



GLOBAL STRATEGY FOR THE *EX SITU* CONSERVATION OF TEMPERATE FORAGES

With support from



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COVER

Medicago sativa subsp. *sativa* at Waite Institute, Adelaide, South Australia. Photo: Michael Major for Crop Trust

DISCLAIMER

This report aims to provide a framework for the efficient and effective *ex situ* conservation of globally important collections of temperate forages. The Crop Trust commissioned AgResearch to coordinate the development of the strategy. 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 is expected to continue to evolve and be updated as and when circumstances change or new information becomes available.

ACKNOWLEDGMENTS

Thanks are due to the following people: Genebank curators, staff and managers; and genebank users from various organizations, for providing survey data. Hannes Dempewolf (Crop Trust) for project oversight; Peter Giovaninni (Crop Trust) for project oversight, database extraction, data analysis and workshop support (transcription and translation) and Emily Drummond for workshop support (transcription). Wendy Boyce, Michelle Williamson (AgResearch) and Graham Kerr (Barenbrug Agriseeds) for feedback on initial survey design. Kioumars Ghamkhar, Zane Webber and Michelle Williamson (AgResearch) for data provision and additional discussions. Drafts of the strategy document were reviewed by Brent Barrett (AgResearch) and Alan Stewart (PGGWrightson), Kioumars Ghamkhar (AgResearch, NZ), Jim Crush (AgResearch, NZ), Alan Stewart (PGG Wrightsons, NZ), Brian Irish (USDA Washington, USA), Axel Diederichsen (Agriculture and Agri-Food Canada), Ken Friesen (Agriculture and Agri-Food Canada), Külli Annamaa (Estonian Crop Research Institute), Evelin Willner (IPK, Germany), Federico Condon (INIA, Uruguay), Fernando Ortega (INIA, Chile), Peter Giovaninni (Crop Trust), Luigi Guarino (Crop Trust).

Thanks to workshop participants: Alan Humphries (PIRSA-SARDI, Adelaide AU), Axel Diederichsen (PGRC, Saskatoon CA), Ken Friesen (PGRC, Saskatoon CA), Kioumars Ghamkhar (Margot Forde Forage Germplasm Centre, Auckland NZ), Michelle Williamson (Margot Forde Forage Germplasm Centre, Auckland NZ), Barbara Hellier (USDA-ARS, Pullman WA, USA), Brian Irish (USDA-ARS, Prosser WA, USA), Xuefeng Ma (Noble Research Institute, Ardmore OK, USA), Malay Saha (Noble Research Institute, Ardmore OK, USA), Michael Udvardi (Noble Research Institute, Ardmore OK, USA), Ali Shehadeh (ICARDA, Lebanon), Bernadette Julier (INRA, France), Külli Annamaa (ETKI, Estonia), Francisco Galea (CICYTEX, Spain), Fernando Ortega-Klose (INIA-Carillanca, Temuco CL), Federico Condon (INIA-La Estanzuela, Colonia UY), Jean-Paul Sampoux (INRA, France), Evelin Willmer (IPK, Malchow).

Online genebank accession data were acquired through the [Genesys](#) global portal on plant genetic resources. All intellectual property rights (including copyright) in the data are owned and retained by the institution that provided the accession-level data to Genesys.

The development of this Crop Conservation Strategy was funded by the Government of Germany (BMEL) as part of the three-year project led by the Crop Trust: *Breathing new life into the Global Crop Conservation Strategies: Providing an Evidence Base for the Global System of Ex Situ Conservation of Crop Diversity*. The Crop Trust also cooperated with the Secretariat of The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) in the development of this document.

The information in Annex 9.10 of this document is a summary of "The plants that feed the world: baseline information to underpin strategies for their conservation and use" a study produced as a collaboration led by the Treaty Secretariat, and funded by NORAD, also involving the Alliance of Bioversity and CIAT and the Crop Trust.

[Supplementary data file](#) available on Figshare.

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RECOMMENDED CITATION

Dodd, M. 2021. Global strategy for the *ex situ* conservation of temperate forages. Global Crop Diversity Trust. Bonn, Germany. DOI: [10.5281/zenodo.8192993](https://doi.org/10.5281/zenodo.8192993).

DOI

[10.5281/zenodo.8192993](https://doi.org/10.5281/zenodo.8192993)



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Forage seeds. Photo: Kioumars Ghamkhar and Zane Webber (AgResearch)

1 EXECUTIVE SUMMARY

1.1 Rationale for the strategy

Livestock systems are valued at over USD 1.4 trillion and employ 1.3 billion people globally. They cover 70% of agricultural land and supply 26% of human protein and 13% of human energy intake. The forage input for these systems is a critical component of the global food supply, and demand for forage continues to grow alongside growing demand for livestock products. Livestock systems also represent an important contribution to rural livelihoods across the socio-economic spectrum, especially for rural communities that are unable to manage land resources. Temperate grazing lands (grass-dominant but inclusive of legume and forb plant functional types) cover 13% of the global land area and contribute 11% of the total feed intake of cattle, sheep and goat enterprises, for the production of meat and milk.

The use of plant genetic resources for the development of improved temperate forage cultivars has an

established and proven history in developed countries. However, there has traditionally been a strong focus on a small group of species and a limited set of traits, namely, total and seasonal herbage production, animal nutritive value and tolerance of the major climatic stressors (drought, heat and cold). The reality of accelerating climate change provides the incentive to more deeply and intensely explore the adaptability of a wider range of germplasm to these conditions and others (e.g. waterlogging, pests).

In addition, concerns around the impact of livestock systems on the environment (soil loss, greenhouse gas emissions, nutrient losses to water, losses of endemic biodiversity) provide another dimension to the need to secure germplasm diversity. This is specifically relevant to capturing mitigating traits, such as reduced methanogenesis, high nutrient uptake rates and dietary partitioning of nitrogen. Harnessing genetic diversity is one of the key strategies for mitigating the environmental impact of intensive livestock systems.

1.2 Mission

To maximize the diversity and utility of germplasm in secure mid- to long-term storage and improve global accessibility of germplasm and associated passport and characterization data, for those temperate forages of proven or demonstrated potential value to the sustainability of the global temperate livestock sector.

1.3 Vision

An international network of genebanks and germplasm users with high levels of open exchange of temperate forage germplasm and comprehensive passport and characterization data.

1.4 Core values

To be effective, a global strategy for temperate forages should reach broad acceptance of a set of core values among all stakeholders, including a) the security of genetic diversity, b) a utilitarian focus, c) assured data quality, d) maximized accessibility of both germplasm and data.

1.5 Scope

The strategy incorporates the *ex situ* conservation of herbaceous plant species (and subordinate taxa) used for grazing livestock forages collected from or used within the temperate zone (30–60° latitude), excluding subtropical and tropical forages used within the temperate zone.

1.6 Characteristics of the temperate forage “crop” and *ex situ* germplasm conservation

Some characteristics of the temperate forage taxa as a group, which make them distinct from other “crops,” include:

- There are a wide range of taxa, with potentially thousands of species and subordinate taxa, dominated by Poaceae and Fabaceae. Taxonomic revision is ongoing, which contributes to issues in identifying duplicates.
- A small proportion of these species dominate global use (e.g. those from *Lolium*, *Festuca*, *Medicago*, *Phleum*, *Trifolium*).
- There is a history of extensive collection by “high income” countries focused on centers of origin in the Mediterranean and Eurasian regions.
- There is a strong cultivar development industry, supported by established legislation to protect rights to plant varieties. This industry has shifted from government to commercial entities.
- Many species have multiple uses beyond livestock forage, including biomedical uses, biofuels, soil con-

servation, ecological restoration, crop support and amenity uses (e.g. *Lolium perenne*, *Festuca arundinacea*). The amenity sector is large in high-income nations, involving several forage grass wild relatives.

- Fungal and microbial symbionts, notably grass endophytes and legume rhizobia, are important biotic influences on temperate forage performance.

Characteristics of the temperate forage germplasm conservation sector include:

- Collections of relevant material are held in more than 160 organizations across more than 70 countries worldwide.
- An estimated 80% of accessions are held by 19 genebanks, and 50% of all accessions are from nine species, based on a search in the *Genesys database* of a sample set of 11 temperate forage genera.
- Most genebanks appear to have fundamentally secure storage facilities and adequate policies and processes but lack regeneration capacity.
- Global accessibility to accession passport and characterization data is improving, but greater attention to data quality is a priority. Germplasm users (i.e. researchers and breeders) probably now hold a significant share of this data.
- Redundant duplication is a major issue for curators, who seek to rationalize their collections and free up resources for priority regeneration and characterization activity.
- Collection activity has declined in recent decades, and several challenges are hindering the new collection activity that is needed to fill known gaps.
- Core collections are seen as a useful tool, but development is hampered by limited access to germplasm and basic characterization data, as well as limited molecular and phenomics data.
- Genebanks are demonstrating an increasing local focus, in terms of field collection of indigenous and naturalized material, and in terms of meeting the needs of local users.
- Some potentially valuable material is held in genebanks or commercial working collections to which access is restricted.
- Collaborative networks have reduced in recent years and, with the exception of CGIAR and ECPGR, are now mainly focused within countries.

1.7 Strategic actions

The following high-level strategic actions are proposed:

A. Taxa categorization and prioritization

Given the wide range of taxa, which are used to varying degrees across many ecogeographic zones and held by many genebanks, an important first step is to

categorize temperate forage germplasm and prioritize activity within these groups. For categorization, several factors may be considered to determine useful groups, including existing collection status, global relevance, ecogeographic zone (within the temperate zone) and type of use. Prioritization will require consideration, within the above categories, of which taxa should be focused on and the specific needs for those taxa or that group, such as standardization of descriptors, urgent collection, underrepresented traits and requirements for new research. A key step in prioritization would be the identification of a lead agent (or agents) with an organizational mandate to focus on the conservation of those taxa. The most likely candidates would be those organizations with existing strong collections of particular taxa, existing responsibilities (e.g. through CGIAR, NPGS or ECPGR) and the ability to deliver a step change in characterization and prioritization activity during the next decade.

B. Improvement of data curation

The passport and characterization data associated with the species already in *ex situ* genebanks around the world vary in quality. In many cases, the data are incomplete, relative to current FAO standards (Multi-Crop Passport Descriptors). For many taxa, standard descriptors are dated or absent. For many descriptors, measurement standards vary, having been adopted by diverse providers. The process of addressing these various issues is likely to involve intensive work, requiring collaboration between database specialists and individual germplasm curators and other experts (e.g. taxonomists, systematists, botanists). Given the almost universal feedback from curators that they are under-resourced in terms of staff capacity, the investment for this activity will need to be externally sourced. Data held by users must be included in this activity wherever possible, given potential commercial sensitivities for breeding companies. Implementing this strategic action would also go some way to the development of human resources (Strategic action D) within individual genebanks—and this represents the *quid pro quo* value proposition for them to engage. This step is considered a priority strategic action ahead

of germplasm activity rationalization (Strategic action C), given that any assessment of genetic resource rationalization for a given taxon must begin with analysis of the data and accessions already held. This is necessary both for minimizing redundancy and for filling gaps, tasks that will contribute to germplasm rationalization, as set out in Strategic action C.

C. Germplasm activity rationalization

In a context of limited resources (in terms of people's time, storage space and regeneration capacity), two major tasks emerge: to minimize redundant activity within the global collection of any given taxon; and to fill gaps in global collections of prioritized taxa, to best represent the true diversity of a crop. Two main methods for achieving this have been applied to specific temperate forages and could be more widely used for priority taxa. Core collections have already been developed for temperate forages (e.g. *Trifolium subterraneum*) and some are in progress (e.g. *Trifolium repens*, *Lolium perenne*); and trait-based sub-setting has been applied to *Lathyrus*. The prioritization exercise in Strategic action A would identify future candidates for the appropriate application of these approaches.

D. Human resource development

Human capacity was almost universally cited as a major constraint to progress in global collaboration. Curators and staff are already fully occupied with attending to their core genebank functions of storage, regeneration and distribution. However, all respondents, including users, saw value in collaboration and coordination at a wider scale. A feature of the temperate forage conservation community appears to be collaborative goodwill. At the global scale, initiatives in this regard should initially focus on support for data curation (Strategic action B). In addition, support for wider participation in existing regional networks or the establishment of regional networks would be valuable. The aim would be to increase the engagement of those countries less connected to global networks.



Alfalfa in Inner Mongolia. Photo: L.M. Salazar/Crop Trust

2 INTRODUCTION

2.1 Rationale for the strategy

2.1.1 The context of forage systems

The safeguarding and use of genetic resources underpin food security, climate adaptation, soil conservation and sustainable development. These genetic resources include not only food crops for direct human consumption, but also the pasture and fodder crops consumed by livestock. Livestock are an important part of the human food resource, comprising 26% of global protein consumption and 13% of calorific consumption. The livestock sector is valued at over USD 1.4 trillion, employs 1.3 billion people and accounts for 70% of agricultural land (Thornton 2010). Ruminant livestock systems are effective converters of high-cellulose plant material into protein and energy products that are human edible, an energy-efficient process in free-range systems. Demand for animal protein is increasing globally and will continue to do so for the foreseeable future (Global Agenda for Sus-

tainable Livestock 2014). However, there is evidence that, as a result of efforts to improve the quality of animal diets, livestock now consume more human-edible protein than they produce (Steinfeld et al. 2006). The genetic improvement of temperate forages offers a means of returning livestock systems to their core value proposition: to produce protein from grazing lands that are unsuitable or undesirable for growing crops.

