch in the presence of root exudates, they invade roots of the host and start feeding causing symptoms of nutrient deficiency including yellow leaves. The juvenile stages form a large syncytium and develop into adult females and males. After about 6 weeks, the adult males leave the root to fertilize the female bodies that are still attached to the root. The fertilized females form a cyst with the next generation of eggs waiting for optimum conditions to hatch (Price et al., 2021). In DEU159, out of 749 accessions tested, 78 accessions of *S. brevicaule*, *S. demissum* and *S. microdontum* wild species showed resistance to *Globodera pallida* (Bachmann-Pfabe et al., 2019).

The description of some of the pests and diseases and the available protection instruments has shown that none of them can be easily defeated by chemical, biological protection, sanitation or cultivation approaches on their own. To minimize the use of pesticide and avoid the loss of their efficacy and the loss of plant-pathogen resistance mechanisms, a combination of different protection approaches has been promoted by most researchers (Kroschel et al., 2020). The so-called Integrated Pest Management involves a combination of: (1) best agricultural practice, including the use of healthy propagules, crop rotation, biological control, and sanitizing tools; (2) the application of monitoring, modelling and prediction tools to prevent pest population growth; (3) the control rather than the complete elimination of pests; and (4) continuous evaluation of the results and adjustments.

### Abiotic stresses

Climate change and growth under sub-optimal conditions affect potato development. Depending on the type of stress, and its intensity, duration and occurrence during the vegetation period, potato yield and quality can be severely changed. Potato in particular is sensitive to **drought** due to its flat root system and inefficient recovery of photosynthetic systems (George et al., 2017). With reduced water availability, lateral roots proliferate and root elongation and root-hair production are significantly reduced, affecting the root-soil contact (Wishart et al., 2014). In addition, amino acids accumulate, ascorbate peroxidase levels increase and transcripts associated with photosystem II light harvesting complex decrease (Demirel et al., 2020), among other changes. Varieties with larger root systems have more and longer stolons, more plantlets and tend to be more stress tolerant as the canopy closes earlier, reducing evaporation from the soil (Wishart et al., 2014). During tuber initiation (BBCH 50) and tuberization (BBCH 70) (Figure 4.2.1), drought has the greatest impact and leads to significant changes in tuber yield and shape, i.e. dumbbell-shaped, knobbly, pointy tubers (George et al., 2017).

**Low temperatures**, in particular below -3°C, damage the foliage in the early and late season and limit the vegetative period and yield potential. **High temperatures**, above 30°C, affect tuber quality and yield (Waterer et al., 2010). High temperatures modulate carbon transport to sink organs, facilitate sucrose accumulation in the phloem, which reduces sucrose transfer to the sink and impairs starch syntheses. In combination with the accumulation of amino acids, Maillard reactions are promoted, producing color and flavor changes and acrylamide accumulation during frying. Furthermore, among other effects, the expression of genes related to anthocyanin and steroidal glycoalkaloid pathways is modulated, altering the beneficial impact on human health. Besides brown spots and necrosis, high temperatures affect tuber development, causing irregular shapes, cracks, secondary tuber formation and reduced tuber dormancy that can result in early sprouting (George et al., 2017).

Extensive use of fertilizers, chemicals and irrigation have considerable impacts on **soil salinity**. Increased salinity induces detrimental changes in the root system, with decrease in number, diameter and length of roots (Chourasia et al., 2021) affecting photosynthesis, protein metabolism, respiration, protection mechanisms and nutrient balances, among others. The impairment of metabolism leads to lower tuber yield, browning and cracking of the tuber surface (George et al., 2017).

Most genebanks have started to screen for abiotic stresses (Figure 11.8.5.1). Of the 32 survey participants, 11 potato collections (ARG1347, CHL023, CHN116, CHN122, CUB005, ESP016, GBR251, GTM001, PER001, SVN019, USA004) were fully or partially screened for drought. Six collections were able to evaluate their collections for high and low temperatures and salinity. In particular, CAN064, CUB005, GBR251, IND665, PER001, and USA004 were interested in the response to high temperatures. CHL028, CHN116, CHN122, GTM001, PER001, and USA004 had the chance to evaluate parts of their collection for frost resistance or response to low temperatures and ARG1347, CHL028, CHN122, NLD037, and USA001 for salinity. Other abi-

otic stresses and traits investigated by some collections were nitrogen deficiency (CAN064, DEU159), mechanical damage (CZE027, PER001), waterlogging (CHN116, DEU159), phosphorus deficiency (DEU159), long-/short day adaptation (PER001), shade adaptation (PER001).

## 11.9 Challenges and Priorities

Potato breeding programs are challenged to introduce new quality traits, and pest and diseases resistances, in combination with increased tuber yield, which is difficult due to the complex genetic nature of the crop. As a result, yield has hardly improved in the last century (Douches et al., 1996). Climate change is leading to more frequent occurrence of frost, heat waves and drought, including effects on increased soil salinity and changes in the distribution and incidence of pest and diseases (Dahal et al., 2019). According to the predictions of Raymundo et al. (2018), potato production will be only moderately affected until 2055. However, the potato yield is predicted to decline by 26% by the end of the century. Significant impacts on potato yield and quality are forecast at high latitudes, such as Eastern Europe and North America, the lowlands of sub-Saharan Africa, though less in mid-latitude and tropical highlands (Raymundo et al., 2018).

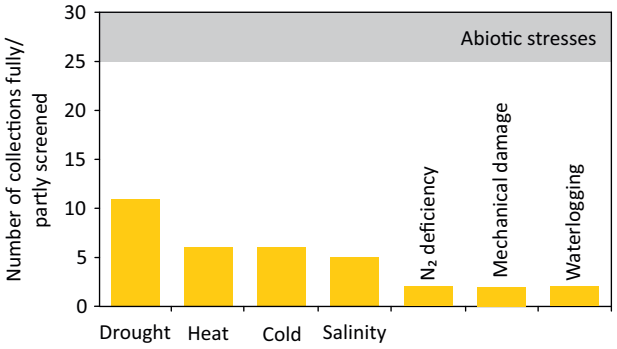



**Figure 11.8.5.1.** Number of collections partially/fully screened for abiotic stresses. Responses are provided from 32 participating genebanks.

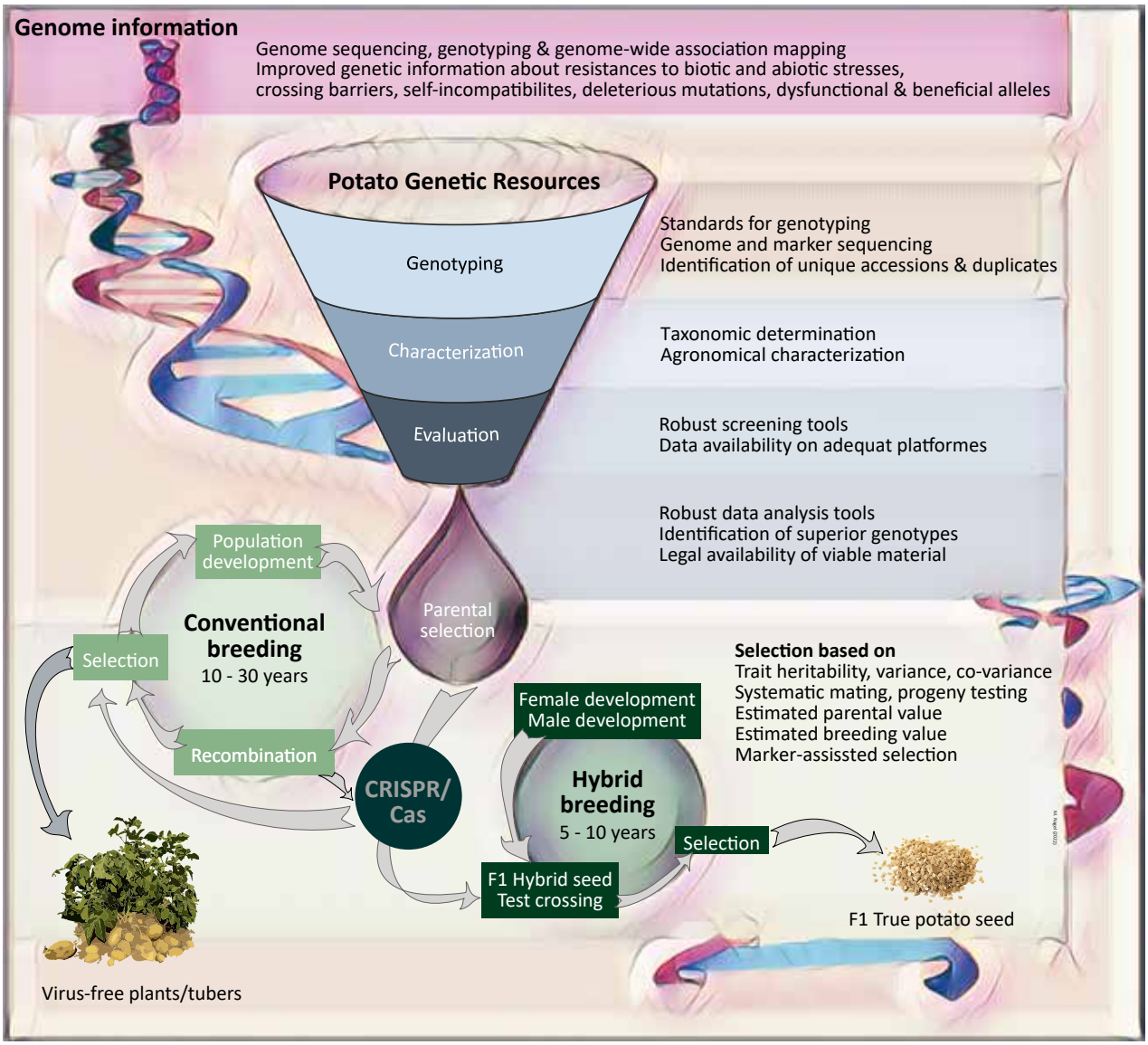



**Figure 11.9.1.** The use of potato genetic resources in potato breeding programs and information needed to increase tuber yield and improve quality.

To improve the productivity of potato, genomic information, characterization and evaluation and plant breeding have to be further developed, and will affect *ex situ* conservation (Figure 11.9.1). In detail, specific requirements include:

1. **Improve genome information** of cultivated and wild potato species, including improved assembly algorithms, increased read lengths, and *de novo* sequences of additional haplotypes to elucidate a full catalogue of genes that provide the genetic basis for resistances, deleterious mutations, dysfunctional and beneficial alleles
2. **Improved genotyping and** phenotyping of germplasm collections using robust and standardized approaches and data analyses tools to identify resistances, beneficial traits and superior individuals
3. **Increased accessibility of the germplasm and associated information**, including the continuous development of databases (Genesys, EURISCO) to provide characterization, evaluation and genotyping information
4. **Broadening genetic diversity** in cultivated potato by a) introduction of stress resistant genotypes of landraces or wild species, or b) improvement of diploid potato germplasm before introgression into tetraploid material
5. **Application of advanced breeding tools** such as a) genomic selection using estimated breeding value and marker-assisted selection, and b) hybrid breeding systems
6. **Enhanced interdisciplinary and international collaboration** to develop Integrated Pest Management systems and to improve tuber yield and quality (breeders, geneticists, conservation biologists, phytopathologists, data managers, agronomists)

Potato flower. Photo: Michael Major/Crop Trust

# 12 RECOMMENDED PRIORITIES

The 32 institutions participating in the survey conserve more than 69,000 accessions, representing more than 80% of the global potato collections. The Latin American countries, plus CIP (PER001) and DEU159, GBR251, NLD037, RUS001, and USA004 maintain large collections of wild species and landraces, whereas most other European and Asian collections maintain extensive collections of heirloom varieties, varieties and breeding lines. Thus, based on the data provided by the survey participants, a comprehensive overview of the conservation status of potato genetic resources can be obtained, and strategic priorities can be recommended.

## Action Point 1: Comprehensive genotyping of *ex situ* and *in situ* collections.

Genotyping is needed in various fields of conservation activities, in particular for taxonomic classification, collection management (including identification of duplicates and unique accessions), gap analysis and use of collections. Therefore, **1)** comprehensive genotyping of all accessions maintained *ex situ* and of material preserved *in situ* and on farm is required. However, to coordinate activities and to ensure adequate data analysis, the international community needs to agree on **2)** standards for genotyping, and the definition of duplicates and unique accessions, and **3)** to establish user-friendly analysis platforms, **4)** ensure effective linkage between passport and genomic data of accessions, and **5)** support further genome research and broaden genetic information on resistances, deleterious mutations, dysfunctional and beneficial alleles.

## Action Point 2: Harmonization of potato taxonomy

Correct taxonomic identification is a foundation for the conservation of genetic diversity. Currently, potato collections are classified according to three different systems, with VIR (RUS001) following Bukasov (1978), yet most genebanks apply Hawkes (1990) due to the precise characterization of species and detailed and comprehensive morphological descriptions. Although GRIN does not obligate genebanks to use the more recent classification system of Spooner et al. (2014), most genebanks using GRIN follow that revision of the 228 wild potato species, seven cultivated species and

19 taxonomic series recognized by Hawkes (1990). On basis of molecular and morphological data, Spooner et al. (2014) combined the Hawkes (1990) taxa into 107 wild and four cultivated potato species. This poses some challenges for use of the collections and the identification of gaps. Therefore, the international community needs to agree on **1)** a universal and predictive taxonomy and/or **2)** the classification system used needs to be stated in documentation systems and respective synonyms need to be transparent and be provided in public databases (EURISCO, Genesys, GRIN). Furthermore, if Spooner et al. (2014) will be more widely applied in future **3)** a suitable system for subdividing large groups of species is required because gaps can be more easily identified in smaller groups. Also, **4)** names of sub-groups should be associated with traits and **5)** intermediate forms could be given an appropriate name indicating their origin.