Beyond human food supply, livestock systems provide a range of other products for human consumption, such as fuel, fertilizer, leather, fiber and pharmaceutical products. Livestock systems are thus an important contributor to rural livelihoods across the whole spectrum of economic and social development. In developing nations, livestock production systems represent one of the most accessible economic activities for alleviating poverty (Steinfeld et al. 2006), directly supporting 600 million smallholder farmers in the developing world (Thornton 2010).

In terms of livestock production systems, grazing lands support 10% of global beef and 30% of global sheep and goat meat (FAO 1997). Grasslands and grass-dominant vegetation types are a substantial biome globally, covering approximately 35% (Ramankutty et al. 2008) to 37% (O'Mara 2012) of the terrestrial area, excluding Greenland and Antarctica. Agricultural land use change has contributed to this area via conversion of 15% of the forest biome to pastureland, but also conversion of 15% of the grassland biome to cropland (Ramankutty et al. 2008). These changes have left the more marginal grassland areas exposed to degradation through overgrazing, acidification, salinization, erosion and weed ingress (Suttie et al. 2005). In terms of genetic resources, global grasslands provide the genetic material for a focus on both efficient livestock production and enhancing the sustainability of this biome.

Temperate grazing lands represent 13% of the world's grassland biome (Conner et al. n.d.). They contribute approximately 18% of global grazing feed consumption in bovine meat, bovine milk, small ruminant meat and small ruminant milk production systems, or approximately 11% of global total feed consumption in these systems (Herrero et al. 2013). Temperate grazed livestock systems in North and South America, Africa and Asia are predominantly on native grassland, while Europe, Australia and New Zealand have a high proportion of derived (sown) grazing land based on introduced grass and legume species.

Further selected metrics for forage crops are presented in Annex 9.10.

2.1.2 Challenges for temperate livestock grazing systems

Rangeland degradation, in terms of soil loss and botanical change, is a long-standing issue in the temperate zone (Steinfeld et al. 2006). While the seasonal phenology of grassland plants and livestock reproductive cycles represents a well-adjusted ecosystem, inflated stocking rates supported by imported supplementary feed can result in ecosystem damage. The ruminant livestock sector has recently come under increased scrutiny for its contribution to environmental degradation (Steinfeld et al. 2006). This scrutiny has focused on three major themes: global warming via biogenic methane emissions, loss of biodiversity via conversion of natural ecosystems to grazing lands, and contamination of water resources.

Biogenic methane emissions are strongly influenced by forage quantity and quality. Therefore, a critical element in the potential for mitigating global warming is the use of genetic variation in forages to develop cultivars that demonstrate reduced rumen methano-

genesis (Clark et al. 2011). There is also recent evidence that specific forage genotypes have a role in the mitigation of soil nitrification processes that lead to nitrous oxide emissions, a further major source of global climate forcing (de Klein et al. 2020). While not directly related to genetic diversity, grasslands also have the potential to mitigate global warming via carbon sequestration in soils, to a level of 1.5 Gt CO₂-e by 2030 (O'Mara 2012).

Biodiversity loss is influenced by both the intensity and the expansion of livestock enterprises. It has been argued that an improvement in forage productivity can mitigate biodiversity loss through land sparing; that is, a smaller area is required for a given quantum of animal production. Although this debate is ongoing (e.g. Kremen 2015), the use of genetic diversity in the development of productive cultivars of high feed quality could contribute to mitigating biodiversity loss.

Water quality is also influenced by the intensity of animal enterprises. Nitrate leaching to groundwater is a function of the excess soil nitrogen over plant requirements caused by urine deposition (Cameron et al. 2013). Plant genotypes with high growth rates, and associated high water- and nutrient-uptake rates, can mitigate this effect. Furthermore, recent research has demonstrated the potential for specific forage genotypes to reduce this impact via urinary dilution and soil nitrification inhibition (de Klein et al. 2020). Surface erosion of sediment and nutrients can be minimized by forage genotypes that are well adapted to their environment and persistent under grazing, and therefore retain maximum ground cover (Zuazo and Pleguezuelo 2009).

2.1.3 Conservation threats and opportunities

Many of the generic threats to crop biodiversity conservation also apply to temperate forages. Losses of original habitat in centers of origin, domestication and diversity are occurring through global change (Epstein et al. 2002) and land-use change (Baldock 1990). Ironically, in some cases, this results from the spread of intensive grazing systems using introduced temperate forages (Krause et al. 2011). Biotic threats include competition from exotic adventive plant species, overgrazing and the global spread of pests and diseases.

Fu (2017) has summarized a range of interconnected issues for *ex situ* conservation of germplasm, including insufficient investment and a long-term decline in funding efficacy, regeneration backlogs, declining political and stakeholder support, inadequate germplasm evaluation and characterization, outdated data management systems, inadequate genebank capacity, unbalanced research support and lack of professional

development support. At the country scale, some of these issues are noted by Diez et al (2018), who go on to propose a focus on rationalizing the network, deep germplasm characterization, optimize regeneration protocols and develop accessible data platforms.

On the other hand, many of the more generic opportunities for plant biodiversity conservation also apply to temperate forages. These include substantial genotypic diversity at the level of families (i.e. grasses, legumes, forbs) and genera (multiple genera within families), and within genera a wealth of crop wild relatives in secondary gene pools. The emergence of new analytical tools can support cost-effective diversity characterization (e.g. phenomics, core collections). A potential advantage for temperate forage conservation is their extensive use by high-income nations (e.g. Europe, North America, Australasia) with ready access to such tools.

2.1.4 Scope of the strategy

The scope of a “temperate forage” strategy is potentially wide, and the boundaries are hard to define. The temperate zone can be defined both latitudinally (35–50°) and climatically. Köppen-Geiger classifications are Csa, Csb, Cfa, Cfb, Cfc, Cwa, Cwb, Cwc (Figure 1; Peel et al. 2007; Beck et al. 2018). However, cold zone classifications such as Dfb, Dfc, Dwb and Dwc may also

be relevant. A more simplistic characterization is to consider the *in situ* distribution of temperate forage germplasm, based on collection records of representative taxa such as the *Trifolium* genus. This indicates that the relevant geographic zone is probably between 30° and 60° latitude (Figure 1).

There is clearly widespread use of temperate zone-origin species within both cooler and warmer zones. Conversely, cooler and warmer zone-origin species are used within the temperate zone, as plant breeders and livestock practitioners seek access to genetic resources that can help them manage climate variability and change. It should be noted that the Global Crop Diversity Trust (Crop Trust) has already completed a strategy for tropical and subtropical forages (Crop Trust 2017), and many of the elements in that strategy are relevant in the realm of temperate forages.

It is also worth noting that some taxa are used globally both as livestock forages and as crops for direct human consumption (e.g. *Pisum* spp., *Hordeum* spp.), and thus characterizations of genetic diversity need to consider these dual purposes. The scope for this strategy includes those species intended for use as livestock forages and either collected from or adapted to the temperate zone. A list of relevant temperate zone countries defined by the 30–60° latitude band is in Annex 9.1.

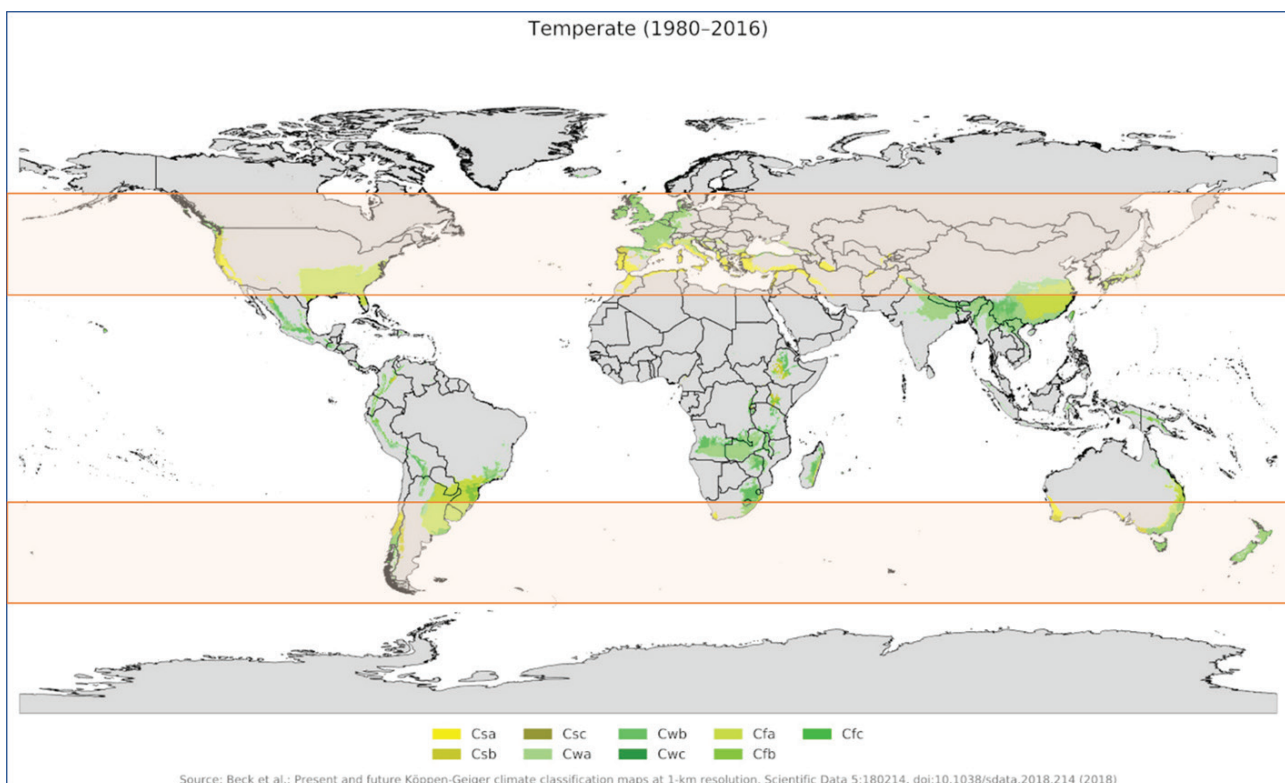


Figure 1 Temperate zone according to updated Köppen-Geiger classifications from Beck et al. (2018) and estimated latitudinal range of temperate forage collection activity (30–60°).

2.2 Objectives of the strategy development

The objective of this project was to develop a global strategy to assess the status of conservation activities around the world and to define priority actions to safeguard and harness the inherent diversity of temperate forage species. Most of these species are derived from grassland systems. The strategy will provide the basis for future conservation activities that are designed to deliver an optimum set of pasture and fodder germplasm that is robustly prioritized, carefully secured and widely available. Key aims of the strategy are as follows:

1. Identify global gaps and redundancies in *ex situ* germplasm collections of the most economically important temperate forage and pasture species.
2. Identify exemplars of successful *ex situ* germplasm collections in terms of conservation and provision of germplasm to users and make recommendations to strengthen future conservation efforts.
3. Identify the needs of temperate forage germplasm holders and users and determine how genebanks can effectively meet the needs of all stakeholders.
4. Provide recommendations for priority conservation activities.

2.3 Process of developing the global strategy

Under the circumstances of a global pandemic, which hindered travel and adjusted priorities for potential participants, it was not possible to follow the Crop Trust's usual process for developing strategies. Taking these limitations into consideration, the revised process was as follows:

1. Identification of 15 temperate forage taxa, based on limited consultation, to form a sample set for consultation with genebank curators, emphasizing diversity in life form, the extent of global use and centers of origin.

2. An initial online survey of a diverse set of genebank curators that focused on the sample set of taxa and key issues affecting germplasm conservation; less consideration was given to the finer detail on temperate forage germplasm collections (e.g. documenting within-species diversity). The survey was sent to 35 potential respondents, and 17 responses were received (49%; Annex 9.2).
3. An initial survey of germplasm users that focused on the sample set of taxa, objectives for use and key challenges. The survey was sent to 80 potential respondents, and 20 responses were received (25%; Annex 9.2). Note that, for previous strategies, data gathering focused only on genebank curators. However, there is considerable value to be gained from surveying a diverse group of genebank users, including academics, breeders, conservationists, geneticists, private and public sector, to understand:
 - which temperate forage species are of particular interest to them;
 - the data they have been gathering on the focal species and other species of interest, which might augment genebank databases;
 - the traits they consider important in the focal species, relative to those considered important by curators (and, by inference, collectors);
 - the degree to which the genebanks they interact with meet their needs;
 - which genebanks and networks they interact with; and
 - whether they held additional genetic material outside of recognized genebanks that could be accessible to networks.
4. Background research and survey of relevant literature and online resources.
5. Analysis of the origin and storage location of unique accession data retrieved from major online germplasm databases, at the genus level for the 15 taxa in the sample set and taxonomic relatives.
6. Four online consultation workshops with the genebank curators who responded to the survey in #2 above. Notes from these discussions were compiled.



Measuring plant height of alfalfa at the Waite Institute, South Australia. Photo: Michael Major for Crop Trust

3 BACKGROUND RESEARCH ON TEMPERATE FORAGES

3.1 Crop overview

The “crop” defined here is a large group of temperate herbaceous taxa, defined by climate and geography as originating from, or used in, the temperate zone (defined here as 30–60° latitude). Many woody browse shrubs could also be considered relevant to the broad definition of the temperate forage “crop.” However, it was decided that woody forage plants were beyond the scope of this study.

The temperate forages “crop” includes a wide range of taxa that originate from temperate grasslands around the world, occurring in every continent except Antarctica. The temperate grassland biome area is estimated to be 49M km² or 36% of the Earth’s land area, in terms of potential natural vegetation (Sala 2001). However, more than half of this area has been modified, either by agriculture (41%) or by urban and industrial uses (13%; Heidenreich 2009). While natural temperate grasslands may contain thousands of unique species, a limited number of these—probably fewer than 100—have been developed into cultivated varieties.