## Action Point 3: Documentation and monitoring of *in situ* populations and traditional landraces maintained on farm in American countries

To successfully conserve wild potato species and traditional landraces *in situ* and on farm, more information is required on natural populations and traditional landraces grown in different places. Therefore, **1)** inventories of crop wild relatives, including IUCN Red List status, ecology, distribution patterns, taxonomy, traditional knowledge and use should be conducted, **2)** changes in diversity in wild populations and of potato landraces should be monitored. A global early warning and monitoring system such as the *in situ* conservation monitoring system for root and tuber crops and bananas currently being developed by the Alliance of Bioversity and CIAT could provide such a platform for monitoring potato diversity globally. Furthermore, the international community needs to agree on **3)** standard procedures to measure conservation status and robustly monitor the dynamics of landrace pools in selected hotspots, especially in the Andes and on the Chiloé islands.

## Action Point 4: Capacity building for *in situ* conservation and improved strategic concepts for on farm conservation

Indigenous families still passionately maintain potato diversity for the benefit of all humanity, and yet they live in poverty. Therefore, **1)** incentives for *in situ* conservation and on farm management of native potato varieties and crop wild relatives need to be provided to compensate for the low economic profitability of this local biodiversity. Further, support is required **2) for** the development of marketing strategies to achieve higher prices for local varieties, and **3)** to improve the local seed system and enhance the availability of healthy and good quality planting material for further propagation and distribution of local varieties among the members of local communities. In addition, **4)** collaborations between landowners and local universities should be promoted to raise the awareness and improve the assessment of the available diversity of wild relatives and native landraces. Universities may run courses, research projects and improve the technical skills of farmers and indigenous families to support the identification of unique material and further *in situ* conservation.

## Action Point 5: Collecting missions and linkage between *in situ*/on farm and *ex situ* conservation

Effective complementary conservation strategies are needed in the potato center of origin. Activities need to be intensified **1)** to repatriate native potato genetic resources, and the diversity they contain, to local communities as needed and **2)** to support on farm management by providing healthy disease-free propagules. In the local communities, **3)** the local on farm and *in situ* diversity needs to be assessed and conserved *ex situ*. Due to habitat changes or introduction of invasive species **4)** missions to collect wild species are urgently required and must be supported by local policy makers, well-experienced collectors and gap analysis. **5)** Missions to re-collect material may be considered because mutations, natural selection, genetic drift and gene flow have a significant impact on local genetic diversity. **6)** The international community must support collecting missions through international collaboration, which is highly appreciated by the Latin American genebanks. **7)** The impact of the repatriation work and collecting missions needs to be evaluated to determine and improve their success.

## Action Point 6: Capacity building to maintain high quality *ex situ* collections, in particular in Latin American countries

Long-term *ex situ* conservation of potato genetic resources can only be successful if appropriate storage conditions and best conservation practices are applied. In particular, in Latin American countries, genebanks need facilities for cold storage, cryopreservation and tissue culture to preserve their material according to internationally agreed Genebank Standards. In particular, to **1)** store field-grown tubers under optimum conditions, **2)** back up field collections *in vitro* or *in cryo*, **3)** improve plant health and eliminate viruses and diseases, 4**)** preserve seeds and **5)** to support safety back ups at different sites. In addition, **6)** full documentation of all procedures is required to ensure an appropriate guidance for technical staff, and thus high conservation quality.

## Action Point 7: Cryopreservation is needed to ensure long-term survival of potato genetic resources

Clonal potato genetic resources, and possibly true potato seeds, can be securely conserved for the long-term at minimal costs by cryopreservation. Therefore, the international community needs to **1)** support the Global Plant Cryopreservation Initiative and cryopreserve all unique potato accessions, **2)** agree on standards for 'best practice' and storage, and **3)** study fundamental processes and optimum preservation conditions to ensure high shoot-tip and seed survival after cryopreservation.

## Action Point 8: Further digitalization, better linkage and visibility of publicly available data for *ex situ* and *in situ* conservation management

Data management is fundamental for the success and the quality of the genebank management and *in situ* conservation. The electronic availability of protocols, procedures, workflows, specific know-how, as well as continuous documentation, secure data storage and registration of *in situ* inventory linked to traditional knowledge, can ensure the high quality of available material, and thus long-term conservation of potato genetic resources. To date, no global data management system is in place for *in situ* conservation, and thus the data are marginally if at all accessible. Therefore, there is an urgent need for the **1)** implementation of *in situ* and genebank information systems recording all data, including inventory, passport, characterization and evaluation data, digitalization of voucher specimen, and for **2)** the improvement of the linkage between *in situ*, genebank and other publicly available data, in particular sequencing data and voucher specimens. Here, the **3)** integration of Digital Object Identifiers (DOI) available to PGR collections through the GLIS DOI portal can support the linkage of material across genebanks and beyond. Furthermore, the accessibility of *in situ* and genebank material will be improved when **4)** the data are integrated into other platforms i.e. GRIN, EURISCO or Genesys and **5)** the data available in the Intergenebank Potato Database (IPD) that matches wild species accessions between eight genebanks are also integrated into GRIN, EURISCO or Genesys. The IPD should be embedded in data management systems that transfer their data to the public domain. Public availability of data is a prerequisite for identifying unique accessions and duplicates, analyzing gaps, assessing the threat potential to wild populations and traditional landraces, and the use of in potato genetic resources.

## Action Point 9: Accessibility of collections for breeding and use

Potato breeding suffers from stagnating yields and faces challenges related to climate change. Therefore, to improve the third most consumed crop, it is commonly agreed that there is a need to broaden the genetic diversity in cultivated potato, including the introduction of resistant landraces and wild species. Therefore, there is a need for **1)** well-documented core collections and **2)** easy access to genebank data, genomic information, characterization and evaluation data, which includes further development of databases (GRIN, EURISCO, Genesys) and **3)** indentification of the specific needs of the international community of users. **4)** FAIR principles (findable, accessible, interoperable, reusable) may be introduced as standard for all phenotypic data (descriptors) and **5)** healthy and virus-free plant material **6)** must be available in required quantities and **7)** via the SMTA. **8)** Further research to overcome self-incompatibilities and sterility barriers, and on molecular and hybrid breeding tools, is essential for the future of this important crop.

## Action Point 10: Networking and training

To address specific challenges related to potato in the future, to raise awareness of the need conservation and to efficiently manage pests and diseases, **1)** interdisciplinary and international collaboration between breeders, curators, geneticists, conservation biologists, phytopathologists, data managers, and agronomists are required **2)** to develop efficient staff training programs, **3)** to monitor *in situ* conservation status and **4)** to implement global conservation planning and **5)** Integrated Pest Management systems. Further discussions are needed to **6)** adapt descriptors and genebank information for breeders and users.

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# ANNEXES

## Annex 1. A survey to build a global conservation strategy for potato

### Background

The Global Crop Diversity Trust ("The Trust") is supporting efforts to develop strategies for the efficient and effective conservation of crop diversity, particularly in *ex situ* collections. The Trust has commissioned an independent external consultant (Manuela Nagel) to coordinate the development of a conservation strategy for germplasm holdings of the 'tuber bearing *Solanums*', commonly known as potato. This questionnaire has been developed for the purpose of seeking the advice and input of representatives of relevant stakeholders around the world in the development of the conservation strategy. In particular, the questionnaire seeks to assess the status of the conservation and management of crop genetic resources of potato, both wild and cultivated, throughout the world.

If you or one of your colleague's curate a collection that includes accessions of potato, either wild or cultivated, we would kindly ask you to complete all sections of the questionnaire. If there are no ex situ collections of potato within your institute, please complete questions 74 and 75 only.

The Crop Trust are keen to have your active participation in the development of the potato conservation strategy and will be pleased to keep you informed on its progress and consult with you, either during its development or at completion. If you have any questions about this questionnaire or about the proposed strategy in general, please contact.

**Does your institution maintain an *ex situ* collection of potato?**

Yes | No

### ORGANIZATION INFORMATION

**Name and address of organization holding/maintaining the potato collection**

Address | City | Postal Code | Country | Website

**Curator in charge of the potato collection**

Name | Address | City | Fax |Email

**Name of respondent to this questionnaire if not as above**

Contact details | Date of response

**Additional key contact person for the above germplasm collections**

Name | Title/Function | Email Address

**Please describe the organization**

Governmental organization | University | Private organization |NGO or charity | Other: please describe

**Is the institution in charge of the potato collection the legal owner of the collection?**

Yes | No | If no, who is the owner (including no owner identified)?

**Is the collection subject to the terms and conditions of the International Treaty on Plant genetic Resources for Food and Agriculture?**

Yes | No

**If yes, has the material been assigned to the Multilateral System (MLS)?**

Yes, already assigned | Not currently assigned to the MLS
In the process of preparing for the materials to be assigned to the MLS

**If no, is it expected to become part of the International Treaty in the near future?**

If yes, indicate expected date | No

**Could you summarize your use of Material Transfer Agreements?**

SMTA ( % of total MTA's) | Nagoya Protocol ( % of total MTA's) | Institute specific ( % of total MTA's)

## OVERVIEW OF THE POTATO COLLECTION

**Main objective of the collection (long-term conservation, working collection, breeding collection, reference collection)**

Long-term conservation | Working collection | Breeding collection | Reference collection
Other (Please specify)

**Please indicate the number of species by type of germplasm**

| Type of germplasm (where known) | Number of species |
|---|---|
| Wild potato species | |
| Potato landraces | |
| Improved potato cultivars | |
| Breeding/research materials | |
| Unknown | |
| Other, specify: | |

**Please indicate the number of accessions by type of germplasm**

| Type of germplasm (where known) | Number of accessions |
|---|---|
| Wild potato species | |
| Potato landraces | |
| Improved potato cultivars | |
| Breeding/research materials | |
| Unknown | |
| Other, specify: | |

**Please indicate the proportion (%) of accessions available for distribution by type of germplasm**

| Type of germplasm (where known) | % available for distribution |
|---|---|
| Wild potato species | |
| Potato landraces | |
| Improved potato cultivars | |
| Breeding/research materials | |
| Unknown | |
| Other, specify: | |

**Origin of the collection: please indicate the proportion (%) of accessions on the total amount that were**

| | Percentage % |
|---|---|
| collected originally in your own country (national origin) | |
| collected originally in your own region (regional origin) | |
| introduced from a collection abroad | |
| from other origin (please define): | |

**If you were asked to describe your collection in general terms, which of the following categories would best you place your collection.**

Good Global coverage | Good regional coverage: which regions? | Good National / multinational coverage? which countries? | If regional or national/multinational coverage applies, please highlight what regions or countries are included:

**Do you consider there to be any major gaps in the collection?**

Species coverage of the crop: Yes ( ), No ( ) | Population (sample) representation per species: Yes ( ), No ( ) | Ecological representation of the species: Yes ( ) , No ( ) | Other, please specify:

**If yes, are there any plans to fill such gaps and if so, please provide details on the plans.**

**Are there any specific aspects or specialist dimensions relating to your collection that you consider to be unique or that you actively promote e.g. sets of heritage cultivars, old native cultivars, host differentials or type lines)?**

**Has your Potato collection at least partially been screened for biotic stresses?**

Yes | No | If yes, for which major diseases or insect pests?

**Has your Potato collection at least partially been screened for abiotic stresses?**

Yes | No | If yes, for which abiotic stresses?

**Has there been any genotyping or marker studies conducted on your Potato collection?**

Yes | No

**If not no, could you indicate the scale of these studies (number of accessions);**

Partial (no. accessions) | Focused subsets (no. accessions) | Major or near complete collection (no. accessions)

**If so, is this data publicly available?**

Yes | No | Website for the data:

**Please describe the main potential/importance of your collection for use and breeding**

## CONSERVATION STATUS (GERMPLASM MANAGEMENT)

**Conservation facilities. Please indicate the proportion of the accessions maintained under the following conditions: Note: if accessions are maintained under more than one storage condition the total percentage may exceed 100%)**

| Condition | Percentage % |
|---|---|
| Short-term storage | |
| Medium-term storage | |
| Long-term storage | |
| Other, please specify: | |

**Please describe the storage facilities (1)**

| | Facility 1 |
|---|---|
| Type of facilities | |
| Temperature | |
| Relative Humidity (%) | |
| Packing material | |
| Other, please specify | |

**Please describe the storage facilities (2)**

| | Facility 2 |
|---|---|
| Type of facilities | |
| Temperature | |
| Relative Humidity (%) | |
| Packing material | |
| Other, please specify | |

**Please describe the storage facilities (3)**

| | Facility 3 |
|---|---|
| Type of facilities | |
| Temperature | |
| Relative Humidity (%) | |
| Packing material | |
| Other, please specify | |

**Have you established a genebank management system or written procedures and protocols for:**

Acquisition (including collecting, introduction and exchange): Yes ( ), No ( ) | Regeneration Yes ( ), No ( ) | Characterization Yes ( ), No ( ) | Storage and maintenance : Yes ( ), No ( ) | Documentation : Yes ( ), No ( ) | Health of germplasm : Yes ( ), No ( ) | Distribution : Yes ( ), No ( ) | Safety-duplication : Yes ( ), No ( )
Other please specify

**In case you have procedures and protocols, are you able to provide the Global Crop Diversity Trust with this information (i.e. provide a copy)?**

Yes | No

**Please describe your quality control activities (in terms of frequency, protocols/methods and actions upon results)**

| Germination tests |
|---|
| Viability testing (including from *in vitro* storage) |
| Health testing |
| Other, please specify |