This suite of taxa is dominated by the Poaceae (grass) and Fabaceae (legume) families. Within these families, a small number of genera dominate global use: *Bromus*, *Dactylis*, *Festuca*, *Lolium*, *Phleum* and *Poa* within the grasses; and *Medicago* and *Trifolium* within the legumes (Annicchiarico et al. 2015).

A second, more diverse tier of genera within grasses and legumes are regionally relevant, with cultivars being developed: *Agropyron*, *Agrostis*, *Elymus*, *Holcus*, *Phalaris* and *Thinopyrum* (grasses); and *Biserrula*,

Hedysarum, *Lotus*, *Lupinus*, *Melilotus*, *Onobrychis*, *Ornithopus* and *Vicia* (legumes).

It should be noted that some temperate grain crops and their wild relatives are also commonly used as animal forages, including the genera *Avena* and *Secale*. Genebank users identified these as important forage species, but they are not dealt with here. Several annual crops are also important forages for livestock, including species in *Brassica* (mustards) and *Beta* (beets).

Use of perennial grassland species from other families (i.e. non-leguminous dicotyledonous forbs) is much more limited. However, notable species for which cultivars have been developed and used at the regional level are *Cichorium intybus* and *Plantago lanceolata* (i.e. in Australasia).

An initial sample list of species for the survey was chosen based on expert knowledge of existing global conservation and use and on expert assessment of potential for future use. The list includes only grasses and legumes (Table 1). Note that two of these species are included in other crop strategies, as they belong to taxa normally associated with crops: *Hordeum* (barley) and *Lathyrus* (grasspea). Respondents to the survey were invited to suggest additional species to the sample set, based on their view of regional or global significance.

All taxa included in the sample set, with the exception of *Biserrula pelecinus*, are covered in Annex I of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) under Forages (grasses and legumes) or Crops (*Hordeum* and *Lath-*

yrus). Annex I of the ITPGRFA includes additional temperate forage species within the genera included in the sample (5 spp. of *Festuca*, 3 spp. of *Lolium*, 2 spp. of *Lotus*, 2 spp. of *Lupinus*, 5 spp. of *Medicago*, 11 spp. of *Trifolium*), as well as additional temperate forage genera and selected species (2 spp. of *Agropyron*, 2 spp. of *Agrostis*, 1 spp. of *Arrhenatherum*, 3 spp. of *Astragalus*, 1 spp. of *Coronilla*, 2 spp. of *Melilotus*, 1 spp. of *Ornithopus*, 1 spp. of *Phleum*, 3 spp. of *Poa*). Annex I of the ITPGRFA also lists a number of crop genera that include temperate species of relevance to animal forages (*Phaseolus*, *Secale*, *Triticosecale*, *Vicia*) and tropical species used for animal forages in the temperate zone (*Pennisetum*, *Sorghum*, *Zea*).

3.2 Crop descriptions

Biserrula pelecinus is a winter-spring annual legume (Table 1) of Mediterranean origin (Table 2) and is the only species in the genus (Ghamkhar et al. 2012b). It is valued for its tolerance of acid soils, high levels of hard-seededness and deep taproot, making it well adapted to deep free-draining soils in summer-dry climates (Loi et al. 2014). Additional morphological characteristics of interest include pod architecture, flowering date, flower color and seed size (Loi et al. 2006). It has also been shown to have lower levels of methane output from *in vitro* fermentation compared with other commonly used legumes, which implies

Table 1 Sample list of temperate forage germplasm taxa used in the online survey (alphabetical order by accepted Latin binomial). The list of synonyms is not exhaustive.

Species name	Selected synonyms	Common name(s)	Family	Habit
<i>Biserrula pelecinus</i> L.	<i>Astragalus pelecinus</i> (L.) Barneby <i>Pelecinus biserrula</i> Moench	Biserrula	Fabaceae	Annual ± pillose herb up to 40 cm TSW ¹ ~1.2 g
<i>Dactylis glomerata</i> L.	<i>Bromus glomeratus</i> (L.) Scop. <i>Festuca glomerata</i> (L.) All. <i>Koeleria dactylis</i> Chaub. <i>Phalaris glomerata</i> (L.) Gueldenst.	Orchardgrass Cocksfoot	Poaceae	Coarsely tufted perennial TSW ~0.9 g
<i>Festuca arundinacea</i> Schreb. ²	<i>Schedonorus arundinaceus</i> (Schreb.) Dumort. <i>Lolium arundinaceum</i> (Schreb.) Darbysh.	Tall fescue	Poaceae	Caespitose, short-rhizome perennial TSW ~2.6 g
<i>Hordeum spontaneum</i> K.Koch		Wild barley Spontaneous barley	Poaceae	Caespitose annual TSW ~20–50 g
<i>Lathyrus sativus</i> L.	<i>Cicerula sativa</i> (L.) Medik.	Grasspea	Fabaceae	Branched annual herb up to 170 cm TSW ~30–300 g
<i>Lolium multiflorum</i> Lam.		Annual ryegrass Italian ryegrass	Poaceae	Caespitose annual or biennial up to 100 cm TSW ~2–4 g
<i>Lolium perenne</i> L.	<i>Festuca perennis</i> (L.) Columbus & J.P.Sm	Perennial ryegrass	Poaceae	Caespitose perennial up to 90 cm TSW ~2.0 g
<i>Lotus corniculatus</i> L.	<i>L. japonicus</i> (Regel) K. Larsen	Birdsfoot trefoil	Fabaceae	Perennial herb TSW ~1.2 g
<i>Lupinus luteus</i> L.		Yellow lupin	Fabaceae	Annual herb TSW ~140 g
<i>Medicago sativa</i> L.		Alfalfa Lucerne	Fabaceae	Perennial branched herb up to 60 cm TSW ~2.0 g
<i>Onobrychis viciifolia</i> Scop.	<i>Hedysarum onobrychis</i> L.	Sainfoin	Fabaceae	Perennial herb TSW ~13–16 g
<i>Trifolium pratense</i> L.		Red clover Carreton	Fabaceae	Perennial herb up to 60 cm TSW ~2–3.5 g
<i>Trifolium repens</i> L.	<i>Amoria repens</i> (L.) C. Presl	White clover Ladino clover	Fabaceae	Perennial herb TSW ~0.7 g
<i>Trifolium resupinatum</i> L.	<i>Amoria resupinata</i> (L.) Roskov	Persian clover Reversed clover Shaftal clover	Fabaceae	Annual prostrate herb up to 60 cm TSW ~1.1 g
<i>Trifolium subterraneum</i> L.	<i>Calycomorphum subterraneum</i> (L.) C. Presl	Subterranean clover	Fabaceae	Annual herb TSW ~6–7 g

¹ TSW = thousand seed weight.

² The current accepted name is *Lolium arundinaceum* (Schreb.) Darbysh. However, the traditional synonym is used in this context, as the common name reflects placement in the genus *Festuca* and the change is not widely accepted in the agricultural user community.

potential for reducing biogenic livestock methane emissions (Banik et al. 2013). All known accessions are diploid $2n = 16$. Outside its center of origin, most research and development activity has occurred in Western Australia since 2005. Two cultivars have resulted from this effort (Banik et al. 2013). A core collection represented by ~10% of known accessions has been developed, based on agro-morphological traits, ecogeographic specifications and amplified fragment length polymorphism markers (Ghamkhar et al. 2012b).

Dactylis glomerata (cocksfoot, orchardgrass) is a densely caespitose perennial grass (Table 1) of temperate Eurasian origin (Table 2) and is one of only two accepted species in the genus *Dactylis* (cf. *Dactylis smithii* Link). It is well adapted to summer-dry environments on coarse-textured soils of moderate fertility, having a deep root network. It is of moderate forage quality in terms of animal nutrition (Stewart and

Charlton 2003). While it is originally diploid ($2n = 14$), some tetraploids and one hexaploid exist, with most forage genotypes being tetraploid; the inheritance mechanism is autopolyploid (Stewart and Ellison 2011). It has a high level of phenotypic plasticity and variability (Last et al. 2013) and includes at least 20 accepted subspecies. However, marker analysis from collections across four regions (China, Europe, North America, Australia) indicated that the genetic base in each was distinct and highest in China and the USA (Zeng et al. 2008). Breeding has focused on flowering date, tiller size and density, winter growth and levels of summer dormancy (Stewart and Charlton 2003). More than 50 cultivars have been produced, mainly from Europe, North America and Australasia (Knight 1968; Stewart and Charlton 2003). Rare examples of cross-genus hybridization with *Festuca*, *Lolium* and *Phleum* have been reported (Matzk 1981; Oertel et al. 1996; Nakazumi et al. 1997, respectively). Stewart and Ellison (2011) suggest that the genetic resources of the

Table 2 Centers of origin, indigenous range and regions of introduction for 16 taxa in the sample set (source: [Plants of the World Online](#)). Secondary centers of diversity are also noted.

Species name	Center of Origin	Indigenous	Introduced
<i>Biserrula pelecinus</i> L.	Mediterranean ¹	Mediterranean to N Ethiopia, Macaronesia	Australia
<i>Dactylis glomerata</i> L.	Temperate Eurasia ²	Mediterranean to Temperate Eurasia, Scandinavia, Macaronesia	N, C & S America, Russia, E Asia, Australasia, South Africa
<i>Festuca arundinacea</i> Schreb.	Europe, Mediterranean, Eurasia ²	Europe, Scandinavia, Eurasia to NW China and Himalaya, Mediterranean, Macaronesia	N, C & S America, Russia, Australasia; South Africa
<i>Hordeum spontaneum</i> K.Koch	E Mediterranean ³	Mediterranean to Central Asia and S China	Belarus, Morocco
<i>Lathyrus sativus</i> L.	Balkans ⁴	Eurasia	Europe, W China, Mediterranean, E Africa, Australia
<i>Lolium multiflorum</i> Lam.	Italy ²	Macaronesia, Sahara, Mediterranean to Central Asia, Himalaya	N Europe, S China, India, Ethiopia, S Africa, N, C & S America, E Russia, Japan, Australasia
<i>Lolium perenne</i> L.	Mediterranean ²	Mediterranean, N Africa, Europe to Siberia and Himalaya, Macaronesia	N, C & S America, Arabia; S Africa, E China, Australasia
<i>Lotus corniculatus</i> L.	Europe, Eurasia, N Africa ²	Europe, Scandinavia, Eurasia, N & E Africa, S Arabia, Macaronesia, Japan	N & S America, Iceland, S Africa, Australasia, China
<i>Lupinus luteus</i> L.	Turkey ²	Spain, Italy	Europe, Eurasia, China, India, NW, S & E Africa, Australasia
<i>Medicago sativa</i> L.	Eurasia ² N Africa*	Mediterranean, Eurasia	N, C & S America, Europe, Arabia, N & S Africa, China, Japan, E Russia Australasia
<i>Onobrychis viciifolia</i> Scop.	SE Europe ²	Central & SE Europe	N America, Bolivia, NW Africa, Scandinavia, Eurasia, S & E China, E Australia
<i>Trifolium pratense</i> L.	Mediterranean ⁵	Europe, Scandinavia, Mediterranean, Eurasia, Asia, NW Africa, S Arabia	N, C & S America, S & E Africa, S & E China, E Russia, Japan, Australasia, Iceland
<i>Trifolium repens</i> L.	Mediterranean ⁶	Europe, Scandinavia, Mediterranean, Eurasia, Asia, NW & E Africa, Iceland	N, C & S America, S Africa, E China, E Russia, Japan, Australasia, Indonesia
<i>Trifolium resupinatum</i> L.	Mediterranean, Persia ²	Mediterranean, Persia to Pakistan	NE & SE America, S Africa, N Europe, S Eurasia, Japan, Australasia
<i>Trifolium subterraneum</i> L.	Europe, Mediterranean ² W Australia**	Europe, Mediterranean, Caucasus, Persia	NW & SE America, S Africa, India, Japan, Australasia

*Algeria is considered a secondary center of diversity²

**Australia is considered a secondary center of diversity²

¹ Ghamkhar et al. (2012b); ² Zeven and Zhukovsky (1975); ³ Harlan and Zohary (1966); ⁴ Kislev (1989); ⁵ Vavilov (1926); ⁶ Vavilov (1951)

primary and secondary tetraploid gene pools are well represented in *ex situ* genebanks, but that the tertiary diploid gene pool is underrepresented and at risk *in situ* from habitat degradation and climate change.

Festuca arundinacea (tall fescue) is a densely caespitose perennial grass (Table 1) with a wide center of origin that encompasses Europe, the Mediterranean and Eurasia (Table 2). It is well adapted to summer-dry environments and relatively heat-tolerant (Stewart and Charlton 2003). It is the major temperate forage grass from the very large genus *Festuca*, which comprises approximately 450 species (Clayton and Renvoize 1986). Along with another major forage species, *Festuca pratensis*, it is the subject of taxonomic debate and has been placed in the genus *Lolium* (Darbyshire 1993). *Festuca* and *Lolium* species can often hybridize naturally, and several *Festulolium* hybrid cultivars have been developed in Europe and North America since the 1970s (Yamada 2011) and more recently in Australasia. Tall fescue is allohexaploid ($2n = 42$) and an obligate outcrosser (Sleper 1985). Two broad types are recognized in breeding programs, namely 'Continental' and 'Mediterranean,' based on relative levels of winter activity and summer dormancy (Stewart and Charlton 2003). Sought-after traits, besides absolute yield, include flowering date (related to forage quality), growth habit, seed yield and disease resistance. The large size of the genus *Festuca* gives rise to considerable potential for using wild relatives to improve the few agriculturally important species; an example is *F. gigantea*, which has leaves of high nutritive value (Thomas and Humphries 1991). However, this diversity is under threat from intensification of forage production in natural grasslands through fertilizer use and sowing of improved cultivars (Yamada 2011).