**Is the collection affected by diseases that can restrict the distribution of the germplasm?**

Yes | No

**If yes or slightly, are knowledge and facilities available at your institution for eradication of these diseases?**

Yes | No

**Please indicate the proportion (%) of the collection that requires urgent regeneration (apart from the normal routine regeneration)**

| Type of germplasm | % of accessions with urgent regeneration need |
|---|---|
| Wild potato species | |
| Potato landraces | |
| Improved potato cultivars | |
| Breeding/research materials | |
| Unknown | |
| Other, specify | |

**Please indicate the current and expected situations of the collection with respect to the following factors, where: 1 = high/good, 2 = adequate/moderate, 3 = not sufficient/bad, NA = not applicable**

| Factors | Current situation | Expected situation in 2025 |
|---|---|---|
| Funding for routine operations and maintenance | | |
| Retention of trained staff | | |
| Interest for Plant Genetic Resource Conservation by donors | | |
| Genetic variability in the collection as needed by users/breeders | | |
| Access to germplasm information | (passport, characterization, evaluation) | | |
| Active support/feedback by users | | |
| Level of use by breeders | | |
| Level of use by researchers | | |
| Other factors (please specify) | | |

## SAFETY DUPLICATION

(defined as the storage of a duplicate/copy of an accession in another location for safety back-up in case of loss of the original accession)

**Are accessions safety-duplicated in another genebank?**

Yes | No

**If you answered yes to previous question, please specify (safety duplcation1):**

| | |
|---|---|
| Name of institute maintaining your safety duplicates | (name) |
| Number of accessions | (number ) |
| Storage conditions \| (short, medium, long term) | (short, medium, long term) |
| Nature of the storage \| (e.g. black box, fully integrated in host collection, etc.) | (e.g. black box, fully integrated in host collection, etc.) |
| Add lines as necessary | |

**If there is a second site for safety duplications, please specify:**

| | |
|---|---|
| Name of institute maintaining your safety duplicates | (Name) |
| Number of accessions | (number ) |
| Storage conditions \| (short, medium, long term) | (short, medium, long term) |
| Nature of the storage \| (e.g. black box, fully integrated in host collection, etc.) | (e.g. black box, fully integrated in host collection, etc.) |
| Add lines as necessary | |

**If there is a third site for safety duplications, please specify:**

| | |
|---|---|
| Name of institute maintaining your safety duplicates | (Name) |
| Number of accessions | (number ) |
| Storage conditions \| (short, medium, long term) | (short, medium, long term) |
| Nature of the storage \| (e.g. black box, fully integrated in host collection, etc.) | (e.g. black box, fully integrated in host collection, etc.) |
| Add lines as necessary | |

**Is there any germplasm of other Potato collections safety-duplicated at your facilities?**

Yes | No

**If yes, please specify (1):**

| |
|---|
| Name of holder of original collection |
| Number of accessions |
| Storage conditions \| (short, medium, long term) |
| Nature of the storage \| (e.g. black box, fully integrated in host collection, etc.) |

**If accessions from other collections are safety duplicated at your genebank (2), please specify:**

| |
|---|
| Name of holder of original collection |
| Number of accessions |
| Storage conditions \| (short, medium, long term) |
| Nature of the storage \| (e.g. black box, fully integrated in host collection, etc.) |

**To what extent do you consider the potato accessions in your collection to be unique and not duplicated extensively elsewhere (i.e. EXCLUDING safety-duplication)? | Are there any specific aspects relating to these unique accessions that are associated with this attribution e.g. National heritage, genetic stocks or host differentials.**

Fully unique | Mostly unique | Partially unique | Fully duplicated elsewhere

**Are there any constraints to duplicating the collection elsewhere outside your country?**

Yes | No | If yes, please specify.

## INFORMATION MANAGEMENT

**Do you use an electronic information system for managing the collection (data related to storage, germination, distribution, etc.)?**

Yes | Partly | No | If yes, what software is used?

**Please specify the proportion (%) of the collection with data available in electronic format.**

| | |
|---|---|
| Passport data | % |
| Characterization data | % |
| Evaluation data | % |

**Please specify the proportion (%) of the collection with data available in paper form.**

| | |
|---|---|
| Passport data | % |
| Characterization data | % |
| Evaluation data | % |

**In case the collection is not computerized, are there plans to do so in the future?**

No plans | Computerization planned within 3 years | Other

**Is information of the collection accessible through the Internet?**

Yes | Partly | No | If yes, please specify web address

**Are data of the collection included in other databases?**

National Yes ( ), Partly ( ), No ( ) | Regional Yes ( ), Partly ( ), No ( ) | International Yes ( ), Partly ( ), No ( )
If yes or partly, specify the databases

## DISTRIBUTION AND USE OF MATERIAL

**What proportion (%) of the total collection is AVAILABLE for the following distributions?**

Nationally: % | Regionally: % | Internationally: %

**Please fill in the number of accessions DISTRIBUTED annually (average of last 3 years)**

| | Number of accessions distributed annually (average of last 3 years) |
|---|---|
| Nationally | % |
| Regionally | % |
| Internationally | % |

**How do you expect your distributions to change over the next 3–5 years? Indicate any expected change over the next 3–5 years?**

| | Expected change for the next 35 years |
|---|---|
| Nationally | Increasing ( ), No change ( ), Decreasing ( ), Don't know ( ) |
| Regionally | Increasing ( ), No change ( ), Decreasing ( ), Don't know ( ) |
| Internationally | Increasing ( ), No change ( ), Decreasing ( ), Don't know ( ) |

**Regarding the amounts of seed, do you set specific conditions for distribution? Please specify**

**Is the germplasm sufficiently available in terms of QUANTITY for distribution?**

Seeds: Yes ( ), Partly ( ), No( ) | Other, please specify: Yes ( ), Partly ( ), No( )

**Is the germplasm sufficiently available in terms of HEALTH for distribution?**

Yes | Partly | No

**Do you have adequate procedures in place for**

Phytosanitary certification? Yes ( ), Partly ( ), No( x ), I don't know ( ) | Packaging? Yes ( ), Partly ( ), No ( ), I don't know ( ) | Shipping? Yes ( ), Partly ( ), No ( ), I don't know ( ) | Other: Yes ( ), Partly ( ), No ( ), I don't know ( ) | If Other please specify

**Do you keep records of the distribution?**

Yes | No

**Which type of the following users received germplasm from you in the past 3 years?**

| Type of users | Proportion of total distribution % |
|---|---|
| Farmers and farmers' organizations | |
| Other genebank curators | |
| Academic researchers and students | |
| Domestic users | |
| Foreign users | |
| Plant breeders - public sector | |
| Plant breeders - private sector | |
| NGOs | |
| Others, please specify: | |

**How do you inform potential users about the availability of accessions and their respective data in your collection?**

**What are the most important factors limiting the use of the material maintained in your collection?**

**Please describe your policy regarding accessibility and distribution of Potato germplasm | (i.e. free or cost. If cost, please specify the amount)**

Cost of accessions: Free ( ), Cost ( ) | Cost of shipment: Free ( ), Cost ( ) | Cost of phytosanitary/growing season inspections: Free ( ), Cost ( )

**Do you have any restrictions on who can receive materials?**

Yes | No | If yes, please specify

## COLLABORATION WITH OTHER GENEBANKS AND/OR BREEDERS OF THE PUBLIC OR PRIVATE SECTOR IN TERMS OF GERMPLASM MANAGEMENT?

**Does your genebank collaborate with other genebanks and/or breeders of the public and/or private sector on aspects of germplasm management (regeneration, characterization, preliminary evaluation), apart from safety duplication?**

Yes | No

**If YES, please provide the following information on your collaboration: (1)**

| |
|---|
| Name of institution |
| Name of institution |
| Location |
| Type (public or private) |
| Type of collaboration (national, regional, international) |
| Area of collaboration (regeneration, characterization, preliminary evaluation) |
| Starting date and frequency of collaboration (annually, once every few years, seldom) |

**If YES, please provide the following information on your collaboration: (2)**

| |
|---|
| Name of institution |
| Name of institution |
| Location |
| Type (public or private) |
| Type of collaboration (national, regional, international) |
| Area of collaboration (regeneration, characterization, preliminary evaluation) |
| Starting date and frequency of collaboration (annually, once every few years, seldom) |

**If YES, please provide the following information on your collaboration: (3)**

| |
|---|
| Name of institution |
| Name of institution |
| Location |
| Type (public or private) |
| Type of collaboration (national, regional, international) |
| Area of collaboration (regeneration, characterization, preliminary evaluation) |
| Starting date and frequency of collaboration (annually, once every few years, seldom) |

**Do you collaborate in (a) network(s) as a Potato collection holder?**

Yes | No

**If YES, please provide the following information for each of the networks: (1)**

| |
|---|
| Name of network |
| National/ Regional/ Worldwide |
| Objectives |
| Reasons for participation |

**If YES, please provide the following information for each of the networks: (2)**

| |
|---|
| Name of network |
| National/ Regional/ Worldwide |
| Objectives |
| Reasons for participation |

**If your institute does not maintain an ex situ collection of Potato, please help us by indicating to the best of your knowledge, the following**

| |
|---|
| Current conservation activities |
| Institute focal person to contact for further details |
| Plans for any ex situ conservation |
| Any other information |

**Please add any further comments you may have**

**Please return the questionnaire to Glenn Bryan (Glenn.Bryan@hutton.ac.uk) as soon as possible.**

## Annex 2. Selected metrics for potato and cassava (as comparison)

*The summary in this annex was written by Dr. Felix Frey, International Consultant, Global Crop Diversity Trust.*

Khoury et al. (2022) compiled a comprehensive dataset as part of a project funded by the International Treaty on Plant Genetic Resources for Food and Agriculture, with the collaboration of the Crop Trust, led by the International Center for Tropical Agriculture (CIAT). The aim was to introduce five normalized, reproducible indicators to serve as an evidence base when prioritizing actions on the conservation and use of plant genetic resources for food and agriculture. The indicators encompass metrics associated with the USE of a crop (Global importance), the INTERDEPENDENCE between countries with respect to genetic resources, the DEMAND among researchers for genetic resources, the SUPPLY of germplasm by genebanks and the SECURITY of germplasm conservation. Graphs of the indicator results are publicly available on an interactive website. To generate the five indicators, Khoury et al. (2022) collected a comprehensive dataset from multiple sources. We do not present those indicators here, but rather discuss the underlying raw data to shed light on the aspects represented by the indicators with respect to potato.

To put numbers into context, we compare potatoes with cassava (Annex Table A2.1). Both crops are grown for their starchy tubers, which are important sources of carbohydrates and protein for human consumption. Both originate from the Americas. Potatoes are represented by the genus *Solanum* and the species *S. tuberosum*, *S. ajanhuiri*, *S. juzepczukii* and *S. curtilobum*. *Manihot* and *Manihot esculenta* are the genus and species names of cassava, respectively.

The metrics for "Global production," "Food supply" and "Quantity exported globally" under the indicator domain "Crop use" are annual average values drawn from FAOSTAT for the years 2010–2014 (Khoury et al., 2022). The percentage of countries producing and consuming (being supplied with) the crop is calculated as the number of countries where the respective crop is within the top 95% of most important crops, divided by the number of countries that report respective numbers (can be different between metrics and crops). The global production of potatoes is estimated at 363 million tons annually, which is close to 50% more than the global cassava production (254 million tons). The quantity of food supply by potatoes, i.e. the average global consumption, is at about 94 g $cap^{-1}day^{-1}$, which is more than double (241%) of food supply by cassava (39 g $cap^{-1}day^{-1}$). Potato food supply is thus relatively high, compared to its production. Percentage of countries producing potatoes is relatively high compared to cassava. Potatoes are produced in 74% of reporting countries, where cassava is only produced in 48% of the world's countries. Potatoes are consumed in all reporting countries in the world (100%), whereas the percentage of countries consuming cassava is 62%. Although both crops are internationally traded tubers, potato trade is of lower importance than cassava trade. Only 18 million tons of potatoes are exported, which is 47% of the exported amount of cassava production (39 million tons). Exports represent 5 and 15% of global production of potatoes and cassava, respectively.

The crop use metrics with respect to research were assessed using a manual search on Google Scholar, searching for the respective genus or species in the titles of publications, including patents and citations, between the years 2009 and 2019 (Khoury et al., 2022). Search hits on Google Scholar indicate the level of scientific interest in a crop. The *Solanum* genus is found in 16,500 publication titles, which is almost four times as much as publication titles including the cassava genus *Manihot* (4,220). However, it should be accounted for that the genus *Solanum* includes other globally important crops, such as tomato and eggplant. Publications with titles including the species names of potato and cassava are more comparable. The potato species names *S. tuberosum*, *S. ajanhuiri*, *S. juzepczukii* and *S. curtilobum* appear in 6,160 publication titles, where *Manihot esculenta* is included in 3,120 publication titles. If related to the comparison of production between both crops presented previously, potato research is slightly overrepresented when compared to cassava research.

Khoury et al. (2022) defined interdependence as a measure of the degree of dependence of global cultivation and use of a certain crop on the primary center of diversity of the crop. Primary centers of diversity are not represented by countries, but by 23 agroecological zones (Khoury et al., 2016), as crop diversity does not follow national borders but rather climatic and agroecological boundaries. Interdependence is high in crops that originate from a small area and are cultivated and used globally. For production, interdependence is calculated by dividing a crop's production outside the primary center of diversity by its global production. If all production is outside the primary center of diversity, interdependence would be 100%. For food supply, interdependence is calculated by dividing the food supply by the world average. Food supply outside can be higher than that inside the primary center of diversity and thus also higher than the global mean. Therefore, interdependence with respect

to food supply can be above 100%. The primary center of diversity of potato is located in Andean South America. As China and India are the most important potato producers (FAOSTAT, 2021b), interdependence of global production is at 98 % very high. Centers of diversity of cassava are located in Tropical South America as well as Central America and Mexico, while the main countries producing cassava are Nigeria, the Democratic Republic of the Congo and Thailand (FAOSTAT, 2021b). Interdependence of global production of cassava is thus also relatively high, with a value of 89%. The interdependence of food supply per capita of potatoes and cassava are also relatively high, with values of 100 and 94%, respectively. This is putatively due to the fact that potatoes are commonly consumed globally, and cassava is mostly consumed on the African and Asian continents (FAOSTAT, 2021a), outside of their primary centers of diversity.