Hordeum spontaneum (wild barley) is a caespitose annual grass (Table 1) with a narrow center of origin in the eastern Mediterranean (Table 2). It is a close wild relative of *H. vulgare* (barley), (i.e. its ancestor), and it is a predominantly self-fertile diploid ($2n = 14$). The wild form is two-rowed, but cultivated varieties are typically four- or six-rowed, with the hulled form grown for animal forage. Genetic variation for growth rate, yield, nitrogen content, drought tolerance, salinity tolerance and disease resistance has been explored (Nevo 1992).

Lathyrus sativus (grasspea) is a branched erect annual herb (Table 1) of Eurasian origin (Table 2). It is adapted to a wide range of environments, both drought-affected and flood-affected, given its hardy taproot system (Campbell et al. 1994). It is mainly used in the subtropics as a winter crop for human consumption, but it has also adapted to the temperate zone as a summer crop for animal forage. The species is dip-

loid ($2n = 28$) and mainly self-fertile, although rates of outcrossing vary (Rahman et al. 1995). Accessions are distinguished based on flower, pod and seed traits. All parts of the plant contain a neurotoxin called ODAP, which is associated with lathyrism, a motor neuron disease in humans (Campbell et al. 1994). The plant also exhibits variable levels of condensed tannins (Deshpande and Campbell 1992). Genetic improvement has mainly focused on reducing the ODAP content in seed; a comprehensive description of this species is given in Campbell (1997).

Lolium multiflorum (annual ryegrass, Italian ryegrass) is a caespitose annual or biennial (Table 1) with a narrow center of origin in Italy (Table 2). *Lolium perenne* (perennial ryegrass) is a caespitose perennial grass of Mediterranean origin. Both are diploid ($2n = 14$), as are all other annual species in the genus *Lolium* (Clayton and Renvoize 1986). The genus *Lolium* is derived from the *Schedonorus* section of the genus *Festuca*, and hence the broad-leaved fescues are an important secondary gene pool (Cai et al. 2011). These two outcrossing *Lolium* species are the most widely used forages in the temperate zone, with thousands of cultivars developed, including hybrids, artificial tetraploids and *Festuca* hybrids. The other two outbreeders in the genus include *L. rigidum* and *L. canariense*, the former having greater genetic diversity indices than *L. perenne* (Balfourier et al. 1998). Key traits of interest beyond forage yield include flowering date (which is related to forage quality), low aftermath heading and seed yield, with some interest in root growth and rhizomatous habit.

Lotus corniculatus is a short-lived perennial legume (Table 1) with a wide center of origin that encompasses Europe, Eurasia and North Africa (Table 2). Given its deep tap root, it is well adapted to dry regions, and it appears to be more tolerant of low soil fertility than other temperate forage legumes (Stewart and Charlton 2003). A key trait of interest for animal nutrition is its high content of condensed tannins, which improve amino-acid digestion, prevent bloat and suppress internal parasites through anthelmintic properties.

Lupinus luteus is an annual herbaceous legume (Table 1) with a narrow center of origin in Turkey (Table 2). However, the genus *Lupinus* includes over 200 annual and perennial species distributed throughout the Mediterranean and Eurasia (Drummond 2008), used for both human and animal feed. *Lupinus luteus* in particular is valued for its high protein content relative to other lupins. However, like other conspecifics, it can accumulate alkaloids that affect the nervous system of animals (Allen 1998). It has moderate rates of outcrossing (Wallace et al. 1954).

Medicago sativa (alfalfa, lucerne) is an erect perennial legume (Table 1) of Eurasian origin, with a secondary center of diversity in North Africa (Table 2). It is adapted to dry, well-drained soils thanks to its deep taproot, but it requires higher fertility and alkaline soils. Diploid ($2n = 16$) and tetraploid ($2n = 32$) forms occur naturally; these are classified as subspecies *falcata* where yellow-flowered, and as subspecies *caerulea* and *sativa*, respectively, if purple-flowered (Brummer et al. 1999). Cultivated forms are mainly tetraploid. Alfalfa is outcrossing and, in addition to the more common interspecific crosses, it has been hybridized with *Medicago arborea* (Nenz et al. 1996) and *Onobrychis viciifolia* (Li et al. 1993). It is susceptible to several pests and diseases, such as bacterial wilt, stem nematode and aphids (Stewart and Charlton 2003). Alfalfa causes bloat in ruminants, and breeding programs have focused on digestion rate and condensed tannin content (Wang et al. 2012).

Onobrychis viciifolia (sainfoin) is a perennial legume (Table 1) with a narrow center of origin in south-eastern Europe (Table 2). It is a deep-rooted plant with a multi-stemmed crown that is well adapted to alkaline well-drained soils. It is valued for not inducing bloat and for being more resistant to pests than lucerne (Fortune and Withers 1980). Tetraploids are typically used as developed varieties, but natural diploids also exist, and the species is predominantly outcrossing (Kempf et al. 2015).

The genus *Trifolium* is large, comprising more than 250 species, at least 10 of which are globally significant as animal forages; others are cultivated for soil enrichment, bee forage, ornamentals, erosion control and cover crops (Morris and Greene 2001). The forage species are spread across five sections and include self-fertile annuals and self-incompatible perennials (Abberton 2007). Hybridization efforts within the perennials over many decades have been largely focused on *T. repens* and *T. pratense*.

Trifolium pratense (red clover) is a short-lived perennial legume (Table 1) of Mediterranean origin (Table 2). Its widespread use over the last millennia has led to the development of two generalized forms: an erect, open and early flowering form called 'Broad,' and a prostrate, dense and late-flowering form with more winter dormancy, known as 'Montgomery.' Red clover is an insect-pollinated outcrosser with some self-fertility and is generally associated with poor seed development. It is diploid ($2n = 14$). Hybridization with the objective of greater longevity has been attempted with numerous species, but it has only been achieved in terms of hybrid plants with *T. alpestre*, *T. diffusum*, *T. medium*, *T. pallidum* and *T. sarosiense* (Abberton 2007).

Trifolium repens (white clover) is a perennial legume (Table 1) of Mediterranean origin (Table 2). It has a prostrate growth habit with creeping stolons that root at the nodes. Flowering is profuse, and in seasonally dry regions it can behave as a free-seeding annual. White clover is an insect-pollinated outcrosser with limited self-fertility under high-temperature conditions. It is tetraploid ($2n = 4x = 42$), but, for most inherited characters, it behaves as a diploid. Breeding objectives include increasing cool-season growth, stem nematode resistance, leaf size for different grazing and soil fertility regimes, stolon density for persistence under close grazing, and tolerance of low soil phosphorus and drought (Caradus 1994). Close relatives include *T. ambiguum*, *T. uniflorum* and *T. occidentale*, with *T. semipilosum* being more distant. Hybridization has been undertaken with *T. nigrescens* for profuse flowering and resistance to clover cyst nematode, and with *T. ambiguum* for persistence, drought tolerance and biotic stress tolerance (Abberton 2007).

Trifolium resupinatum (Persian clover) is a prostrate annual legume (Table 1) of Mediterranean and Persian origin (Table 2). Abbasi (2008) identified a secondary gene pool comprised of *T. clusii* and wild *T. resupinatum* collections, and a tertiary gene pool of *T. fragiferum*. Persian clover is valued for its tolerance of waterlogged soils and lack of phytoestrogenic compounds (Stewart and Charlton 2003).

Trifolium subterraneum (sub clover) is a prostrate annual legume (Table 1) of Mediterranean origin, with a secondary center of diversity in Western Australia (Table 2). A key adaptive feature is the burial of seeds in burrs. There are three major subspecies, *subterraneum*, *yannicum* and *brachycalycinum*, which favor differing edaphic conditions. Sub clover is diploid ($2n = 16$) and dominantly inbreeding (Abdi et al. 2020). Characteristics important in breeding include flowering date (and associated seasonal growth pattern), growth habit, hard-seededness and embryo dormancy (Ghamkhar et al. 2012a). Leaf tissue contains three isoflavone compounds, which vary independently and have phytoestrogenic effects on sheep fertility (Abdi et al. 2020).

3.3 Crop symbionts

While outside the scope of this strategy, it is critical to note the role of symbionts in the effective use of many temperate forages. Two groups are of particular importance, and conservation of diversity in their germplasm is as important as conservation of the crop germplasm itself. In both cases, there is also a well-developed genetic improvement pathway through to commercial varieties.

The *Epichloë* and *Neotyphodium* fungal endophytes have co-evolved with *Lolium* and *Festuca* and have a major impact on their ecology through the production of secondary compounds that influence the herbivory of both invertebrate pests and vertebrate livestock. It has been suggested that this complex has supported the evolution of perennialism in *Lolium* (Cai et al. 2011). Endophytic diversity is another consideration for the importance of the conservation of *Lolium* and *Festuca* wild relatives. It is also a consideration in that the fungus is seed-borne, and thus represents a challenge to compliance with phytosanitary standards in the process of material transfer.

The *Rhizobium* legume symbionts have co-evolved with the *Fabaceae* and have a major impact on their ecology through biological nitrogen fixation in root nodules. Rhizobial diversity is another consideration for the importance of the conservation of legume wild relatives, as the symbiosis is often highly species specific. In many cases, the lack of effective nodulation limits the usefulness of the legume species. This can occur through a lack of effective rhizobial strains in soil or through infection with ineffective rhizobial strains (Friesen 2012).

From the perspective of *ex situ* germplasm conservation, the prevalence of these organisms also has implications for phytosanitary certification. This is particularly relevant to the endophytes, which are seed-borne “infections” likely to be impacted by sterilization treatment.

3.4 Other temperate forage taxa

In the online survey, genebank curators and users indicated 42 other taxa that they considered important as temperate forages (15 identified by genebank curators, 21 identified by genebank users, 6 identified by both; see Table 13 in Annex 9.3). These are dominantly grasses and legumes. The only forbs included were *Cichorium intybus* and *Plantago lanceolata* (included by the New Zealand genebank curator and user); subsequent discussion with other respondents indicated that forbs are generally not a major focus of activity. Ratings by the users indicated that 24 of the 27 additional species suggested were considered to be of global significance (i.e. relevant to multiple continents; Table 14 in Annex 9.3).

It is a reflection of the broad interest in the potential of a large number of “alternative species” for forages that many are not specifically covered by Annex I of the ITPGRFA. Based on global relevance (indicated in Table 14 in Annex 9.3) and collection activity (Table 15 in Annex 9.3), taxa that could be considered for future inclusion are *Bromus*, *Cichorium*, *Elymus*, additional

Medicago spp., *Plantago* and additional *Trifolium* spp.

The six species identified by both one curator and one user were *Cichorium intybus* L. (chicory), *Festuca pratensis* (now accepted as *Lolium pratensis* (Huds.) Darbysh. but still known as meadow fescue), *F. rubra* L. (red fescue), *Medicago polymorpha* L. (bur clover), *Phleum pratense* L. (timothy) and *Plantago lanceolata* L. (narrow-leaved plantain). In addition, three species were identified by more than one curator: *F. rubra* L., *Poa pratensis* L. (Kentucky bluegrass) and *Astragalus cicer* L. (milkvetch); and four species were identified by more than one user: *Agropyron cristatum* (L.) Gaertn. (crested wheatgrass), *Bromus riparius* Rehm (Asian meadow brome), the *Festulolium* hybrid and *Thinopyrum intermedium* (Host) Barkworth & D.R. Dewey (intermediate wheatgrass). On this basis, these 12 species may be considered as globally important and worth including in any future data-gathering exercises involving curators. Two curator respondents answered the question about additional taxa by giving names at the genus level, which included *Festuca*, *Elymus*, *Poa*, *Lolium* and *Trifolium*. All these genera are globally dispersed with large numbers of species.

The large number of additional species identified suggests that a broader assessment of the relative importance of various temperate forage species would be helpful. There are several potential approaches to this, aside from simply documenting the numbers of accessions in genebanks as an indicator of relative importance, as follows:

- Inclusion in reports of the European Working Group on Forages (Maggioni et al. 2000). During the 1990s, databases were divided by genus, and responsibility for them was allocated to various European partners. The databases covered *Agropyron*, *Agrostis*, *Arrhenatherum*, *Bromus*, *Dactylis*, *Festuca*, *Lathyrus*, *Lolium*, *Medicago*, *Phalaris*, *Phleum*, *Poa*, *Trifolium*, *Trisetum*, minor forage grasses and minor forage legumes.
- Research activity, for example the frequency of occurrence of species in the proceedings of the International Herbage Seed Group (2007, 2010, 2015, 2017, 2019). A wider literature search could possibly identify research activity based on frequency of occurrence and the locations of senior authors, but this would be a substantial exercise.
- Seed trade, for example based on data collected by the Danish Seed Council. These data from 1993-2006 were published in the proceedings of the International Herbage Seed Group (Aamlid et al. 2007), and it would be worth investigating whether the Danish Seed Council has continued to collect these data since 2007 and whether other temperate forage species have been included. Details are given in Table 16 (Annex 9.4).

From these various sources, it seems that global forage species could be categorized into broad activity groups. For example, four of the additional grass species appear to contribute strongly to global forage seed research and seed production: *Poa pratensis*, *Festuca rubra*, *Phleum pratense* and *F. pratensis*. This is consistent with their also being identified in the survey as additional species of significance. A second tier of species are in common use but do not dominate the sector (e.g. *Bromus*, annual *Medicago*, *Lotus* spp.), and a third tier might be considered to be of emerging or regional significance (e.g. *Festulolium* spp.). Although we attempted to capture this range in the initial sample set, limits had to be imposed on the initial survey to reduce the burden on respondents.