Demand for germplasm is defined by two metrics (Khoury et al., 2022): (1) the number of distributions of accessions by genebanks, as an annual average between 2014 and 2017, drawn from the Plant Treaty's Global Information System; (2) the number of varieties released during the five years between 2014 and 2018, obtained from the International Union for the Protection of New Varieties of Plants (UPOV). There is a relatively strong use of potato germplasm, reflected by the 13,483 accessions per year distributed by genebanks. In contrast, only 1,388 cassava accessions are distributed annually. There is an even higher difference between the crops considering the development of new cultivars. 21,434 potato varieties were released during a five-year period in comparison with only 21 new cassava varieties per five years.

Khoury et al. (2022) illustrated the supply of germplasm by using the number of accessions available in *ex situ* collections around the world, with respect to the crop genus and the most important species of the respective crop. They also assessed the number of accessions (again with respect to genus and species) available under the multilateral system (MLS) of the Plant Treaty. This assessment was done first, directly, as notation (in MLS/not in MLS) in the public online databases Genesys, FAO WIEWS and GBIF. Secondly, the availability of accessions was assessed by considering whether the country hosting the institution that held the respective germplasm collection was a signatory to the Plant Treaty, in which case the accession was regarded as available via the MLS. According to databases, global *ex situ* collections count a total of 122,252 *Solanum* accessions, including all *Solanum* crops. 27,750 of these accessions are contributed by the potato species. The number of cassava accessions stored in global *ex situ* collections is 18,886 with respect to the genus *Manihot* and 17,831 for the species *Manihot esculenta*. Both potatoes and cassava are listed in Annex I of the Plant Treaty (FAO, 2009b). At the genus level, the percentage of accessions available under the MLS is 32 and 35% for potatoes and cassava, respectively. At the species level, the percentage of accessions available under the MLS is 45% for potato and 34% for cassava. However, a high percentage of accessions of both crops can be made available indirectly by matching institute countries with party status. On the species level 88 and 91% of potato and cassava accessions, respectively, are available in the MLS.

Security of germplasm conservation is represented here by two metrics: safety duplication at the Svalbard Global Seed Vault (SGSV) and the equality of global distribution with respect to several crop use metrics. The numbers of accessions, by genus and species, safety duplicated were taken from the SGSV website and divided by the total number of accessions stored in global *ex situ* collections, with the result giving the percentage of germplasm that is safety duplicated. To represent the equality of distribution across different agroecological regions of the world (Khoury et al., 2016), Khoury et al. (2022) used the reciprocal 1-Gini index with respect to the crop use metrics. The Gini index is the most commonly used inequality index (Gini Index, 2008), known foremost for the quantification of global income inequality. The 1-Gini index, presented here, ranges from 0 to 1, where 0 reflects very unequal distribution across world regions and 1 reflects a completely equal global distribution across regions. It reflects the security of crop cultivation and use, where, for example, small indices of production and thus geographic restriction go hand in hand with a higher vulnerability of supply, for example to natural disasters. The percentage of potato accessions safety duplicated at the SGSV is 43% and thus relatively high, while there are no safety duplicated cassava accessions. The equality of the distribution across the worlds' regions with respect to global production is 0.05 for potatoes and 0.04 for cassava. This is consistent with the fact that more countries produce potatoes than cassava, as stated above. Food supply of potatoes is more equally distributed throughout the world, with an equality of distribution value of 0.20, compared to a value of only 0.07 for cassava.

**Annex Table 2.1.** Selected metrics collected by Khoury et al. (2022) for potatoes and cassava, subdivided by indicator domain.

| Metric | Potatoes | Cassava | Potatoes / Cassava |
|---|---|---|---|
| **Crop use** | | | |
| Global production [tons] | 362,697,957 | 254,352,835 | 143% |
| Food supply (Amount consumed) [g/capita/day] | 94 | 39 | 241% |
| Percentage of countries producing crop * | 74% | 48% | 154% |
| Percentage of countries consuming (being supplied with) crop * | 100% | 62% | 161% |
| Quantity exported globally [t] | 18,287,593 | 39,015,830 | 47% |
| Number of publications between 2009-2019, including patents and citations, searching title of publication (Google scholar search hits) for genus ** | 16,500 | 4,220 | 391% |
| Number of publications between 2009-2019, including patents and citations, searching title of publication (Google scholar search hits) for species *** | 6,160 | 3,120 | 197% |
| **Interdependence** | | | |
| Interdependence of global production from germplasm from primary centers of diversity [0-1] **** | 98% | 89% | 110% |
| Interdependence of global food supply from germplasm from primary centers of diversity [0-1] **** | 100% | 94% | 106% |
| **Demand** | | | |
| Accessions distributed from gene banks (Annual average 2014-2017) | 13,483 | 1,388 | 971% |
| Variety releases in 5 years (2014-2018) | 21,434 | 21 | 102,067% |
| **Supply** | | | |
| Number of accessions in ex situ collections of genus ** | 122,252 | 18,886 | 647% |
| Number of accessions in ex situ collections of species *** | 27,750 | 17,831 | 156% |
| Accessions of the genus ** available through Multilateral System (MLS) directly noted in databases [%] | 32% | 35% | 91% |
| Accessions of the species *** available through Multilateral System (MLS) directly noted in databases [%] | 45% | 34% | 132% |
| Accessions of the genus ** available through Multilateral System (MLS) indirectly by matching institute countries with party status [%] | 84% | 89% | 94% |
| Accessions of the species *** available through Multilateral System (MLS) indirectly by matching institute countries with party status [%] | 88% | 91% | 97% |
| **Security** | | | |
| Accessions of genus ** safety duplicated in Svalbard Global Seed Vault [%] | 14% | 0% | |
| Accessions of species *** safety duplicated in Svalbard Global Seed Vault [%] | 43% | 0% | |
| 1-GINI index for equality of production across the world [0-1] ***** | 0.05 | 0.04 | 125% |
| 1-GINI index for equality of food supply across the world [0-1] ***** | 0.20 | 0.07 | 286% |

* Counting countries which list the crop as within top 95 % (FAOSTAT); Calculated as: Number of countries counting crop (top 95%) / Total number of countries (production 216, food supply 175)

** Potatoes: *Solanum*; Cassava: *Manihot*

*** Potatoes: *Solanum tuberosum, Solanum ajanhuiri, Solanum juzepczukii* and *Solanum curtilobum*; Cassava: *Manihot esculenta*

**** Global metric / Metric at primary center of diversity

***** Relative equality of crop use across world regions (same regions as used in interdependence domain), high equality give high indicator value

## Annex 3. Number and category of potato accessions

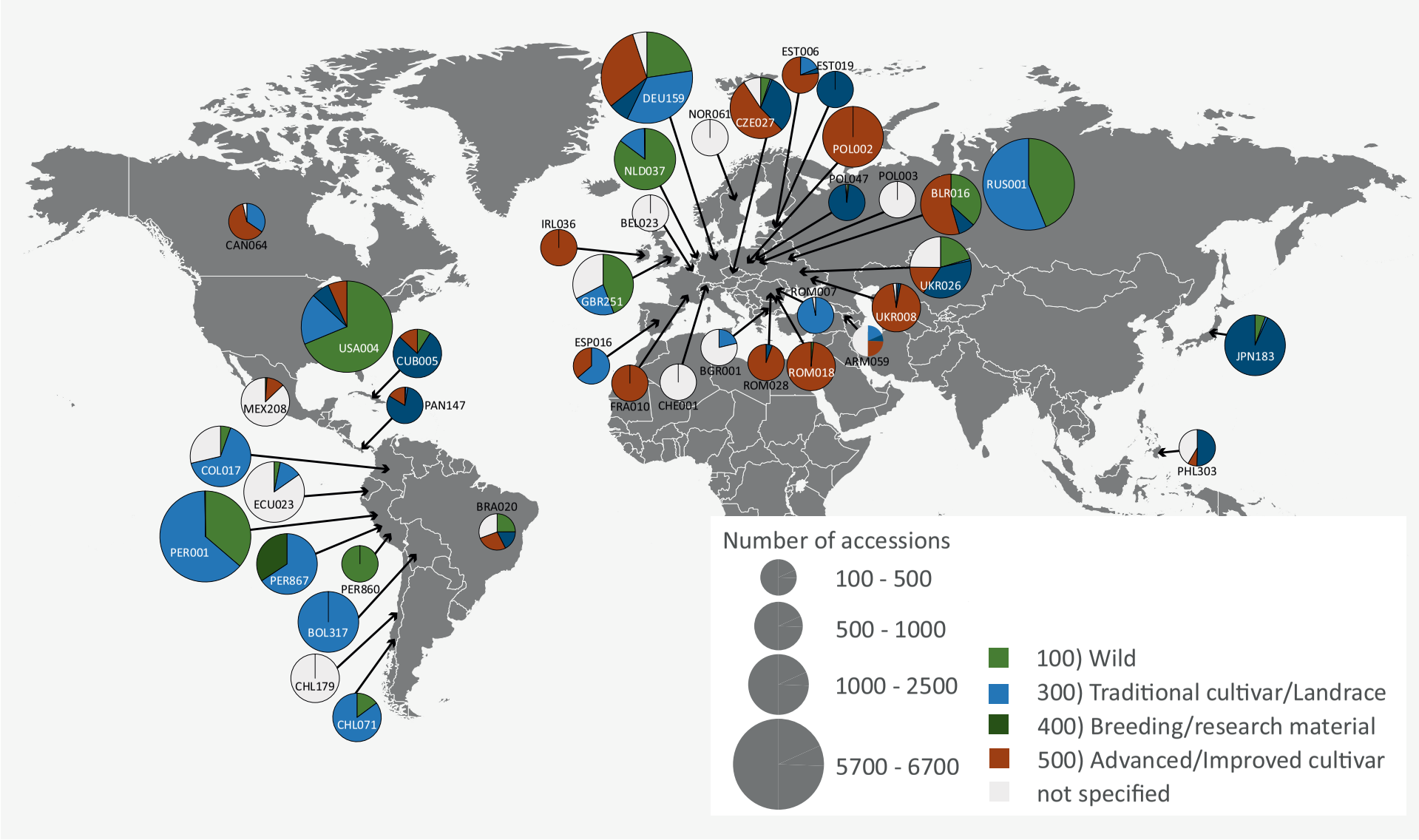


Figure A3. Number and category of potato accessions listed for each institute having > 100 accessions in the World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture (WIEWS) ©FAO 2021, http://www.fao.org/wiews/en/, accessed on 20 Sept 2021.

## Annex 4. Potato germplasm collections classified as wild species

**Table Annex 4** Potato germplasm collections classified as wild species in the World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture (WIEWS). WIEWS ©FAO 2021, http://www.fao.org/wiews/en/, accessed on 20th Sept 2021. Species name according to WIEWS were transferred to those names accepted by Spooner et al. (2014). In addition, country of origin, ploidy level is provided for the nine largest collection holders. na, not accepted names were found at https://solanaceaesource.myspecies.info/; *cultivated species listed incorrectly

| Genebank species | *Accepted by Spooner et al. (2014)* | Code | Country | Ploidy | Total | USA004 | RUS001 | PER001 | DEU159 | NLD037 | GBR251 | BLR016 | UKR026 | PER860 | CZE027 | BRA020 | JPN183 | POL003 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S. japonicum | *Lycianthes rantonnetii* | | | | 1 | | | | | | | | | | | | | |
| S. aemulans | *Solanum ×aemulans* Bitter & Wittm. | aem | ARG | 3x, 4x (2EBN) | 20 | 18 | | | | | | | | | | | | 1 |
| S. blanco-galdosii | *Solanum ×blanco-galdosii* Ochoa | blg | PER | 2x (2EBN) | 10 | 4 | | 4 | 1 | | 1 | | | | | | | |
| S. doddsii | *Solanum ×doddsii* Correll | dds | BOL | 2x (2EBN) | 41 | 16 | 8 | 4 | 4 | 3 | 3 | 1 | 2 | | | | | |
| S. michoacanum | *Solanum ×michoacanum* (Bitter) Rydb. | mch | MEX | 2x | 10 | 1 | 2 | | | | 1 | 2 | 2 | | | | | 1 |
| S. neoweberbaueri | *Solanum ×neoweberbaueri* Wittm. | nwb | PER | 3x | 1 | | | 1 | | | | | | | | | | |
| S. vallis-mexici | *Solanum ×vallis-mexici* Juz. | vll | MEX | 3x | 6 | | 1 | | | | | 1 | 3 | | | | | |
| S. acaule | *Solanum acaule* Bitter | acl | ARG, BOL, PER | 4x (2EBN), | 1488 | 421 | 335 | 377 | 64 | 142 | 62 | 9 | 16 | 35 | 5 | | | 18 |
| S. schreiteri (na) | *Solanum acaule* Bitter | acl | ARG, BOL, PER | 4x (2EBN), | 1 | | | | | | | | | | | | | |
| S. uyunense (na) | *Solanum acaule* Bitter | acl | ARG, BOL, PER | 4x (2EBN), | 2 | | 1 | | | | | | | | | | | |
| | *Solanum acaule* Bitter Total | | | | 1491 | 421 | 336 | 377 | 64 | 142 | 62 | 9 | 16 | 35 | 5 | 0 | 0 | 18 |
| S. acroglossum | *Solanum acroglossum Juz.* | acg | PER | 2x (2EBN) | 5 | 2 | 1 | 2 | | | | | | | | | | |
| S. acroscopicum | *Solanum acroscopicum* Ochoa | acs | PER | 2x | 35 | 4 | 3 | 16 | 1 | 1 | | | | 10 | | | | |
| S. lopez-camarenae | *Solanum acroscopicum* Ochoa | acs | PER | 2x | 3 | | | 1 | | | | | | 2 | | | | |
| | ***Solanum acroscopicum* Ochoa Total** | | | | **38** | **4** | **3** | **17** | **1** | **1** | **0** | **0** | **0** | **12** | **0** | **0** | **0** | **0** |
| S. agrimoniifolium | *Solanum agrimonifolium* Rydb. | agf | GUA, HON, MEX | 4x (2EBN) | 49 | 21 | 8 | 6 | 5 | 3 | 2 | 1 | 3 | | | | | |
| S. albicans | *Solanum albicans* (Ochoa) Ochoa | alb | ECU, PER | 6x (4EBN) | 144 | 27 | 13 | 81 | 4 | 12 | 1 | | | 1 | | | | 2 |
| S. albornozii | *Solanum albornozii* Correll | abz | ECU | 2x (2EBN) | 13 | 4 | | 4 | 2 | 1 | | | | | | | | |
| S. amayanum | *Solanum amayanum* Ochoa | amy | PER | 2x (2EBN) | 7 | | | 4 | | 2 | | | | 1 | | | | |
| S. anamatophilum | *Solanum anamatophilum* Ochoa | amp | PER | 2x (2EBN) | 1 | | | 1 | | | | | | | | | | |
| S. peloquinianum | *Solanum anamatophilum* Ochoa | amp | PER | 2x (2EBN) | 4 | | | 4 | | | | | | | | | | |
| | ***Solanum anamatophilum* Ochoa Total** | | | | **5** | **0** | **0** | **5** | **0** | **0** | **0** | **0** | **0** | **0** | **0** | **0** | **0** | **0** |
| S. andreanum | *Solanum andreanum* Baker | adr | COL, ECU | 2x (2EBN), 4x (4EBN) | 80 | 43 | 5 | 10 | 4 | | | | | | | | | |
| S. paucijugum | *Solanum andreanum* Baker | adr | COL, ECU | 2x (2EBN), 4x (4EBN) | 31 | | 5 | 20 | 2 | 2 | 2 | | | | | | | |

| Genebank species | *Accepted by Spooner et al. (2014)* | Code | Country | Ploidy | Total | USA004 | RUS001 | PER001 | DEU159 | NLD037 | GBR251 | BLR016 | UKR026 | PER860 | CZE027 | BRA020 | JPN183 | POL003 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S. tuquerrense | *Solanum andreanum* Baker | adr | COL, ECU | 2x (2EBN), 4x (4EBN) | 20 | | 4 | 10 | 3 | 1 | 1 | | | | | | | |
| | ***Solanum andreanum* Baker Total** | | | | **131** | **43** | **14** | **40** | **9** | **3** | **3** | **0** | **0** | **0** | **0** | **0** | **0** | **0** |
| S. augustii | *Solanum augustii* Ochoa | agu | PER | 2x (1EBN) | 4 | | | 4 | | | | | | | | | | |
| S. ayacuchense | *Solanum ayacuchense* Ochoa | ayc | PER | 2x (2EBN) | 3 | | | 1 | | | | | | 2 | | | | |
| S. Berthaultii | *Solanum berthaultii* Hawkes | ber | ARG, BOL | 2x (2EBN), | 308 | 135 | 49 | 29 | 15 | 32 | 14 | 8 | 5 | | 15 | | | 2 |
| S. litusinum | *Solanum berthaultii* Hawkes | ber | ARG, BOL | 2x (2EBN), | 2 | | | 2 | | | | | | | | | | |
| S. tarijense | *Solanum berthaultii* Hawkes | ber | ARG, BOL | 2x (2EBN), | 186 | | 95 | 18 | 19 | 27 | 13 | 6 | 1 | | | | | 2 |
| | ***Solanum berthaultii* Hawkes Total** | | | | **496** | **135** | **144** | **49** | **34** | **59** | **27** | **14** | **6** | **0** | **15** | **0** | **0** | **4** |
| S. boliviense | *Solanum boliviense* Dunal in DC. | blv | ARG, BOL, PER | 2x (2EBN) | 307 | 222 | 9 | 10 | 11 | 18 | 4 | 29 | 2 | | | | | |
| S. megistacrolobum | *Solanum boliviense* Dunal in DC. | blv | ARG, BOL, PER | 2x (2EBN) | 242 | | 93 | 44 | 19 | 68 | 10 | | 1 | 7 | | | | |
| S. sanctae-rosae | *Solanum boliviense* Dunal in DC. | blv | ARG, BOL, PER | 2x (2EBN) | 31 | | 6 | | 7 | 11 | 4 | 1 | 2 | | | | | |
| | ***Solanum boliviense* Dunal *in* DC. Total** | | | | **580** | **222** | **108** | **54** | **37** | **97** | **18** | **30** | **5** | **7** | **0** | **0** | **0** | **0** |
| S. bombycinum | *Solanum bombycinum* Ochoa | bmb | BOL | 4x | 2 | | | 2 | | | | | | | | | | |
| | ***Solanum bombycinum* Ochoa Total** | | | | **2** | **0** | **0** | **2** | **0** | **0** | **0** | **0** | **0** | **0** | **0** | **0** | **0** | **0** |
| S. alandiae | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 63 | | 12 | 18 | 7 | 12 | 10 | 3 | | | | | | |
| S. avilesii | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 13 | | 2 | 4 | 3 | 3 | | | 1 | | | | | |
| S. brevicaule | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 632 | 551 | 8 | 14 | 7 | 13 | 13 | | | | 20 | | | 1 |
| S. gourlayi | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 229 | | 119 | | 22 | 62 | 14 | 8 | 3 | | | | | |
| S. hondelmannii | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 54 | | 16 | | 12 | 6 | 2 | 10 | 8 | | | | | |
| S. hoopesii | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 10 | | 2 | 2 | 2 | 4 | | | | | | | | |
| S. incamayoense | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 26 | | 7 | 4 | 3 | 6 | | 5 | 1 | | | | | |

| Genebank species | *Accepted by Spooner et al. (2014)* | Code | Country | Ploidy | Total | USA004 | RUS001 | PER001 | DEU159 | NLD037 | GBR251 | BLR016 | UKR026 | PER860 | CZE027 | BRA020 | JPN183 | POL003 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S. leptophyes | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 105 | | 20 | 34 | 4 | 37 | 6 | | 2 | | | | | 1 |
| S. oplocense | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 188 | | 46 | 81 | 14 | 23 | 9 | 13 | 2 | | | | | |
| S. saltense | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 4 | | 1 | | | | | 1 | 1 | | | | | |
| S. setulosistylum | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 4 | | | | 2 | 1 | | | | | | | | |
| S. sparsipilum | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 220 | | 41 | 58 | 45 | 33 | 25 | | 6 | 8 | | | | 3 |
| S. spegazzinii | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 195 | | 74 | 3 | 57 | 40 | 12 | 6 | 1 | | | | | 2 |
| S. sucrense | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 101 | | 26 | 13 | 10 | 41 | 9 | 1 | | | | | | |
| S. ugentii | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 14 | | 6 | 2 | 3 | 2 | | 1 | | | | | | |
| S. vidaurrei | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 16 | | 4 | 12 | | | | | | | | | | |
| S. virgultorum | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 7 | | 1 | | 2 | 4 | | | | | | | | |
| S. brevimucronatum (na) | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 1 | | | | | | | | | | | | | |
| S. ruiz-zeballosii (na) | *Solanum brevicaule* Bitter | brc | ARG, BOL, PER | 2x (2EBN), 4x (4EBN), 6x (4EBN) | 14 | | 2 | | | | | 9 | | | | | | 2 |
| | *Solanum brevicaule* Bitter Total | | | | **1896** | **551** | **387** | **245** | **193** | **287** | **100** | **57** | **25** | **8** | **20** | **0** | **0** | **9** |
| S. buesii | *Solanum buesii* Vargas | bue | PER | 2x (2EBN) | 27 | 3 | 22 | 2 | | | | | | | | | | |
| | ***Solanum buesii* Vargas Total** | | | | **27** | **3** | **22** | **2** | **0** | **0** | **0** | **0** | **0** | **0** | **0** | **0** | **0** | **0** |

| Genebank species | *Accepted by Spooner et al. (2014)* | Code | Country | Ploidy | Total | USA004 | RUS001 | PER001 | DEU159 | NLD037 | GBR251 | BLR016 | UKR026 | PER860 | CZE027 | BRA020 | JPN183 | POL003 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S. bulbocastanum | *Solanum bulbocastanum* Dunal in Poir. | blb | GUA, HON, MEX | 2x (1EBN), 3x | 219 | 54 | 41 | 7 | 37 | 19 | 14 | 16 | 14 | | 17 | | | |
| S. burkartii | *Solanum burkartii* Ochoa | brk | PER | 2x | 15 | 2 | | 8 | | | | | | 5 | | | | |
| S. irosinum | *Solanum burkartii* Ochoa | brk | PER | 2x | 7 | | 2 | 5 | | | | | | | | | | |
| | ***Solanum burkartii* Ochoa Total** | | | | 22 | 2 | 2 | 13 | 0 | 0 | 0 | 0 | 0 | 5 | 0 | 0 | 0 | 0 |
| S. cajamarquense | *Solanum cajamarquense* Ochoa | cjm | PER | 2x (1EBN) | 27 | 2 | | 17 | 1 | | | | | 7 | | | | |
| S. abancayense | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 22 | | | | | | | | | | | | | |
| S. achacachense | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 8 | | 1 | 1 | 1 | 4 | 1 | | | | | | | |
| S. ambosinum | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 26 | | 3 | 12 | 8 | 3 | | | | | | | | |
| S. aymaraesense | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 8 | | 1 | 4 | | 1 | | | | 2 | | | | |
| S. billhookeri | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 3 | | | 2 | | | | | | 1 | | | | |
| S. bukasovii | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 451 | | | 351 | 18 | 19 | 11 | 1 | 5 | 45 | | | | |
| S. canasense | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 64 | | 10 | | 20 | 15 | 18 | | | | | | | |
| S. candolleanum | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 214 | 177 | 5 | 19 | 6 | 3 | | 4 | | | | | | |
| S. chillonanum | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 3 | | 2 | | | 1 | | | | | | | | |
| S. coelestispetalum | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 53 | | 1 | 38 | 3 | 7 | | 1 | | 3 | | | | |
| S. longiusculus | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 5 | | | 3 | | | | | | 2 | | | | |
| S. marinasense | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 67 | | 3 | 43 | 5 | 1 | 8 | | | 7 | | | | |
| S. multidissectum | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 35 | | 16 | | 9 | | 8 | | 1 | | | | | |
| S. orophilum | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 30 | | 1 | 23 | 2 | 3 | | | | 1 | | | | |
| S. ortegae | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 3 | | | 2 | | | | | | 1 | | | | |
| S. pampasense | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 26 | | 2 | 7 | 6 | 3 | 6 | | | 1 | | | | |
| S. sarasarae | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 5 | | | 5 | | | | | | | | | | |
| S. saxatilis | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 3 | | | 3 | | | | | | | | | | |
| S. tapojense | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 9 | | | 9 | | | | | | | | | | |
| S. tarapatanum | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 11 | | | 10 | | | | | | 1 | | | | |

| Genebank species | *Accepted by Spooner et al. (2014)* | Code | Country | Ploidy | Total | USA004 | RUS001 | PER001 | DEU159 | NLD037 | GBR251 | BLR016 | UKR026 | PER860 | CZE027 | BRA020 | JPN183 | POL003 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S. amabile (na) | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 1 | | | | | 1 | | | | | | | | |
| S. catarthrum (na) | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 6 | | 4 | | | | | | 1 | | | | | |
| S. soukupii (na) | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 4 | | | | | 2 | | 2 | | | | | | |
| S. velardei (na) | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 8 | | 1 | 4 | | 1 | | | | 2 | | | | |
| | ***Solanum candolleanum* Berthault Total** | | | | **1065** | **177** | **50** | **536** | **78** | **64** | **52** | **8** | **7** | **66** | **0** | **0** | **0** | **0** |
| S. cantense | *Solanum cantense* Ochoa | cnt | PER | 2x (2EBN) | 9 | | | 7 | | | | | | 2 | | | | |
| S. cardiophyllum | *Solanum cardiophyllum* Lindl. | cph | MEX | 2x (1EBN), 3x | 102 | 11 | 55 | 4 | 16 | 3 | | | 10 | | | | | |
| S. arnezii | *Solanum chacoense* Bitter | chc | ARG, BOL, BRA, PAR, PER, URU | 2x (2EBN), 3x | 16 | | 3 | | 4 | 1 | | 8 | | | | | | |
| S. calvescens | *Solanum chacoense* Bitter | chc | ARG, BOL, BRA, PAR, PER, URU | 2x (2EBN), 3x | 1 | | | 1 | | | | | | | | | | |
| S. chacoense | *Solanum chacoense* Bitter | chc | ARG, BOL, BRA, PAR, PER, URU | 2x (2EBN), 3x | 717 | 167 | 212 | 18 | 111 | 72 | 16 | 54 | 28 | | 2 | 16 | | 11 |
| S. tuberosum | *Solanum chacoense* Bitter | chc | ARG, BOL, BRA, PAR, PER, URU | 2x (2EBN), 3x | 154 | 5 | | | 1 | 1 | | | | | 18 | | 108 | |
| S. yungasense | *Solanum chacoense* Bitter | chc | ARG, BOL, BRA, PAR, PER, URU | 2x (2EBN), 3x | 16 | | 2 | 6 | 2 | 3 | | | | 3 | | | | |
| S. boergeri (na) | *Solanum chacoense* Bitter | chc | ARG, BOL, BRA, PAR, PER, URU | 2x (2EBN), 3x | 6 | | 3 | | | | | | 2 | | | | | |
| S. dolichostigma (na) | *Solanum chacoense* Bitter | chc | ARG, BOL, BRA, PAR, PER, URU | 2x (2EBN), 3x | 4 | | | | | | | 1 | | | | | | 2 |
| S. knappei (na) | *Solanum chacoense* Bitter | chc | ARG, BOL, BRA, PAR, PER, URU | 2x (2EBN), 3x | 4 | | 3 | | | | | | | | | | | |
| S. laplaticum (na) | *Solanum chacoense* Bitter | chc | ARG, BOL, BRA, PAR, PER, URU | 2x (2EBN), 3x | 1 | | | | | | | | | | | | | |
| S. parodii (na) | *Solanum chacoense* Bitter | chc | ARG, BOL, BRA, PAR, PER, URU | 2x (2EBN), 3x | 9 | | 3 | | | | | 1 | 1 | | | | | 2 |