A categorization exercise such as this would lead naturally to the prioritization of activities within those categories, such as those indicated in the following.

- High-use species of known value. Such species would include those with large existing numbers of accessions in multiple genebanks. These are species where demand for development of forages has been historically high, and breeders already have a robust business case for the acquisition of more diversity and germplasm development. In terms of identifying and filling any remaining germplasm diversity gaps, it may be possible to rely on the efforts of individual organizations and focus mainly on data curation and incorporation into global databases.
- Emerging species of potential value. Such value likely lies in nonconventional traits, such as those associated with reducing environmental impact (as opposed to conventional traits such as productivity and nutritional value). These species typically have limited collection size and are restricted to fewer genebank collections, and the collections are poorly representative of natural diversity. In this case, support for new collection efforts in any location will be valuable.
- Underappreciated species of poorly known value. Such species are likely to be represented by very small and scattered collections. Further collection and characterization would be of lower priority, until scientific investigations of future trait-based benefits have uncovered a greater value proposition.

3.5 Centers of origin

Centers of origin and regions of domestication for the individual taxa in Table 1 are shown in Table 2. Most are centered on the Mediterranean and Eurasian regions. In particular, the *Lolium* and *Festuca* genera are believed to have originated in the Caucasus/Eurasia/Persia region (Zeven and Zhukovsky 1975), while the *Trifolium* genus has three centers of diversity

in the Mediterranean, Ethiopia and western North America, each proposed to be the center of origin by different authors (Zohary and Heller 1984). Most recently, Zohary (1972) holds that North America is the origin of the genus.

3.6 Uses

All the species in Table 1 are primarily used for livestock forage, except for *Hordeum spontaneum* (a barley wild relative primarily used in breeding) and *Lathyrus sativus* (used primarily for human consumption). In terms of nutritional value for livestock, characteristics such as dry matter digestibility, metabolizable energy content and crude protein content are priorities for selection and cultivar development across all temperate forages. In this respect, the legumes are typically superior and are therefore often used in binary grass/legume mixtures. Comprehensive forage value information for a number of species is available at www.feedipedia.org/.

Various species have several other uses, described in the following.

3.6.1 Crop support

The nitrogen fixation capability of legumes makes them widely useful as cover crops, intercrops and green manures for conventional arable crops (Morris and Greene 2001).

3.6.2 Biofuel

The high biomass accumulation rates and ease of harvest for temperate forage grasses make them good candidates for biofuel feedstock, although less so than tropical grasses. The potential use of temperate forages as biofuel would likely see different characteristics treated as priorities for germplasm conservation compared to forage use, such as cellulose, lignin and ash content of the tissue. Of the species in the sample set (Table 1), the following have been evaluated for biofuel: *Dactylis glomerata* and *Festuca arundinacea* (Godin et al. 2013), *Lolium multiflorum* (Yasuda et al. 2015), *Lolium perenne* (Farrar et al. 2012), *Medicago sativa* (Sanderson and Adler 2008; Godin et al. 2013) and *Onobrychis viciifolia* (Xiong et al. 2008). Other recognized temperate forage grasses that have also been considered include *Phalaris arundinacea* and *Tripsacum dactyloides* (Sanderson and Adler 2008; Varnero et al. 2018).

3.6.3 Amenity

Several of the grass taxa are of interest for amenity use (sports grounds, parks, airfields, lawns), although in general the desirable traits for amenity use are at

odds with those required for forage. Desirable traits for amenity use include a prostrate growth habit, fine leaves, slower growth rates and higher levels of secondary compounds that protect the plant against herbivory (including Endophyte associations). In many cases, other species within the same genera as those used for forage have been the focus of selection and cultivar development for amenity use; for example, *Festuca rubra* and *F. ovina* (turf) vs. *F. arundinacea* (forage). Of the species in the sample set (Table 1), *Lolium perenne* and *F. arundinacea* have been developed for amenity use (BSPB 2019). The amenity market is relatively large in Europe and the United States.

For the legumes, additional generic uses are noted in Table 3, sourced from ILDIS. Environmental uses include soil remediation, and medicinal uses include human dietary phytoestrogens (Morris and Greene 2001).

Some indication of the global extent of use for six of the species (*Dactylis glomerata*, *Festuca arundinacea*, *Lolium multiflorum*, *L. perenne*, *Trifolium pratense* and *T. repens*) in terms of seed quantity is given by the seed production data shown in Annex 9.4 (Danish Seed Council data, Aamlid et al. 2007). These data underscore these species' global significance as dominant temperate forages, alongside *Poa pratensis* and *Phleum pratense*. Note that these data also include seed production for species used extensively in amenity, such as *F. ovina*.

3.7 Genetic resources

3.7.1 Taxonomy

A search across online taxonomic resources (Annex 9.5) for the 11 genera represented in Table 1 was undertaken, and taxonomic lists of accepted names and synonyms were developed for the purpose of standardizing taxa in joint datasets, including data from [Genesys](#) and [WIEWS](#). These taxonomic lists are available in a [separate supplementary data file](#).

Challenges with taxonomy, particularly in relation to properly characterizing crop and wild relative diversity, emerged in the workshop discussions. The taxonomy of many temperate forages is subject to ongoing revision. Name changes make it difficult to identify unique accessions and duplicates both within and across genebank databases, in cases where accessions are only identified by the name assigned at the time of collection. The [GRIN-Global taxonomy](#) was generally regarded by curators as the benchmark that should be widely adopted.

3.7.2 Crop wild relatives

Some components of primary and secondary gene pools for each of the 15 sample species are identified in Table 4.

3.7.3 Core collections

Among the temperate forage genera included in the initial focal list (Table 1), the development of core collections (Brown 1989) has been reported for the following taxa, although the use of the term does not always appear to correspond to a strict definition: *Biserrula pelecinus* (Ghamkhar et al. 2012b, AUS), *Dactylis glomerata* (Lindner et al. 2000, ESP; Studnicki et al. 2013, CZE), *Festuca arundinacea* (Lou et al. 2015, CHN), *Hordeum* (van Hintum et al. 1990, global) *Lathyrus* (Shehadeh 2011, global) and *Lathyrus sativus* (Polignano et al. 2004, ITA), *Lolium* (Sackville Hamilton et al. 1998b, Europe), *Lotus japonicus* (Kai et al. 2010, JAP), *Lupinus angustifolius* (Chen et al. 2016), *Lupinus luteus* (Parra Gonzalez et al. 2010), *Medicago sativa* (Basigalup et al. 1995, USA), annual *Medicago* (Diwan

Table 3 Non-forage uses of legumes, including initial focal species and those nominated by curators and users (source: data from ILDIS, with specific references therein).

Species name	Non-forage uses
<i>Biserrula pelecinus</i> L.	Nil
<i>Lathyrus sativus</i> L.	Chemical products, Environmental, Food, Medicine
<i>Lotus corniculatus</i> L.	Environmental, Food
<i>Lupinus luteus</i> L.	Chemical products, Environmental
<i>Medicago sativa</i> L.	Chemical products, Environmental, Food, Medicine
<i>Medicago truncatula</i> Gaertn.	Nil
<i>Medicago polymorpha</i> L.	Environmental, Food, Medicine
<i>Medicago littoralis</i> Loisel.	Nil
<i>Onobrychis viciifolia</i> Scop.	Environmental
<i>Ornithopus compressus</i> L.	Environmental
<i>Trifolium alexandrinum</i> L.	Chemical products, Environmental
<i>Trifolium michelianum</i> Savi	Nil
<i>Trifolium pratense</i> L.	Domestic, Environmental, Food, Medicine
<i>Trifolium repens</i> L.	Chemical products, Domestic, Environmental, Food, Medicine
<i>Trifolium resupinatum</i> L.	Environmental, Food
<i>Trifolium subterraneum</i> L.	Environmental
<i>Trifolium vesiculosum</i> Savi	Environmental
<i>Vicia villosa</i> Roth	Environmental, Medicine

et al. 1994, USA), *Medicago truncatula* (Ellwood et al. 2006; Ronfort et al. 2006, global), *Trifolium pratense* (Dias et al. 2007, USA; Kouamé and Quesenberry 1993, global; Vymyslický et al. 2012, CZE), *T. repens* (Bortolini et al. 2006, USA; Vymyslický et al. 2010, CZE), *T. spumosum* (Ghamkhar et al. 2008, global) and *T. subterraneum* (Ghamkhar et al. 2015, global).

It has been suggested that core collections may not capture the required variation in traits, particularly rare and adaptive traits. An alternative trait-based sub-setting approach is the Focused Identification of Germplasm Strategy (FIGS), which is based on the assumption of correspondence between the distribution of taxonomy and adaptive traits of interest (Mackay and Street 2004). The FIGS approach has also been applied to *Lathyrus* (Shehadeh 2011).

3.7.4 Diversity trees

Diversity trees are a means of representing the overall structure of within-crop diversity. The trees are created by dividing the crop gene pool in a hierarchical manner based on various factors, including taxonomy, related gene pools (1°, 2°, 3°), cultivated varieties, landraces and geographic ecotypes (van Treuren et al. 2009). The structure of these trees is based on both published information and consultation with experts. Among the genera represented in the sample set (Table 1), diversity trees for grasspea and alfalfa are

available in Genesys on the corresponding crop pages. In addition, *Hordeum spontaneum* is included in the existing barley diversity tree as a wild relative (*Hordeum vulgare* ssp. *Spontaneum*).

To develop diversity trees for temperate forages, a crop species-based approach would necessarily involve numerous individual trees for the various significant forages in Table 1 and Table 13 (Annex 9.3). An alternative approach could focus on genera groups, among which *Trifolium* and *Lolium-Festuca* would deserve priority attention, given their significance in the temperate forage sector and the importance of interspecific crosses in germplasm development (Table 4). A potential structure for *Trifolium* is offered in Figure 7 (Annex 9.6). The initial division into cultivated and wild relatives could be based on those species for which cultivars have been developed, with some recognition of those close relatives already in use, as distinct from other intrageneric species. Deeper divisions by “crop type” (*sensu* van Treuren et al. 2009) would need to reflect those traits for which selection has been a priority in the past (Table 5) or might be in the future. Such traits typically include timing of maturity, growth habit, forage quality and ploidy level.

3.7.5 Cultivated species

All species in the sample set (Table 1) are cultivated for both forage and seed production. Global estimates

Table 4 Summary of components of primary and secondary gene pools for species in the sample set. ¹Ploidy levels: D = diploid, T = tetraploid, H = hexaploid, O = octoploid, Dd = dodecaploid, A = aneuploid; natural ploidy in bold; ² bracketed number = Intra-specifics, regarded as synonyms (POTW); ³ *Biserrula* has been included in the genus *Astragalus*.

Species name	Primary		Secondary	
	Ploidy	Number of sub-taxa	Intra-genera crosses	Number of species within genus
<i>Biserrula pelecinus</i> L.	D	1		2 (<i>Biserrula</i>) 534 (<i>Astragalus</i>) ³
<i>Dactylis glomerata</i> L.	D,T,H ¹	22		2
<i>Festuca arundinacea</i> Schreb.	T,H,O,Dd	2		650
<i>Hordeum spontaneum</i> K.Koch	D	0 (2) ²	<i>H. vulgare</i> , <i>H. bulbosum</i>	39
<i>Lathyrus sativus</i> L.	D	0 (11) ²	<i>L. cicero</i> , <i>L. amphicaropus</i>	182
<i>Lolium multiflorum</i> Lam.	D,T	0 (3) ²		27
<i>Lolium perenne</i> L.	D,T,A	0 (9) ²	<i>L. rigidum</i>	27
<i>Lotus corniculatus</i> L.	T	6		123
<i>Lupinus luteus</i> L.	D	0		615
<i>Medicago sativa</i> L.	D,T	3	<i>O. viciifolia</i>	89
<i>Onobrychis viciifolia</i>	D,T,A	0 (1) ²		192
<i>Trifolium pratense</i> L.	D,T	1	<i>T. sariosense</i> , <i>T. medium</i> , <i>T. alpestre</i> , <i>T. ambiguum</i> , <i>T. diffusum</i>	284
<i>Trifolium repens</i> L.	D,T	2	<i>T. ambiguum</i> , <i>T. occidentale</i> <i>T. nigrescens</i> , <i>T. uniflorum</i>	284
<i>Trifolium resupinatum</i> L.	D,A	2		284
<i>Trifolium subterraneum</i> L.	D	3		284

of seed production quantities for a number of these are given in Annex 9.4.

3.7.6 Landraces, varieties and cultivars

All species included in the sample list have at least one commercial cultivar, and some have up to hundreds of cultivars (e.g. *Trifolium repens*, *Lolium perenne*). In the latter case, many cultivars are no longer commercially produced, as they have been superseded by more recent releases. A partial list of cultivars and their country of origin, based on a brief online search as a starting point, is provided in a [separate supplementary data file](#). The degree to which the suite of developed cultivars represents the diversity within a species could be analyzed in two ways: 1) by comparing the origins of genetic material used to develop cultivars with the native range of those species; or 2) by comparing the range in traits expressed in cultivars with the range in traits across all accessions of the species (e.g. flowering date, although this is likely to be quite difficult given the lack of data on relevant traits for all accessions). Table 5 provides a list of traits and characteristics selected for cultivars (this list should be considered incomplete).

The substantive role of the commercial sector in the development of temperate forage germplasm presents some challenges for forage germplasm conservation. There has been a long-term shift in cultivar development from governmental organizations to private companies (Williams et al. 2007; Nichols et al. 2012), which themselves have merged into multinational organizations (e.g. Barenbrug, DLF). They hold germ-

plasm collections that may not be publicly accessible under the terms of the ITPGRFA's Multilateral System (MLS), since the MLS agreement is between member states. One survey respondent, a plant breeder, reported that their use of genebank-derived germplasm had declined, due to a focus on crossing within elite material to avoid losing genetic gain for valued traits (e.g. yield). Genebank curators cited examples of local negative reaction to foreign entities collecting plants, and one raised a concern about the retention of older cultivar material once commercial entities had ceased production and distribution.

3.8 Major vulnerabilities and threats

There are several major sources of vulnerability for temperate forages that may lead to local extirpation of taxa in centers of diversity or to the inability to access those areas for collection of germplasm:

- Climate change: movement of the temperate zone (Zhang et al. 2017), leading to reductions in species' abundance (Epstein et al. 2002).
- Development: overgrazing, land-use change patterns such as urbanization, cultivation and afforestation. This is occurring in both developed and developing nations.
- Biosecurity failure: competition from exotic adventive weeds, introduction of pests and diseases.
- Political disputes: conflict zones present a safety risk to potential collectors.
- Administrative obstacles: inability to carry out collection activities due to a lack of local approval roles or processes.

Table 5 Cultivar traits or characteristics of interest, and their numbers, for the sample set.

Species name	Traits (other than yield)	Number of cultivars found ¹
<i>Biserrula pelecinus</i> L.	Flowering date	2
<i>Dactylis glomerata</i> L.	Tiller density, growth habit	58
<i>Festuca arundinacea</i> Schreb.	Winter activity, flowering date, summer dormancy	18
<i>Hordeum spontaneum</i> K.Koch	Salinity tolerance, disease resistance	2
<i>Lathyrus sativus</i> L.	ODAP content	6
<i>Lolium multiflorum</i> Lam.	Flowering date, ploidy	23
<i>Lolium perenne</i> L.	Flowering date, ploidy, water soluble carbohydrate, aftermath heading, tiller density, rhizomatous growth	99
<i>Lotus corniculatus</i> L.	Growth habit, winter hardiness	14
<i>Lupinus luteus</i> L.	Alkaloid content, shattering level	6
<i>Medicago sativa</i> L.	Disease resistance, drought resistance, salt tolerance	60
<i>Onobrychis viciifolia</i> Scop.	Flowering date, winter hardiness, seed yield	18
<i>Trifolium pratense</i> L.	Disease resistance, persistence	55
<i>Trifolium repens</i> L.	Leaf size, winter activity, summer dormancy, flowering date, seed production, growth habit, stolon density	254
<i>Trifolium resupinatum</i> L.	Leaf size, hard-seededness, flowering date, growth habit	8
<i>Trifolium subterraneum</i> L.	Leaf size, flowering date, hard-seededness, phytoestrogen content, growth habit, leaf marking	38

¹ Minimum numbers; lists are incomplete due to time constraints

These threats probably apply to all genetic diversity conservation efforts. Global maps of some of these threats are increasingly becoming available and can be used in conjunction with spatial data on centers of diversity for specific taxa to identify priorities for future collection missions.

3.9 Key observations on temperate forages

Characteristics of the temperate forage taxa as a group that make them distinct from other “crops” include the following:

- There are a wide range of taxa, potentially thousands of species and subordinate taxa, dominated by Poaceae and Fabaceae. Within these families, a small number of genera dominate global use: *Bromus*, *Dactylis*, *Festuca*, *Lolium*, *Phleum* and *Poa* within the grasses; and *Medicago* and *Trifolium* within the legumes.
- A second, more diverse tier of genera within grasses and legumes are regionally relevant, with multiple cultivars being developed: *Agrostis*, *Elymus*, *Holcus*, *Phalaris*, *Thinopyrum* (grasses); *Biserrula*, *Hedysarum*, *Lotus*, *Lupinus*, *Melilotus*, *Onobrychis*, *Ornithopus*, *Vicia* (legumes).
- There is limited use of non-legume dicot species from other families (notably *Cichorium intybus* and *Plantago lanceolata* and annual crops from *Beta* and *Brassica*).
- Taxonomic revision is ongoing and impacts some of the significant temperate forage taxa, such as *Lolium/Festuca*, *Astragalus/Biserrula* and *Hedysarum/Onobrychis*. This creates difficulties in identifying duplications within and across collections.

- Fungal and microbial symbionts support the effective use of temperate forages, principally endophytic fungi and nitrogen-fixing rhizobia.
- Many species have multiple uses beyond livestock forage, including Biomedical uses, biofuels, soil conservation, ecological restoration and crop support. Many crop wild relatives are used in the amenity sector (e.g. sports turf), among them genera such as *Agrostis*, *Festuca*, *Lolium* and *Poa*.
- “High-income nations” have a century-long history of extensive collection of mainly grasses and legumes, focused on centers of origin in the Mediterranean and Eurasian regions.
- There is a strong cultivar development industry, supported by established legislation to protect rights to plant varieties. From the middle of the 20th century, cultivar development was mainly undertaken by government agricultural agencies, but cultivar development is now dominated by commercial entities.
- Interest is emerging in the conservation of native rangeland species in both North and South America. The focus is mainly on ecosystem restoration, but future forage value is a consideration.

These key observations suggest that considerable work is needed in terms of prioritizing species for global collaborative efforts. Clearly, there is insufficient global capacity to assess the *ex situ* conservation status and determine priority needs for securing the genetic diversity of all temperate forage taxa. Therefore, some form of categorization and prioritization process is needed as a precursor to this work, which is suggested as the first strategic action in this global strategy.



Medicago sativa L. subsp. *varia* accession in Australian Pastures Genebank. Photo: Michael Major for Crop Trust

4 EX SITU CONSERVATION STATUS

4.1 Genebank collections

Searches within the Genesys (www.genesys-pgr.org) and FAO-WIEWS (www.fao.org/wiews) databases for accession information on the taxa in the initial sample set were conducted at the genus level, on the basis of the taxa standardization. Three extra genera were included because of relatedness to the sample set genera through taxonomic revision: *Astragalus* (crossover with *Biserrula*), *Bromus* (crossover with *Lolium* and *Festuca*) and *Hedysarum* (crossover with *Onobrychis*). *Hordeum* was excluded, having been considered in a previous strategy. Unique accessions were filtered where passport data enabled identification of duplicates¹. Thus, 11 genera were included in the search, which encompassed 1,534 individual taxa. Of interest were the holdings by genebank and by country of origin. At the genus level, a total of 166 entities across 74 countries held material (Figure 2; Table 17 in Annex 9.7), with between 38 and 62 countries holding material for individual genera (Table 6). A similar small grouping of 12 countries tend to hold the majority of accessions for individual genera across all genera (AUS, USA, RUS, GBR, LBN, NZL, DEU, ESP, JPN, POL,

¹DONORNUMB and DONORCODE information from passport data were used to identify duplicates. In most cases, it is not possible to identify duplicates from passport data as the DONORNUMB and DONORCODE are often not recorded.

ITA, CHL; Table 6). It should be noted that, of this core list of countries, the online survey did not include any responses from Russia, Great Britain or Italy, which were identified in Figure 2 as significant participants in the temperate forage germplasm sector (see also Annex 9.7). These search data indicate that an estimated 80% of accessions are held by 19 genebanks in 16 countries.

It is also worth noting that some of the countries identified in Table 17 (Annex 9.7) as holding temperate forage germplasm are not signatories to the ITPGRFA. These countries include Azerbaijan, Belarus, Bosnia and Herzegovina, Colombia, Israel, Macedonia, Mexico, Russia, Taiwan and Ukraine. Of these, Russia and Ukraine hold 5.9% and 1.7% of the accessions in the 11 genera, respectively, while the others each hold less than 0.3%. China is another significant non-signatory to the treaty, but an independent search of the accessible forage genebank online resource for the Chinese Academy of Agricultural Sciences (www.cgris.net) indicated that they hold only a small number of temperate forage accessions.

At the taxon level, there is also a high level of skewness in the number of accessions held. Sixty-seven species comprise 80% of the total number of accessions, and 12 species comprise 50% of the total acces-

sions (*Lolium perenne*, *Dactylis glomerata*, *Trifolium pratense*, *Lathyrus sativus*, *Medicago sativa*, *T. repens*, *Medicago truncatula*, *Festuca arundinacea*, *F.*, *Lupinus albus*, *T. subterraneum* and *Lupinus angustifolius*). Within each genus in Table 6, there was also a high level of skewness in the taxonomic distribution of accession numbers. For most genera, between one and seven taxa represented 80% of the accessions. The more balanced genera included *Astragalus* (41 taxa), *Trifolium* (25 taxa), *Bromus* (19 taxa) and *Medicago* (17 taxa).

For individual genera, a very large proportion of material (10–40%) had no record of country of origin in these databases (on average 25% across all taxa). Each genus also had a number of accessions identified only by genus name (“spp.” Or “hybr.”). For most genera, this was 4% or less; it was much higher for *Astragalus*, *Bromus* and *Onobrychis*.

Data from the curator survey indicated that the proportion of the surveyed genebanks’ accessions that were temperate forage species varied from 3% to 100%. Curators were asked to categorize their sample species collections, as an indicator of collection strength distinct from numbers, into: a) a whole collection of diverse geographic origins; b) a core collection; c) a subset collection of restricted origin; and

d) a small incidental collection. These categories were assigned rank scores (4, 3, 2 and 1, respectively) and the rankings were tallied to get an indication of the overall strength of global collections for those species in the sample set.

Four of the species in the sample set were well represented in many genebanks (12 or 13), with high collection strength scores and large numbers of accessions: *Medicago sativa*, *Trifolium pratense*, *T. repens* and *Lolium perenne* (Table 7). Note that the accession numbers for the latter two species are strongly influenced by very large collections in New Zealand (>28,000). Other species varied in terms of these indicators. For example, *Dactylis glomerata*, *Lotus corniculatus*, *Lolium multiflorum* and *Onobrychis viciifolia* were all present in 10–11 collections but varied by size and strength of those collections. *Hordeum spontaneum* and *Trifolium subterraneum* were present in fewer collections (8–9) but had more “whole collections of diverse origin” (3 and 4, respectively).

Curators were also asked to indicate collection activity, in terms of whether their collections of species in the sample set were expanding, whether users were requesting accessions and whether they were gathering genotypic or phenotypic data. Positive responses were tallied across respondents for individual species

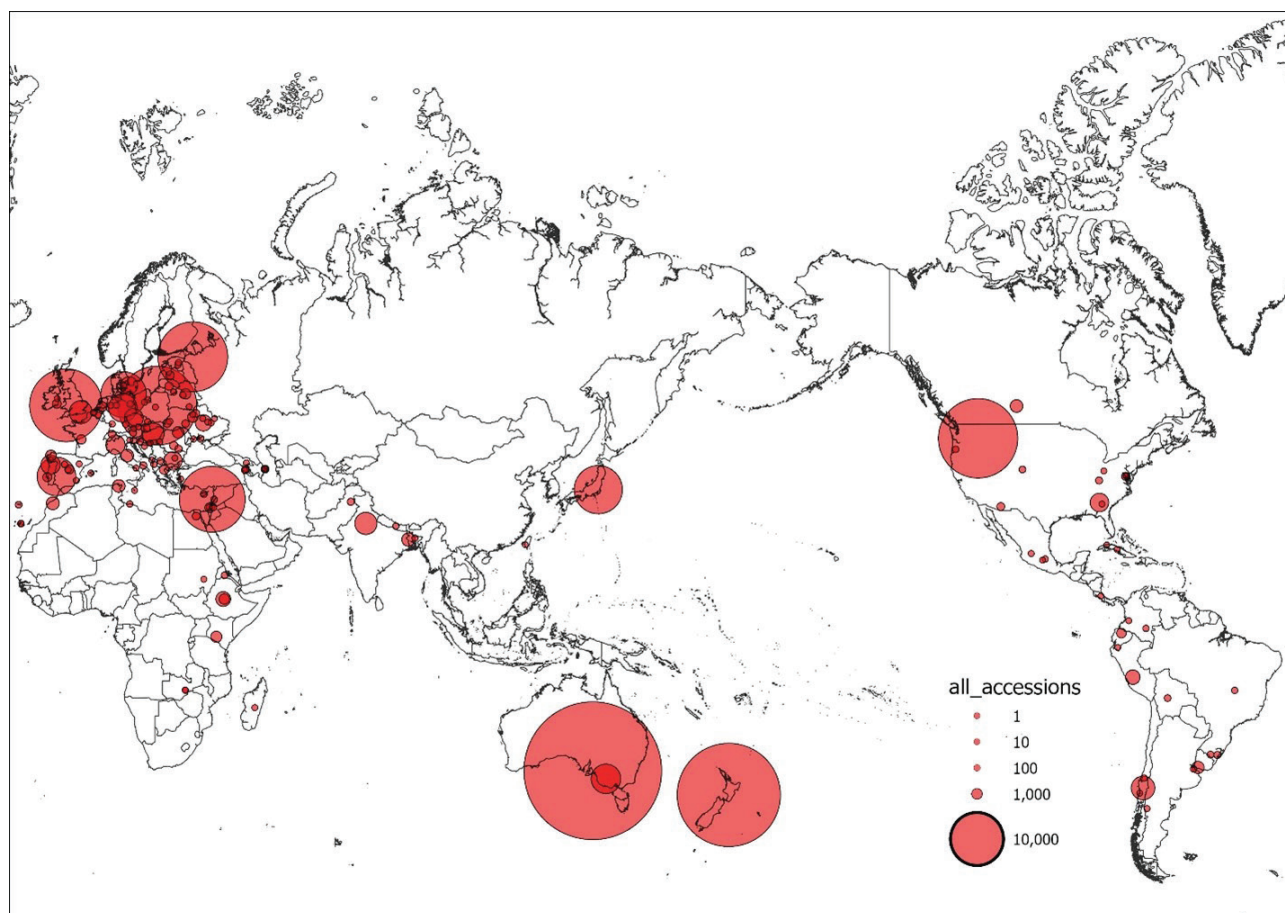


Figure 2 Locations of temperate forage genebanks and relative collection size, based on a Genesys/WIEWS search on the sample set of 11 genera.