| Genebank species | *Accepted by Spooner et al. (2014)* | Code | Country | Ploidy | Total | USA004 | RUS001 | PER001 | DEU159 | NLD037 | GBR251 | BLR016 | UKR026 | PER860 | CZE027 | BRA020 | JPN183 | POL003 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S. subtilius (na) | *Solanum chacoense* Bitter | chc | ARG, BOL, BRA, PAR, PER, URU | 2x (2EBN), 3x | 8 | | 5 | | | | | 1 | 1 | | | | | |
| | ***Solanum chacoense* Bitter Total** | | | | **936** | **172** | **231** | **25** | **118** | **77** | **16** | **65** | **32** | **3** | **20** | **16** | **108** | **15** |
| S. chilliasense | *Solanum chilliasense* Ochoa | chl | ECU | 2x (2EBN) | 3 | 1 | | 2 | | | | | | | | | | |
| S. ariduphilum | *Solanum chiquidenum* Ochoa | chq | PER | 2x (2EBN) | 1 | | | 1 | | | | | | | | | | |
| S. chiquidenum | *Solanum chiquidenum* Ochoa | chq | PER | 2x (2EBN) | 33 | 5 | | 18 | 1 | | | | | 9 | | | | |
| | ***Solanum chiquidenum* Ochoa Total** | | | | **34** | **5** | **0** | **19** | **1** | **0** | **0** | **0** | **0** | **9** | **0** | **0** | **0** | **0** |
| S. chomatophilum | *Solanum chomatophilum* Bitter | chm | ECU, PER | 2x (2EBN) | 124 | 15 | 1 | 77 | 9 | 5 | 2 | | | 13 | | | | |
| S. huarochiriense | *Solanum chomatophilum* Bitter | chm | ECU, PER | 2x (2EBN) | 11 | | | 10 | | 1 | | | | | | | | |
| S. jalcae | *Solanum chomatophilum* Bitter | chm | ECU, PER | 2x (2EBN) | 10 | | | 6 | | | | | | 4 | | | | |
| S. pascoense | *Solanum chomatophilum* Bitter | chm | ECU, PER | 2x (2EBN) | 6 | | | 4 | 2 | | | | | | | | | |
| | ***Solanum chomatophilum* Bitter Total** | | | | **151** | **15** | **1** | **97** | **11** | **6** | **2** | **0** | **0** | **17** | **0** | **0** | **0** | **0** |
| S. clarum | *Solanum clarum* Correll | clr | GUA, MEX | 2x | 21 | 14 | 3 | | 2 | | | 1 | 1 | | | | | |
| S. calacalinum | *Solanum colombianum* Dunal | col | COL, ECU, PER, VEN | 4x (2EBN) | 1 | | | 1 | | | | | | | | | | |
| S. colombianum | *Solanum colombianum* Dunal | col | COL, ECU, PER, VEN | 4x (2EBN) | 212 | 91 | 10 | 38 | 16 | 2 | | | | | | | | |
| S. moscopanum | *Solanum colombianum* Dunal | col | COL, ECU, PER, VEN | 4x (2EBN) | 26 | | 4 | 6 | 2 | 4 | | | | | | | | |
| S. orocense | *Solanum colombianum* Dunal | col | COL, ECU, PER, VEN | 4x (2EBN) | 4 | | 2 | 1 | | 1 | | | | | | | | |
| S. otites | *Solanum colombianum* Dunal | col | COL, ECU, PER, VEN | 4x (2EBN) | 7 | | 1 | 6 | | | | | | | | | | |
| S. subpanduratum | *Solanum colombianum* Dunal | col | COL, ECU, PER, VEN | 4x (2EBN) | 3 | | 1 | 1 | 1 | | | | | | | | | |
| S. sucubunense | *Solanum colombianum* Dunal | col | COL, ECU, PER, VEN | 4x (2EBN) | 2 | | | 1 | | 1 | | | | | | | | |
| S. tundalomense (na) | *Solanum colombianum* Dunal | col | COL, ECU, PER, VEN | 4x (2EBN) | 18 | | | 18 | | | | | | | | | | |
| | *Solanum colombianum* Dunal Total | | | | **273** | **91** | **18** | **72** | **19** | **8** | **0** | **0** | **0** | **0** | **0** | **0** | **0** | **0** |
| S. commersonii | *Solanum commersonii* Dunal | cmm | ARG, BRA, URU | 2x (1EBN), 3x | 259 | 37 | 19 | 42 | 27 | 15 | 2 | 2 | | | | 77 | | |
| S. contumazaense | *Solanum contumazaense* Ochoa | ctz | PER | 2x (2EBN) | 6 | 1 | | 4 | | | | | | 1 | | | | |
| S. Curtilobum* | *Solanum curtilobum Juz. & Bukasov* | cur | BOL, PER | 5x | 3 | | | | | | 1 | | | | | | | |

| Genebank species | *Accepted by Spooner et al. (2014)* | Code | Country | Ploidy | Total | USA004 | RUS001 | PER001 | DEU159 | NLD037 | GBR251 | BLR016 | UKR026 | PER860 | CZE027 | BRA020 | JPN183 | POL003 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S. demissum | *Solanum demissum* Lindl. | dms | GUA, MEX | 6x (4EBN) | 742 | 164 | 134 | 14 | 175 | 76 | 59 | 5 | 67 | | 10 | | | 12 |
| S. semidemissum | *Solanum demissum* Lindl. | dms | GUA, MEX | 6x (4EBN) | 4 | | | | | | 3 | | | | | | | |
| | ***Solanum demissum* Lindl. Total** | | | | **746** | **164** | **134** | **14** | **175** | **76** | **62** | **5** | **67** | **0** | **10** | **0** | **0** | **12** |
| S. dolichocremastrum | *Solanum dolichocremastrum* Bitter | dcm | PER | 2x (1EBN) | 37 | 4 | 1 | 24 | 3 | 2 | | | | 3 | | | | |
| S. ehrenbergii | *Solanum ehrenbergii* (Bitter) Rydb. | ehr | MEX | 2x (1EBN) | 46 | 29 | 8 | | | 1 | 7 | | | | | | | |
| S. flahaultii | *Solanum flahaultii* Bitter | flh | COL | 4x | 44 | 17 | 1 | 9 | | 2 | | | | | | | | |
| S. gandarillasii | *Solanum gandarillasii* Cárdenas | gnd | BOL | 2x (2EBN) | 22 | 7 | 1 | 2 | 5 | 3 | 4 | | | | | | | |
| S. garcia-barrigae | *Solanum garcia-barrigae* Ochoa | gab | COL | 4x | 3 | 1 | | 1 | | | | | | | | | | |
| S. gracilifrons | *Solanum gracilifrons* Bitter | grc | PER | 2x | 4 | | | 3 | | | | | | 1 | | | | |
| S. guerreroense | *Solanum guerreroense* Correll | grr | MEX | 6x (4EBN) | 24 | 2 | 5 | 1 | 3 | 1 | 1 | 2 | 2 | | 5 | | | 1 |
| S. hastiforme | *Solanum hastiforme* Correll | hsf | PER | 2x (2EBN) | 8 | | | 7 | | | | | | 1 | | | | |
| S. hintonii | *Solanum hintonii* Correll | hnt | MEX | 2x | 1 | | | 1 | | | | | | | | | | |
| S. hjertingii | *Solanum hjertingii* Hawkes | hjt | MEX | 4x (2EBN) | 76 | 13 | 24 | 3 | 8 | 4 | 5 | 8 | 11 | | | | | |
| S. hougasii | *Solanum hougasii* Correll | hou | MEX | 6x (4EBN) | 55 | 10 | 9 | 9 | 6 | 2 | 7 | 4 | 6 | | | | | 1 |
| S. huancabambense | *Solanum huancabambense* Ochoa | hcb | PER | 2x (2EBN) | 28 | 5 | 6 | 6 | 5 | 2 | | 3 | | 1 | | | | |
| S. humectophilum | *Solanum humectophilum* Ochoa | hmp | PER | 2x (1EBN) | 5 | | | 3 | 1 | 1 | | | | | | | | |
| S. guzmanguense | *Solanum hypacrarthrum* Bitter | hcr | PER | 2x (1EBN) | 4 | | | 3 | | | | | | 1 | | | | |
| S. hypacrarthrum | *Solanum hypacrarthrum* Bitter | hcr | PER | 2x (1EBN) | 11 | 1 | 1 | 8 | 1 | | | | | | | | | |
| | ***Solanum hypacrarthrum* Bitter Total** | | | | **15** | **1** | **1** | **11** | **1** | **0** | **0** | **0** | **0** | **1** | **0** | **0** | **0** | **0** |
| S. immite | *Solanum immite* Dunal | imt | PER | 2x (1EBN), 3x | 14 | 4 | 1 | 5 | 1 | | | | | 3 | | | | |
| S. incasicum | *Solanum incasicum* Ochoa | ins | PER | 2x (2EBN) | 2 | | | 2 | | | | | | | | | | |
| S. infundibuliforme | *Solanum infundibuliforme* Phil. | inf | ARG, BOL | 2x (2EBN) | 262 | 127 | 60 | 9 | 4 | 41 | 7 | 14 | | | | | | |
| S. brachycarpum | *Solanum iopetalum* (Bitter) Hawkes | iop | MEX | 6x (4EBN) | 60 | | 13 | | 22 | 3 | 13 | 1 | 7 | | | | | |
| S. iopetalum | *Solanum iopetalum* (Bitter) Hawkes | iop | MEX | 6x (4EBN) | 99 | 59 | 4 | 8 | 4 | 4 | 3 | 12 | 2 | | | | | |
| | ***Solanum iopetalum* (Bitter) Hawkes Total** | | | | **159** | **59** | **17** | **8** | **26** | **7** | **16** | **13** | **9** | **0** | **0** | **0** | **0** | **0** |
| S. jamesii | *Solanum jamesii* Torr. | jam | MEX, USA | 2x (1EBN) | 301 | 216 | 43 | 3 | 11 | 2 | 3 | 5 | 16 | | | | | |
| S. juzepczukii* | *Solanum juzepczukii* Juz. | juz | ARG, BOL, PER | 3x | 1 | | | | | | | | | | | | | |
| S. kurtzianum | *Solanum kurtzianum* Bitter & Wittm. | ktz | ARG | 2x (2EBN) | 290 | 94 | 117 | 3 | 13 | 34 | 5 | 6 | 15 | | | | | 2 |
| S. macolae (na) | *Solanum kurtzianum* Bitter & Wittm. | ktz | ARG | 2x (2EBN) | 1 | | | | | | | | | | | | | |
| | ***Solanum kurtzianum* Bitter & Wittm. Total** | | | | **291** | **94** | **117** | **3** | **13** | **34** | **5** | **6** | **15** | **0** | **0** | **0** | **0** | **2** |
| S. angustifolium (na) | *Solanum lanzae* | | | | 4 | | | | | | | | | | | | | |