(Table 7). *Medicago sativa* stood out as consistently the most active temperate forage, while *Trifolium pratense*, *Dactylis glomerata*, *T. subterraneum* and *Lolium perenne* also had relatively high levels of global activity.

Among the other taxa that curators and users identified as being important temperate forages, other species of *Trifolium*, *Festuca* and *Lolium* featured in multiple genebanks with high accession numbers (Table 15 in Annex 9.3). The two annual *Medicago* species had high accession numbers in the Australian genebank. Other notable grass genera included *Poa*, *Elymus* and *Phleum*, while other notable legume genera included *Vicia* and *Astragalus*.

4.2 Genebank structure and management

Planning: Twelve of the respondents cited a planning or policy document that guides management of their associated genebank, although only nine documents were specifically named and only seven were available online (summarized in Annex 9.8). Three respondents indicated that their genebank did not operate under

a national policy, although in the case of ICARDA (Lebanon), a national policy is not strictly relevant to this multinational organization, and ICARDA's planning documentation is readily found online (Annex 9.8). Planning and policy documents are important in establishing national priorities, which are not likely to be undermined by the sort of international collaborative efforts proposed in this strategy. Rather, the documents provide a basis for the alignment of goals that a global strategy can build on. Common elements across national policies include the following:

- Long-term security of diverse germplasm, including the maintenance of health, viability and seed resources through regeneration, as well as safety backup duplication.
- Importance of robust identity, passport and characterization data.
- Provision of managed but ready access to germplasm and associated data.
- Research and development of more effective and efficient processes and methods.
- Mandate for expansion of collection through acquisition.
- Support for germplasm use by researchers, breeders, producers etc.

Table 6 Global database accession search by sample list genera, in order of total accession numbers.

Genus name	Count of taxa ¹	Total accessions	Number of taxa comprising 80% of accessions	% unknown origin	% taxa not identified to spp.	Number of countries holding accessions	Countries holding 80% of accessions
<i>Trifolium</i>	305	82,728	25	23	2	62	AUS, NZL, GBR, USA, LBN, RUS, ESP, ITA, DEU
<i>Medicago</i>	109	78,800	17	10	1	59	AUS, LBN, USA, RUS, MAR, FRA, GBR, ITA, JPN
<i>Lolium</i>	16	27,633	2	40	2	52	GBR, NZL, DEU, POL, JPN, USA, AUS, RUS, CZE, ITA
<i>Lupinus</i>	144	26,099	5	22	4	52	AUS, DEU, RUS, ESP, USA, PRT, PER, UKR, CHL, POL
<i>Festuca</i>	205	25,612	3	31	2	47	POL, JPN, USA, DEU, AUS, RUS, NZL, GBR, SWE
<i>Lathyrus</i>	115	22,279	6	18	2	57	LBN, IND, CHL, BGD, GBR, AUS, UKR, RUS, USA, ETH, DEU
<i>Dactylis</i>	21	21,253	1	24	1	50	POL, JPN, DEU, USA, NZL, RUS, GBR, AUS, ESP
<i>Biserrula/Astragalus</i>	495	6,076	41	12	8	40	AUS, USA, LBN, GBR, ESP, JPN, NZL, RUS
<i>Bromus</i>	101	5,878	19	38	17	41	USA, NZL, CHL, AUS, DEU, CAN, GBR, HUN, URU
<i>Onobrychis</i>	83	4,084	7	16	8	38	LBN, RUS, USA, AUS, GBR, NZL, ITA
<i>Hedysarum</i>	58	1,179	4	12	4	21	AUS, TUN, USA, NZL, LBN, ITA

¹ Including taxa identified only to genera (e.g. *Trifolium* spp.) or as hybrids (e.g. *Medicago* hybr.)

Global collaboration is typically implied rather than consistently mandated in these guiding documents.

Influence: Ten of the respondents indicated that the curator had the greatest influence over the activity of their genebank, with four other genebanks mainly influenced by a parent organization (government agencies in all cases) and another genebank managed by a governing committee. All of the genebanks were subject to the terms of the ITPGRFA, with 12 of those holding material that has been or is being assigned to the Multilateral System (MLS). Two genebank respondents indicated that their genebank material was not assigned to the MLS.

Objectives: Long-term conservation was a high priority for all of the genebanks, maintaining breeding collections was a high priority for nine of the genebanks and maintaining a reference (research) collection was a high priority for four of the genebanks. Other priorities specifically noted included passport and data management, acquisition, germplasm distribution and holding collections of associated microorganisms.

4.3 Regeneration status

In their survey responses, three of the genebanks specifically noted difficulties with carrying out regeneration, although the details varied: technical challenges for nonconventional taxa that require specific methods for pollination, germination and establishment; a lack

of the effective equipment required; and insufficient human resources. Two of these genebanks used long-term collaborative arrangements to assist regeneration.

Low capacity for regeneration emerged as a strong and consistent theme in all four online workshops. This was generally attributed to insufficient human resources (effectively budgetary constraints), but also, in some cases, to insufficient land area (particularly for effectively isolating the numerous outcrossing species) and to technical difficulties with less well-known forage species. It was noted that low capacity for regeneration was one of the factors that contributes to reduced collection activity and to limited enthusiasm for growing the forage collection. The reason is that increases in collections tend to create an obligation to eventually add the new accessions to the priority list for regeneration, and a number of curators felt they were already behind in their plans to work systematically through their collections.

An associated issue that emerged from the online consultation workshops, conducted as part of developing this document, was uncertainty about the need to regenerate all existing accessions, given an awareness that the current forage collections contained an unquantified level of duplication (note that this is distinct from documented safety backup). Identifying redundant duplication was seen as a cost-effective means of reducing the regeneration burden and freeing up human capacity for other priority tasks.

Table 7 Relative size and activity of the collections of sample list species across 16 genebanks (curator survey responses), in order of total number of accessions.

Species name	Number of genebanks with accessions	Relative collection strength ¹ (max=64)	Total accessions ²	Expanding collection (max=16)	Regular requests (max=16)	Gathering data (max=16)
<i>Lolium perenne</i> L.	12	24	35,998	5	4	6
<i>Trifolium repens</i> L.	13	31	30,872	3	5	5
<i>Trifolium subterraneum</i> L.	8	21	14,092	5	5	5
<i>Festuca arundinacea</i> Schreb.	9	19	13,567	3	4	5
<i>Medicago sativa</i> L.	13	36	13,293	7	8	8
<i>Dactylis glomerata</i> L.	11	22	13,191	5	4	7
<i>Trifolium pratense</i> L.	13	31	10,060	4	5	5
<i>Hordeum spontaneum</i> K.Koch	5	14	6,845	2	4	3
<i>Lolium multiflorum</i> Lam.	11	20	6,101	2	4	6
<i>Lotus corniculatus</i> L.	10	25	3,691	2	3	4
<i>Lathyrus sativus</i> L.	6	14	3,207	2	3	4
<i>Trifolium resupinatum</i> L.	9	16	1,437	4	3	4
<i>Lupinus luteus</i> L.	7	16	1,333	1	1	4
<i>Onobrychis viciifolia</i> Scop.	10	15	793	1	4	4
<i>Biserrula pelecinus</i> L.	6	9	733	2	0	4

¹ The survey used four categories, with a score assigned to each category: a) whole collection of diverse geographic origins (score 4); b) core collection (score 3); c) subset collection of restricted origin (score 2); d) small incidental collection (score 1). No respondent indicated a core collection for any species.

² From 15 genebanks, as one of the respondents did not provide this information.

Curators particularly pointed out that redundant duplication should not be a basis for eliminating accessions from genebanks.

4.4 Characterization status

Approximately half of the surveyed genebanks were undertaking some level of characterization activity, although the nature of this work varied greatly between genebanks (Table 8). All users were undertaking some form of characterization. All six types of germplasm characterization activity were more common among the genebank users than the curators. The most common characterization activities are phenotyping for highly heritable traits that aid in taxonomic identity, genetic diversity assessment and screening for abiotic stress. The discussion in one workshop revealed a general lack of characterization data, which are needed to enable a deeper understanding of the collections and support prioritization efforts and the development of core collections. Given the apparently greater level of characterization activity within the user group, it would be worthwhile exploring to what degree these users provide characterization data back to genebank curators to support collaborative efforts to rationalize collections. However, one curator noted that additional work was often required to align such data with the structure of genebank databases.

The pests and diseases that were named under screening for biotic stresses include a wide range of fungal (leaf rust) and bacterial (root and crown rots) pathogens, as well as aphids, nematodes and mites. The common stresses noted under screening for abiotic stresses include drought (21 respondents), cold and/or freezing (13 respondents), salinity (11 respondents), heat (6 respondents), waterlogging (2 respondents) and low soil fertility (2 respondents).

The workshop discussions consistently revealed a widespread desire to undertake more characterization work, to better understand diversity and to support pre-breeding and the development of core collections. The development of more cost-effective methods would be of widespread interest, particularly with regard to molecular work and phenomics. There may be opportunities for specialist facilities in particular countries, if germplasm exchange limitations can be overcome (Section 4.6).

4.5 Crop descriptors

The lack of globally consistent standard descriptor lists for temperate forages was identified in multiple workshops. Generic descriptor lists do exist for legumes (IBPGR 1984) and grasses (IBPGR 1985), and a number of crop-specific lists have been in use for many decades (e.g. by ICARDA, which uses them for *Lathyrus*, *Medicago* and *Trifolium* and has supplied them to Genesys). It was noted that many range and forage species are not covered by descriptor lists; for those that are, the lists need updating to account for new characterization methods. A key issue is gaining collective agreement on a minimum descriptor set for any given species, since it is likely that most genebanks will not have the capacity to collect the data to populate comprehensive descriptor lists. Guidance for the development of crop descriptor lists has been provided by Bioversity International (2007).

4.6 Phytosanitary status

Among curators who responded to the survey, only six were fully confident that the health status of their collections was adequate for distribution, and eight considered that they had adequate procedures in place for phytosanitary certification. This issue also emerged in the workshops, with one curator noting

Table 8 Tally and percentage of genebank curators (total 15) and users (total 17) undertaking characterization activities, underway and planned, among those who provided this information in the survey.

Characteristic	Respondent	Activity underway (Percentage of total)	Activity planned
Phenotyping	Curator	8 (53%)	0
	User	15 (88%)	2
Abiotic stresses	Curator	8 (53%)	0
	User	13 (77%)	2
Marker studies	Curator	6 (40%)	0
	User	12 (71%)	1
Genotyping	Curator	5 (33%)	1
	User	14 (82%)	2
Biotic stresses	Curator	8 (53%)	0
	User	10 (59%)	2
Phenomics	Curator	2 (13%)	0
	User	7 (41%)	4

that some genebanks they interacted with appeared to be unaware of the requirement for certification. There was general agreement that the Nagoya protocol and individual countries' internal biosecurity standards were inhibiting distribution of germplasm, through both increased strictness of importation standards and the inability of source genebanks to supply adequate certification to meet those standards. This was particularly problematic when researchers were looking to access material for characterization in the development of core collections.

4.7 Storage facilities

All genebanks had long-term cool-store facilities held at temperatures of -18 or -20 °C (base storage), but with relative humidity (RH) varying from 5% to 20%, with three facilities not controlling for RH%. Most used aluminum foil as packaging material, with one using plastic, one glass and one paper. Twelve genebanks also had "active" or "medium-term" storage facilities, most held at temperatures of 0–5 °C (one at 15 °C), again with the RH% varying across genebanks. These facilities had greater variation in packaging materials, which included foil, paper, plastic, cloth and glass. Only one genebank indicated that it held other plant tissue types. Based on the survey results across all the genebanks, the fundamental infrastructure required to securely store germplasm seemed to be well placed.

4.8 Safety duplication status

Nine genebanks had full collection duplications of some species at backup facilities, and one had core collection backup. Seven genebanks named the Svalbard Global Seed Vault as one of the backup facilities. Apart from using Svalbard, three genebanks used facilities in other countries, four in other cities and one in a separate building. The survey did not explore the reasons why four of the genebanks had no separate duplicate backup facilities, but this is an obvious way in which genebanks can support one another via global networks.

4.9 Collecting activities

Collections of many temperate forage species are expanding (see Table 8); among the species in the sample list, seven genebanks had at least one collection expanding. However, the expansion is not necessarily the result of collection activities, as some genebank curators reported new germplasm as coming from other genebank or user donations (e.g. private breeding material). There was consensus that the level of collection activity has declined in recent decades, with the following reasons suggested:

- Restrictions to access in certain countries.
- Reduced investment by government and commercial funding sources.
- An inability to identify officials with the authority to approve collection activities in some countries.
- Increasing strictness of phytosanitary and biosecurity standards.
- Lack of human resource capacity to store and regenerate new accessions.
- Local community resistance to international collectors.
- Already well-represented collections from historical acquisition.

A number of countries are refocusing their collection activities domestically, to give more priority to indigenous grassland species with a role in ecosystem restoration or potential as forages (e.g. South America, USA; Barga et al. 2020), or to use naturalized exotic species that have persisted in local environments and therefore represent well-adapted germplasm (e.g. New Zealand).

For those collection activities that are still occurring, it was recognized that a lack of global awareness of the location and timing of those activities may well be leading to duplicated search efforts. One benefit of a global network could be a database of past and planned activities. This was previously documented in Maggioni et al. (2000) for the ECPGR Forages Working Group.