| Genebank species | *Accepted by Spooner et al. (2014)* | Code | Country | Ploidy | Total | USA004 | RUS001 | PER001 | DEU159 | NLD037 | GBR251 | BLR016 | UKR026 | PER860 | CZE027 | BRA020 | JPN183 | POL003 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S. laxissimum | *Solanum laxissimum* Bitter | lxs | PER | 2x (2EBN) | 21 | 5 | 1 | 8 | 1 | 1 | | | | 5 | | | | |
| S. santolallae | *Solanum laxissimum* Bitter | lxs | PER | 2x (2EBN) | 11 | | 1 | 4 | 2 | 2 | 1 | | | 1 | | | | |
| | ***Solanum laxissimum* Bitter Total** | | | | **32** | **5** | **2** | **12** | **3** | **3** | **1** | **0** | **0** | **6** | **0** | **0** | **0** | **0** |
| S. lesteri | *Solanum lesteri* Hawkes & Hjert. | les | MEX | 2x | 18 | 3 | 7 | 3 | 1 | 3 | | | | | | | | |
| S. lignicaule | *Solanum lignicaule* Vargas | lgl | PER | 2x (1EBN) | 26 | 6 | 1 | 9 | 2 | 1 | 2 | 2 | | 3 | | | | |
| S. limbaniense | *Solanum limbaniense* Ochoa | lmb | PER | 2x (2EBN) | 14 | 1 | 1 | 8 | 1 | 1 | | | | 2 | | | | |
| S. lobbianum | *Solanum lobbianum* Bitter | lbb | COL | 4x (2EBN) | 12 | 3 | 1 | 4 | | | | | | | | | | |
| S. longiconicum | *Solanum longiconicum* Bitter | lgc | CRI, PAN | 4x | 34 | 10 | 1 | 8 | 1 | 2 | | | | | | | | |
| S. maglia | *Solanum maglia* Schltdl. | mag | ARG, CHL | 2x, 3x | 29 | 2 | 4 | 2 | 4 | 2 | | 1 | 1 | | | | | |
| S. malmeanum | *Solanum malmeanum* Bitter | 0 | ARG, BRA, PAR, URU | 2x (1EBN), 3x | 50 | 25 | | | | | | | | | | 25 | | |
| S. medians | *Solanum medians* Bitter | med | CHL, PER | 2x (2EBN), 3x | 109 | 13 | 4 | 61 | 3 | 5 | 4 | 1 | | 17 | | | | |
| S. sandemanii | *Solanum medians* Bitter | med | CHL, PER | 2x (2EBN), 3x | 19 | | 1 | 6 | 1 | 3 | 1 | | | 7 | | | | |
| S. tacnaense | *Solanum medians* Bitter | med | CHL, PER | 2x (2EBN), 3x | 23 | | | 12 | | | 1 | | | 10 | | | | |
| | *Solanum medians* Bitter Total | | | | **151** | **13** | **5** | **79** | **4** | **8** | **6** | **1** | **0** | **34** | **0** | **0** | **0** | **0** |
| S. microdontum | *Solanum microdontum* Bitter | mcd | ARG, BOL | 2x (2EBN), 3x | 307 | 114 | 34 | 14 | 44 | 41 | 26 | 3 | 7 | | 1 | | | 1 |
| S. simplicifolium (na) | *Solanum microdontum* Bitter | mcd | ARG, BOL | 2x (2EBN), 3x | 21 | | 7 | | | | | 4 | 7 | | | | | 2 |
| | ***Solanum microdontum* Bitter Total** | | | | **328** | **114** | **41** | **14** | **44** | **41** | **26** | **7** | **14** | **0** | **1** | **0** | **0** | **3** |
| S. minutifoliolum | *Solanum minutifoliolum* Correll | min | ECU | 2x (1EBN) | 18 | 1 | 3 | 2 | | | | | | | | | | |
| S. chancayense | *Solanum mochiquense* Ochoa | mcq | PER | 2x (1EBN) | 15 | | 8 | 2 | 2 | 3 | | | | | | | | |
| S. mochiquense | *Solanum mochiquense* Ochoa | mcq | PER | 2x (1EBN) | 41 | 6 | 4 | 13 | 7 | 4 | 3 | | | 2 | 1 | | | |
| | ***Solanum mochiquense* Ochoa Total** | | | | **56** | **6** | **12** | **15** | **9** | **7** | **3** | **0** | **0** | **2** | **1** | **0** | **0** | **0** |
| S. morelliforme | *Solanum morelliforme* Bitter & Muench | mrl | BOL, GUA, MEX, HON | 2x | 33 | 19 | 3 | 4 | 4 | | | 1 | | | | | | |
| S. multiinterruptum | *Solanum multiinterruptum* Bitter | mtp | PER | 2x (2EBN), 3x | 118 | 8 | 5 | 84 | 6 | | 1 | | | 14 | | | | |
| S. neocardenasii | *Solanum neocardenasii* Hawkes & Hjert. | ncd | BOL | 2x | 39 | 2 | 2 | 5 | 2 | 1 | 2 | 22 | 3 | | | | | |
| S. neorossii | *Solanum neorossii* Hawkes & Hjert. | nrs | ARG | 2x | 32 | 6 | 5 | 3 | 4 | 4 | 8 | 1 | 1 | | | | | |
| S. hannemanii | *Solanum neorossii* Hawkes & Hjert. | nrs | ARG | 2x | 9 | | | | 1 | 8 | | | | | | | | |
| | *Solanum neorossii* Hawkes & Hjert. Total | | | | **41** | **6** | **5** | **3** | **5** | **12** | **8** | **1** | **1** | **0** | **0** | **0** | **0** | **0** |
| S. neovavilovii | *Solanum neovavilovii* Ochoa | nvv | BOL | 2x (2EBN) | 1 | | | 1 | | | | | | | | | | |
| S. nubicola | *Solanum nubicola* Ochoa | nub | PER | 4x (2EBN) | 3 | | | 1 | | | | | | 2 | | | | |
| S. okadae | *Solanum okadae* Hawkes & Hjert. | oka | BOL | 2x | 89 | 16 | 9 | 8 | 4 | 13 | 9 | 24 | 6 | | | | | |
| S. oxycarpum | *Solanum oxycarpum* Schiede | oxc | MEX | 4x (2EBN) | 42 | 20 | 6 | 4 | 10 | 2 | | | | | | | | |
| S. brevidens (na) | *Solanum palustre* | | | | 23 | | 4 | | 2 | | | | | | | | | |

| Genebank species | *Accepted by Spooner et al. (2014)* | Code | Country | Ploidy | Total | USA004 | RUS001 | PER001 | DEU159 | NLD037 | GBR251 | BLR016 | UKR026 | PER860 | CZE027 | BRA020 | JPN183 | POL003 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S. paucissectum | *Solanum paucissectum* Ochoa | pcs | PER | 2x (2EBN) | 20 | 3 | 1 | 11 | 1 | | | | | 4 | | | | |
| S. pillahuatense | *Solanum pillahuatense* Vargas | pll | PER | 2x (2EBN) | 2 | | | 2 | | | | | | | | | | |
| S. pinnatisectum | *Solanum pinnatisectum* Dunal | pnt | MEX | 2x (1EBN) | 233 | 19 | 67 | 1 | 36 | 10 | 12 | 37 | 34 | | 12 | | | 4 |
| S. piurae | *Solanum piurae* Bitter | pur | PER | 2x (2EBN) | 19 | 3 | 3 | 6 | 3 | | | 1 | | 3 | | | | |
| S. polyadenium | *Solanum polyadenium* Greenm. | pld | MEX | 2x | 83 | 18 | 25 | 5 | 7 | 6 | 7 | 7 | 2 | | 1 | | | |
| S. raphanifolium | *Solanum raphanifolium* Cárdenas & Hawkes | rap | PER | 2x (2EBN) | 195 | 37 | 16 | 86 | 14 | 14 | 10 | 6 | | 12 | | | | |
| S. raquialatum | *Solanum raquialatum* Ochoa | raq | PER | 2x (1EBN) | 3 | | | 3 | | | | | | | | | | |
| S. rhomboidei-lanceolatum | *Solanum rhomboideilanceolatum* Ochoa | rhl | PER | 2x (2EBN) | 5 | | | 3 | | | | | | 2 | | | | |
| S. ancophilum (na) | *Solanum rhomboideilanceolatum* Ochoa | rhl | PER | 2x (2EBN) | 7 | | | 7 | | | | | | | | | | |
| | ***Solanum rhomboideilanceolatum* Ochoa Total** | | | | **12** | **0** | **0** | **10** | **0** | **0** | **0** | **0** | **0** | **2** | **0** | **0** | **0** | **0** |
| S. scabrifolium | *Solanum scabrifolium* Ochoa | scb | PER | 2x | 2 | 1 | | 1 | | | | | | | | | | |
| S. schenckii | *Solanum schenckii* Bitter | snk | MEX | 6x (4EBN) | 35 | 15 | 2 | 4 | 9 | 1 | 3 | | | | | | | |
| S. simplicissimum | *Solanum simplicissimum* Ochoa *(1989b)* | smp | PER | 2x (1EBN) | 4 | | | 3 | | | | | | 1 | | | | |
| S. sogarandinum | *Solanum sogarandinum* Ochoa | sgr | PER | 2x (2EBN), 3x | 24 | 2 | 1 | 14 | 2 | 3 | 1 | | | 1 | | | | |
| S. brachistotrichum | *Solanum stenophyllidium* Bitter | sph | MEX | 2x (1EBN) | 34 | | 16 | | 5 | 1 | | 12 | | | | | | |
| S. stenophyllidium | *Solanum stenophyllidium* Bitter | sph | MEX | 2x (1EBN) | 51 | 25 | 13 | 9 | 2 | 1 | | | | | | | | |
| | ***Solanum stenophyllidium* Bitter Total** | | | | **85** | **25** | **29** | **9** | **7** | **2** | **0** | **12** | **0** | **0** | **0** | **0** | **0** | **0** |
| S. capsicibaccatum | *Solanum stipuloideum* Rusby | stp | BOL | 2x (1EBN) | 18 | | | | 4 | 7 | 2 | | 5 | | | | | |
| S. circaeifolium | *Solanum stipuloideum* Rusby | stp | BOL | 2x (1EBN) | 28 | | 1 | | 9 | 5 | 6 | 7 | | | | | | |
| S. stipuloideum | *Solanum stipuloideum* Rusby | stp | BOL | 2x (1EBN) | 26 | 14 | | 12 | | | | | | | | | | |
| | ***Solanum stipuloideum* Rusby Total** | | | | **72** | **14** | **1** | **12** | **13** | **12** | **8** | **7** | **5** | **0** | **0** | **0** | **0** | **0** |
| S. fendleri | *Solanum stoloniferum* Schltdl. | sto | MEX, USA | 4x (2EBN) | 127 | | 52 | | 18 | 7 | 24 | 9 | 12 | | | | | 4 |
| S. papita | *Solanum stoloniferum* Schltdl. | sto | MEX, USA | 4x (2EBN) | 69 | | 36 | | 7 | 6 | | 1 | 14 | | | | | 5 |
| S. polytrichon | *Solanum stoloniferum* Schltdl. | sto | MEX, USA | 4x (2EBN) | 101 | | 44 | | 12 | 5 | 16 | 9 | 10 | | | | | 4 |
| S. stoloniferum | *Solanum stoloniferum* Schltdl. | sto | MEX, USA | 4x (2EBN) | 921 | 520 | 103 | 48 | 94 | 10 | 52 | 8 | 52 | | 13 | | 1 | 13 |
| S. ajuscoense (na) | *Solanum stoloniferum* Schltdl. | sto | MEX, USA | 4x (2EBN) | 2 | | 1 | | | | | | | | | | | |
| S. antipoviczii (na) | *Solanum stoloniferum* Schltdl. | sto | MEX, USA | 4x (2EBN) | 6 | | 4 | | | | | | | | | | | |
| S. malinchense (na) | *Solanum stoloniferum* Schltdl. | sto | MEX, USA | 4x (2EBN) | 1 | | | | | | | | | | | | | |
| S. neoantipoviczii (na) | *Solanum stoloniferum* Schltdl. | sto | MEX, USA | 4x (2EBN) | 26 | | 1 | | | | | 23 | 1 | | | | | 1 |
| S. tlaxcalense (na) | *Solanum stoloniferum* Schltdl. | sto | MEX, USA | 4x (2EBN) | 2 | | | | | | | 1 | 1 | | | | | |
| | ***Solanum stoloniferum* Schltdl. Total** | | | | **1255** | **520** | **241** | **48** | **131** | **28** | **92** | **51** | **90** | **0** | **13** | **0** | **1** | **27** |

| Genebank species | *Accepted by Spooner et al. (2014)* | Code | Country | Ploidy | Total | USA004 | RUS001 | PER001 | DEU159 | NLD037 | GBR251 | BLR016 | UKR026 | PER860 | CZE027 | BRA020 | JPN183 | POL003 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S. suaveolens | *Solanum suaveolens* | | | | 6 | | | | | 5 | | | | | | | | |
| S. tarnii | *Solanum tarnii* Hawkes & Hjert. | trn | MEX | 2x | 25 | 11 | 7 | 3 | 4 | | | | | | | | | |
| S. trifidum | *Solanum trifidum* Correll | trf | MEX | 2x (1EBN) | 57 | 14 | 13 | 1 | 18 | 3 | 1 | 2 | 4 | | | | | |
| S. trinitense | *Solanum trinitense* Ochoa | trt | PER | 2x (1EBN) | 1 | | | 1 | | | | | | | | | | |
| S. andigenum* | *Solanum tuberosum* 'Andigenum group' tetraploids | tbr | Landraces from W Venezuela South to N Argentina | 4x (4EBN) | 14 | | | | | | | 14 | | | | | | |
| S. phureja* | *Solanum tuberosum* 'Andigenum group' diploids | tbr | Landraces from W Venezuela South to N Argentina | 2x (2EBN) | 15 | | | | | 1 | | 1 | | | | | | |
| S. stenotomum* | *Solanum tuberosum* 'Andigenum group' diploids | tbr | Landraces from W Venezuela South to N Argentina | 2x (2EBN) | 10 | | | | | | | | | | | | | |
| S. leptostigma (na) | *Solanum tuberosum* 'Chilotanum group' | tbr | Landraces from W Venezuela South to N Argentina | 4x (4EBN) | 2 | | 1 | | | | | | | | | | | |
| S. Ochoanum (na) | 'Chilotanum group' | tbr | Landraces from W Venezuela South to N Argentina | 4x (4EBN) | 1 | | | | | | | | | | | | | |
| S. parvicorollatum (na)* | *Solanum tuberosum* 'Chilotanum group' | tbr | Landraces from W Venezuela South to N Argentina | 4x (4EBN) | 1 | | | | | | | | | | | | | |
| S. rybinii* | *Solanum tuberosum* 'Andigenum group' diploids | tbr | Landraces from W Venezuela South to N Argentina | 2x (2EBN) | 3 | | | | | | | 3 | | | | | | |

| Genebank species | *Accepted by Spooner et al. (2014)* | Code | Country | Ploidy | Total | USA004 | RUS001 | PER001 | DEU159 | NLD037 | GBR251 | BLR016 | UKR026 | PER860 | CZE027 | BRA020 | JPN183 | POL003 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ***Solanum tuberosum Andigenum group* Total** | | | | **46** | **0** | **1** | **0** | **0** | **1** | **0** | **18** | **0** | **0** | **0** | **0** | **0** | **0** |
| S. venturii | *Solanum venturii* Hawkes & Hjert. | vnt | ARG | 2x (2EBN) | 22 | 4 | 3 | 2 | 6 | 3 | 2 | 1 | 1 | | | | | |
| S. vernei | *Solanum vernei* Bitter & Wittm. | vrn | ARG | 2x (2EBN) | 192 | 35 | 36 | 10 | 24 | 22 | 7 | 32 | 23 | | 3 | | | |
| S. macropilosum | *Solanum verrucosum* Schltdl. | ver | MEX | 2x (2EBN), 3x, 4x | 3 | | | | 2 | 1 | | | | | | | | |
| S. verrucosum | *Solanum verrucosum* Schltdl. | ver | MEX | 2x (2EBN), 3x, 4x | 163 | 43 | 34 | 8 | 12 | 18 | 20 | 3 | 15 | | 6 | | | 2 |
| | ***Solanum verrucosum* Schltdl. Total** | | | | **166** | **43** | **34** | **8** | **14** | **19** | **20** | **3** | **15** | **0** | **6** | **0** | **0** | **2** |
| S. urubambae | *Solanum violaceimarmoratum* Bitter | vio | BOL, PER | 2x (2EBN) | 14 | | | 11 | | | | | | 2 | | | | |
| S. violaceimar-moratum | *Solanum violaceimarmoratum* Bitter | vio | BOL, PER | 2x (2EBN) | 28 | 7 | 2 | 6 | 3 | 4 | 5 | 1 | | | | | | |
| | ***Solanum violaceimarmoratum* Bitter Total** | | | | **42** | **7** | **2** | **17** | **3** | **4** | **5** | **1** | **0** | **2** | **0** | **0** | **0** | **0** |
| S. wittmackii | *Solanum wittmackii* Bitter | wtm | PER | 2x (1EBN) | 38 | | | 29 | | 1 | | | | 8 | | | | |
| S. woodsonii | *Solanum woodsonii* Correll | wds | PAN | 4x | 4 | | | 4 | | | | | | | | | | |
| S. etuberosum | *Solanum etuberosum* Lindl. | | | | 59 | 30 | 5 | | 1 | 5 | 1 | 8 | | | | | | |
| S. fernandezianum | *Solanum fernandezianum* Phil. | | | | 20 | 7 | 1 | | 3 | 4 | | 2 | | | | | | |
| S. palustre | *Solanum palustre* Schltdl. | | | | 158 | 71 | 9 | | | 3 | 5 | 10 | | | 1 | | | |
| | ***Solanum* sect. *Etuberosum* Total** | | | | **237** | **108** | **15** | **0** | **4** | **12** | **6** | **20** | **0** | **0** | **1** | **0** | **0** | **0** |
| S. juglandifolium | *Solanum* sect. *Juglandifolia* | | | | 19 | | | | | | | | | | | | | |
| S. coriaceifoliolatum (na) | | | | | 4 | | 1 | | | | | 1 | 1 | | | | | |
| S. fraxinifolium | | | | | 9 | | | | | 1 | | | | | | | | |
| S. garciae | | | | | 8 | | 5 | | | | | 1 | 1 | | | | | |
| S. gibberulosum | | | | | 46 | | 10 | | | | | 33 | | | | | | 2 |
| S. hawkesianum | | | | | 5 | | | | | 5 | | | | | | | | |
| S. ingifolium | | | | 2x (1EBN) | 1 | | | 1 | | | | | | | | | | |
| S. pamiricum | | | | | 6 | | 5 | | | | | | 1 | | | | | |
| S. schickii | | | | | 7 | | 5 | | | | | 1 | | | | | | |
| | **Total** | | | | **14400** | **3946** | **2530** | **2428** | **1324** | **1228** | **654** | **560** | **454** | **282** | **130** | **118** | **109** | **104** |

## Annex 5. Collection of landraces maintained in national and international genebank

**Table Annex 5** Collection of landraces maintained in national and international genebanks and listed in data the World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture (WIEWS). WIEWS ©FAO 2021, http://www.fao.org/wiews/en/, accessed on 20th Sept 2021. Species name according to WIEWS and species name accepted by Spooner et al. (2014) including country of origin, ploidy level is provided for nine largest collection holder. na, not accepted names were found at https://solanaceaesource.myspecies.info/; *species classified incorrectly by genebanks.

| Genebank species | Accepted by Spooner et al. (2014) | Code | Country | Ploidy | Total | PER001 | RUS001 | DEU159 | BOL317 | COL017 | USA004 | PER867 | CHL071 | GBR251 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Solanum ajanhuiri** | ***Solanum ajanhuiri* Juz. & Bukasov** | ahj | BOL, PER | 2x (2EBN) | 98 | 14 | 9 | 8 | 64 | | 1 | | | |
| Solanum megistacrolobum* | *Solanum boliviense* Dunal in DC. | blv | ARG, BOL, PER | 2x (2EBN) | 2 | | 2 | | | | | | | |
| Solanum suaveolens* (na) | *Solanum campylacanthum* Hochst. ex A.Rich. | | | | 1 | | | | 1 | | | | | |
| Solanum multidissectum | *Solanum candolleanum* Berthault | buk | PER | 2x (2EBN), 3x | 1 | | 1 | | | | | | | |
| ***Solanum curtilobum*** | ***Solanum curtilobum* Juz. & Bukasov** | cur | BOL, PER | 5x | 121 | | 26 | | 80 | | 7 | | | |
| *Solanum xcurtilobum* see Dodds, 1962 | *Solanum curtilobum* | cur | BOL, PER | 5x | 30 | 8 | | 14 | | | | 16 | | |
| *Solanum etuberosum** | *Solanum etuberosum* Lindl. | | | | 16 | | | | | | | | 16 | |
| ***Solanum juzepczukii*** | ***Solanum juzepczukii* Bukasov** | juz | ARG, BOL, PER | 3x | 163 | | 3 | | 128 | | 1 | | | |
| *Solanum xjuzepczukii* see Dodds, 1962 | *Solanum juzepczukii* Bukasov | juz | ARG, BOL, PER | 3x | 28 | 31 | | 12 | | | | 16 | | |
| | ***Solanum juzepczukii* Bukasov Total** | | | | **191** | **31** | **3** | **12** | **128** | **0** | **1** | **16** | **0** | **0** |
| *Solanum chaucha* | *Solanum tuberosum* 'Andigenum group' triploids | tbr | Landraces from W Venezuela South to N Argentina | 3x | 131 | | 4 | | | | | | | |
| *Solanum phureja* | *Solanum tuberosum* 'Andigenum group' diploids | tbr | Landraces from W Venezuela South to N Argentina | 2x (2EBN) | 335 | 197 | 88 | | 6 | | | | | |
| *Solanum stenotomum* | *Solanum tuberosum* 'Andigenum group' diploids | tbr | Landraces from W Venezuela South to N Argentina | 2x (2EBN) | 369 | | 108 | | 248 | | | | | |
| *Solanum stenotomum* subsp. *goniocalyx* | *Solanum tuberosum* 'Andigenum group' diploids | tbr | Landraces from W Venezuela South to N Argentina | 2x (2EBN) | 166 | 110 | | 14 | | | | 33 | | |
| *Solanum tuberosum* subsp. *andigena* | *Solanum tuberosum* 'Andigenum group' tetraploids | tbr | Landraces from W Venezuela South to N Argentina | 4x (4EBN) | 7845 | 3308 | | 1215 | 975 | 672 | 940 | 528 | | |
| *Solanum tuberosum Group Andigena* | *Solanum tuberosum* 'Andigenum group' tetraploids | tbr | Landraces from W Venezuela South to N Argentina | 4x (4EBN) | 326 | | | | | | | | | 324 |
| *Solanum stenotomum* subsp. *stenotomum* | *Solanum tuberosum* 'Andigenum group' diploids | tbr | Landraces from W Venezuela South to N Argentina | 2x (2EBN) | 450 | 287 | | 86 | | | | 77 | | |
| | ***Solanum tuberosum* Andigenum group Total** | | | | **9622** | **3902** | **200** | **1315** | **1229** | **672** | **940** | **638** | **0** | **324** |

| Genebank species | Accepted by Spooner et al. (2014) | Code | Country | Ploidy | Total | PER001 | RUS001 | DEU159 | BOL317 | COL017 | USA004 | PER867 | CHL071 | GBR251 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Solanum tuberosum* subsp. *tuberosum* | *Solanum tuberosum* L. 'Chilotanum group' | tbr | CHL (Chilean landraces) | 4x (4EBN) | 1281 | 173 | | 405 | 59 | 23 | 48 | | 492 | |
| *Solanum tuberosum Group Tuberosum* | *Solanum tuberosum* L. 'Chilotanum group' | tbr | CHL (Chilean landraces) | 4x (4EBN) | 9 | | | | | | | | | 9 |
| | ***Solanum tuberosum* L. 'Chilotanum group' Total** | | | | **1290** | **173** | **0** | **405** | **59** | **23** | **48** | **0** | **492** | **9** |
| *Solanum andigenum* (na) | *Solanum tuberosum* 'Andigenum group' tetraploids | tbr | | 4x (4EBN) | 2705 | | 2701 | | | | | | | |
| *Solanum goniocalyx* (na) | *Solanum tuberosum* 'Andigenum group' diploids | tbr | | 2x (2EBN) | 60 | | 54 | | 6 | | | | | |
| *Solanum phureja* subsp. *Phureja* (na) | *Solanum tuberosum* 'Andigenum group' diploids | tbr | | 2x (2EBN) | 625 | | | 229 | | 396 | | | | |
| *Solanum rybinii* (na) | *Solanum tuberosum* 'Andigenum group' diploids | tbr | | 2x (2EBN) | 246 | | 246 | | | | | | | |
| *Solanum yabary* (na) | *Solanum tuberosum* | tbr | | | 1 | | 1 | | | | | | | |
| *Solanum x chaucha* (not found) | *Solanum tuberosum* 'Andigenum group' triploids | tbr | | 3x | 135 | 127 | | 14 | | | | 115 | | |
| *Solanum tuberosum* | *Solanum tuberosum* | tbr | | | 1021 | | | 25 | | | 47 | | 2 | 1 |
| *Solanum tuberosum Group Phureja* | *Solanum tuberosum* 'Andigenum group' diploids | tbr | | 2x (2EBN) | 3 | | | | | | | | | 3 |
| *Solanum tuberosum Group Stenotomum* | *Solanum tuberosum* 'Andigenum group' diploids | tbr | | 2x (2EBN) | 3 | | | | | | | | | 3 |
| | ***Solanum tuberosum* Total** | | | | **4799** | **127** | **3002** | **268** | **6** | **396** | **47** | **115** | **2** | **1** |
| | **Total** | | | | **16171** | **4255** | **3243** | **2022** | **1567** | **1091** | **1044** | **785** | **510** | **340** |

## Annex 6. Consultation agenda

### Consultation to discuss the Global Strategy for the Conservation of Potato (GSPC) 10-12 November 2021

### 10 November 2021 – 14:00–15:45 CET

**Topic 1: Taxonomy**

**14:00–14:30** Manuela Nagel: Introduction and overview of the GSPC
**14:30–14:55** Taxonomy: Potato taxonomy Keynote speaker: Dr. Iris Edith Peralta (Argentina)
**14:55–15:00** 5 Minute Break
**15:00–15:45** Discussion Topic 1

### 10 November 2021 – 16:00–18:00 CET

**Topic 2: Conservation management**

**16:00–16:15** Manuela Nagel: Recent challenges in the conservation management
**16:15–16:55** Reports of the curators
CIP potato collections – Dr. Manrique, Norma (CIP, Peru)
Management at the CGN – Dr. Roel Hoekstra (CGN, The Netherlands);
Conservation at Embrapa – Dr. Caroline M. Castro (Embrapa, Brazil)
**16:45–16:55** Short Questions and Answers
**16:55–17:00** 5 Minute Break
**17:00–17:45** Discussion Topic 2
**17:45–18:00** Summary and conclusions of the day

### 11 November 2021 – 14:00–15:45 CET

**Topic 3: Gap analysis**

**14:00–14:30** Manuela Nagel: Welcome, short survey summary about gaps in the collections
**14:30–14:55** Gap analysis: The spatial gap analysis for potato landraces
Keynote speaker: Prof. Dr. Julian Ramirez-Villegas (Alliance of Bioversity International and CIAT, Italy)
**14:55–15:00** 5 Minute Break
**15:00–15:45** Discussion Topic 3

### 11 November 2021 – 16:00–18:00 CET

**Topic 4: Data quality and safety**

**16:00–16:15** Manuela Nagel: Overview on data availability and challenges
**16:15–16:45** Data management and tools for collection management
Keynote speaker: Matija Obreza (CropTrust, Germany)
**16:45–16:50** 5 Minute Break
**16:50–17:35** Discussion Topic 4

### 12 November 2021 – 14:00 –15:45 CET

**Topic 5: Breeding**

**14:00–14:30** Manuela Nagel: Overview on usability of the collections
**14:30–14:55** Breeding: Genome design of hybrid potato
Keynote speaker: Dr. Chunzhi Zhang (CAAS, Shenzen, China)
**14:55–15:00** 5 Minute Break
**15:00–15:45** Discussion Topic 5

### 12 November 2021 – 16:00–17:15 CET

**Topic: Action Points for GSPC**

**16:00–16:20** Future priorities for the *ex situ* conservation of potato
Zoom Breakout Group: Taxonomy & miscellaneous
Zoom Breakout Group: Conservation management & miscellaneous
Zoom Breakout Group: Gap filling & miscellaneous
Zoom Breakout Group: Data safety & miscellaneous
Zoom Breakout Group: Breeding & miscellaneous
**16:20–16:45** Reports from each Breakout Group (max 5 minutes each)
**16:45–17:15** Summary and conclusions of the meeting

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