4.10 Major constraints to genebank operations

In the online survey, curators were asked to identify up to five limitations they were facing. Ten of the respondents identified staff capability (i.e. skills and knowledge) and/or capacity limitations, with several linking the low capacity to the issue of insufficient financial support. Characterization capacity was an issue for seven respondents, although the specific needs varied, and included constraints on their ability to undertake either genetic, phenotypic, population or molecular data collection. Regeneration capacity and capability was an issue for six respondents, who particularly noted the challenges with wild relatives and native species. Biosecurity issues were also noted by several respondents, although the specifics varied, and included contamination by genetically engineered material, onerous regulations and isolation limitations. Other issues that were unique to each respondent included: public awareness, ineffective or outdated equipment, lack of duplication, challenges in identifying duplicates, multiple stakeholder reporting requirements, supply of new germplasm, seed viability testing capacity, limited accession backup and limited

long-term storage capacity. Implementation of the Nagoya protocol was noted in additional comments as restricting collection activity.

Curators were also asked to identify up to five areas where their collection was performing well; the responses are specific to their situation, rather than serving as comments on global interactions. However, one of the most commonly noted strengths was in the area of collaboration, in terms of other genebanks, breeders, researchers and farmers. Equally commonly cited was their efficiency in operation and basic procedures (e.g. documentation, use of technology and germplasm distribution), aligned with the value of modern online database information resources and the quality of their facilities. Genetic resource availability, staff capability and seed quality were mentioned by more than one respondent. Other comments specific to individual respondents included the supply of new germplasm, the products of germplasm development and associated characterization data.

4.11 Overall status of collections

In the online survey, curators were asked to indicate the status of their temperate forage germplasm collection according to some core genebank functions, as Improving/Increasing, Stable or Regressing/Declining. The results from the 13 responses are summarized in Figure 3. "User access to accession information," "Genetic variability in the collection" and "Phytosanitary standards" were rated by every respondent as

stable or improving. By contrast, "Staff retention and recruitment" were rated by every respondent as declining or stable. "Resources for expansion of the collection" and "Regeneration" were two areas that also had a high proportion of respondents indicating a worsening situation (>30%).

In the online survey, users were asked to rank the severity of several potential issues arising in their interactions with genebanks, from high impact to no impact. The results from the 17 responses are summarized in Figure 4. The most significant issue was lack of metadata associated with accessions, which had at least some impact on all user respondents. Other medium- or high-impact issues for at least 70% of users included the inhibition of material exchange by phytosanitary standards, poor access to information about relevant genebanks and poor representation of genetic diversity within genebank collections. Less problematic were the responsiveness of curators and the utility of databases. Only one additional issue was raised by a single respondent, namely, the need for global standardization of scales used for trait measurements (e.g. disease impact, dormancy and flowering).

Users were also asked to identify positive aspects of their interactions with genebanks. Their free-text responses were manually categorized. Perhaps unsurprisingly, the most frequently mentioned benefit was access to genetic diversity, with a couple of respondents noting the value of access to specific geno-

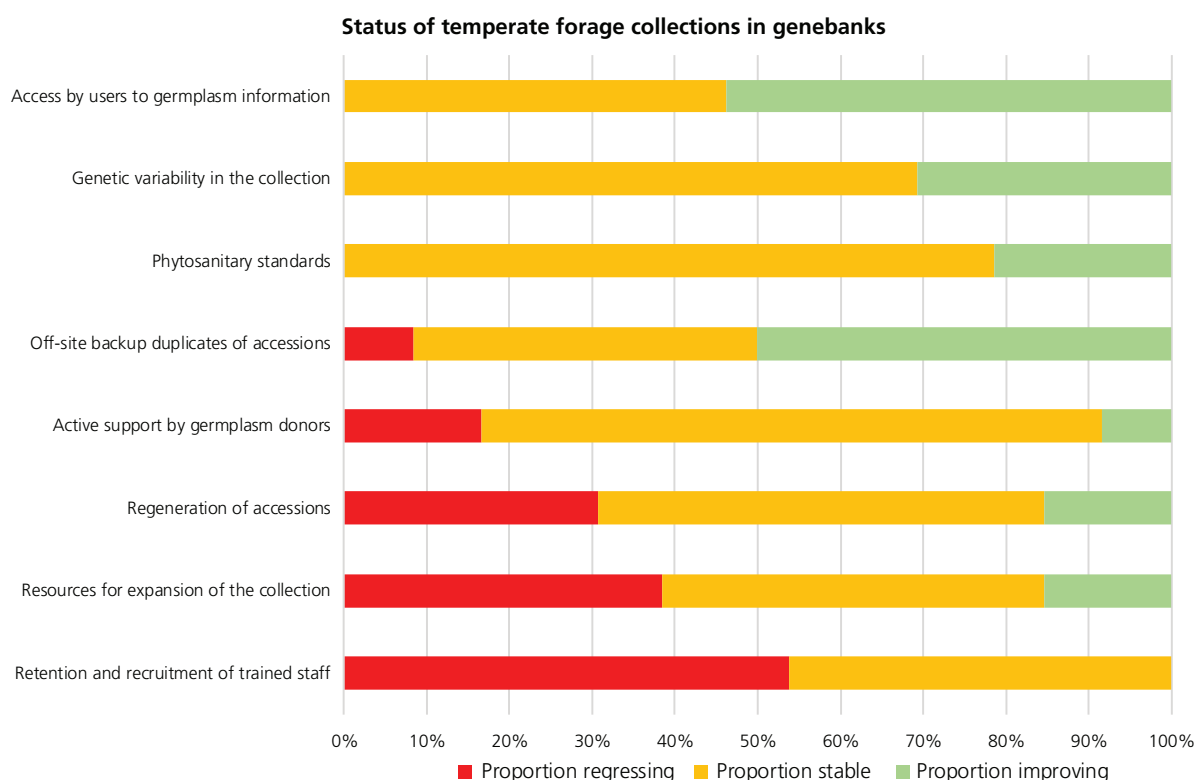


Figure 3 Genebank curators' assessments of the status of their collections across eight core genebank functions.

types or traits. The responsiveness of genebank staff was also often noted, including mention of specific individual curators. Their knowledge and willingness for collaboration were mentioned in a few cases. The availability of associated data was also mentioned by a few respondents. Aspects that were only noted by one or two respondents included seed quality, characterization data and growth in the collections.

4.12 Documentation and information sharing

4.12.1 Data platforms

Twelve of the genebanks have fully electronic information systems to manage accessions and two have a partly electronic system. Four use GRIN-Global (including the curator tool). Three use Microsoft Access and one uses Oracle, as the basis of an in-house database. One uses Microsoft Excel spreadsheets.

4.12.2 Database content

All of the genebanks provide accession numbers and passport data, and the data are accessible on the internet for all but one, which is in the process of implementing this via GRIN-Global. The survey question did not go into detail about the level of passport data available, relative to the current standard (FAO 2015), but incomplete passport data was identified as an issue in the workshops, and there is evidence that some data are missing, such as country of origin, as

noted in Section 4.1. Eleven of the genebanks provide phenotypic data, and four can provide genotypic data. Other available data noted in individual cases included images and climate data for collection locations.

4.12.3 Online access

As indicated above, four of the genebanks that responded to the curator survey provided online access to accession information via GRIN-Global. Two of these, along with another two, provided access via Genesys. One of these also provided access via EURISCO, as did two others. Five others were not connected to any of these three key online resources, although two were in the process of arranging access. A rudimentary network map of database linkages for individual genebanks, based on the survey responses, is shown in Figure 5.

Genesys is a global search and request tool for crop accessions, active since 2008. It is managed by the Global Crop Diversity Trust and now contains passport data for an estimated half of all global genebank accessions. Key data providers to Genesys are EURISCO/ECPGR, the CGIAR genebanks and NPGS/GRIN-Global. Content includes core collection lists (currently only for tropical forages) and descriptor lists. A generic descriptor list is included for tropical forages, and with respect to temperate forages, there are specific descriptor lists for *Lathyrus* and *Trifolium*.

GRIN-Global is the new, scalable version of GRIN

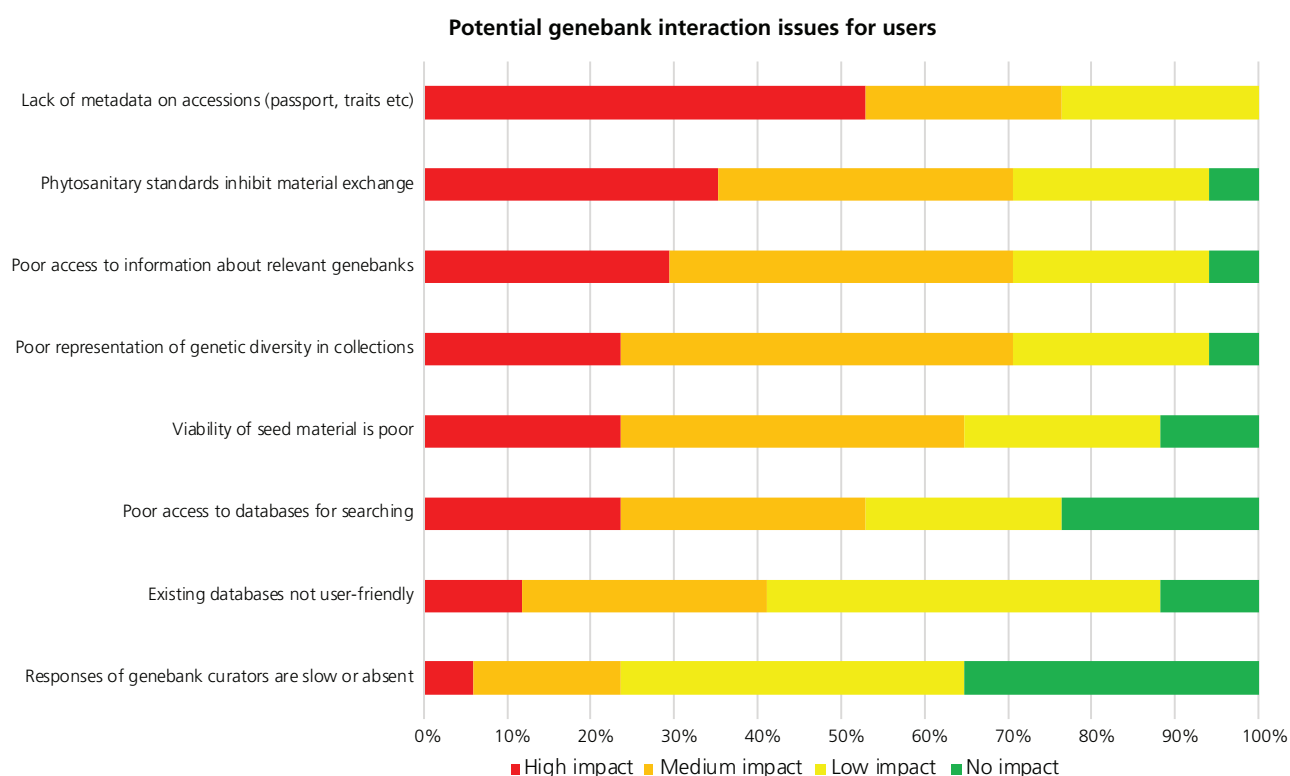


Figure 4 Genebank users' assessments of their interactions with genebanks across eight potential issues.

(Germplasm Resources Information Network), the USDA/ARS genebank information management system. It stores and delivers many types of genetic resource data, including passport, phenotypic, genotypic, distribution, regeneration, health and availability. It also delivers authoritative nomenclatural information through GRIN Taxonomy. GRIN-Global is currently used not only by the US National Plant Germplasm System, but also by genebanks in more than 20 other nations, the NordGen genebanks and several CGIAR centers.

ECPGR (European Cooperative Programme for Plant Genetic Resources) includes a Forages Working Group. The "Forages" database is one of six ECPGR Central Crop Databases. It is divided into 10 taxonomic sections, led by database managers from various countries: Annual medics, *Dactylis*, *Festuca*, *Lolium* & *Trifolium*, Minor forage grasses, Minor forage legumes, Perennial medics, *Phleum*, *Poa* and *Trifolium subterraneum*.

EURISCO is the European Search Catalogue for Plant Genetic Resources, active since 2003. It is maintained at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) on behalf of the ECPGR and contains passport and phenotypic data on more than two million accessions held by 405 institutions in 43 countries.

WIEWS (World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture) is the information system managed by the UN Food and Agriculture Organization (FAO). It is used for periodic assessment of the status of plant genetic

resources conservation. In terms of temperate forages, there is information on *Medicago sativa*, *Trifolium pratense*, *T. repens*, *T. alexandrinum*, *T. subterraneum* and *Lathyrus sativus*.

GENBIS is the Nordic Baltic Genebanks Information System, managed by NordGen (Nordic Genetic Resource Centre), and includes genebank data for five Nordic (Iceland, Denmark, Finland, Sweden, Norway) and two Baltic (Latvia, Estonia) states. It is hosted online by the GRIN-Global platform. Lithuania plans to migrate its data into the common Nordic Baltic system in the future.

Discussions during the workshops highlighted issues around the accessibility, completeness and quality of accession data, including what was considered essential information such as country of origin and type of accession (wild collection, breeding line, etc.). There was consistent support for initiatives to address these issues. At the same time, however, participants recognized that it was necessarily a time-consuming and meticulous process, which would, in some cases, involve the development of suitable consistent descriptor lists and the collaboration between database, curator and taxonomy expertise. There was an awareness that a number of countries do not provide open access to accession passport data and a collective desire to improve this situation. The availability of accession passport data would support curators in identifying unnecessary duplication and robustly developing core collections and would support users in identifying promising germplasm for desirable traits and tolerances.

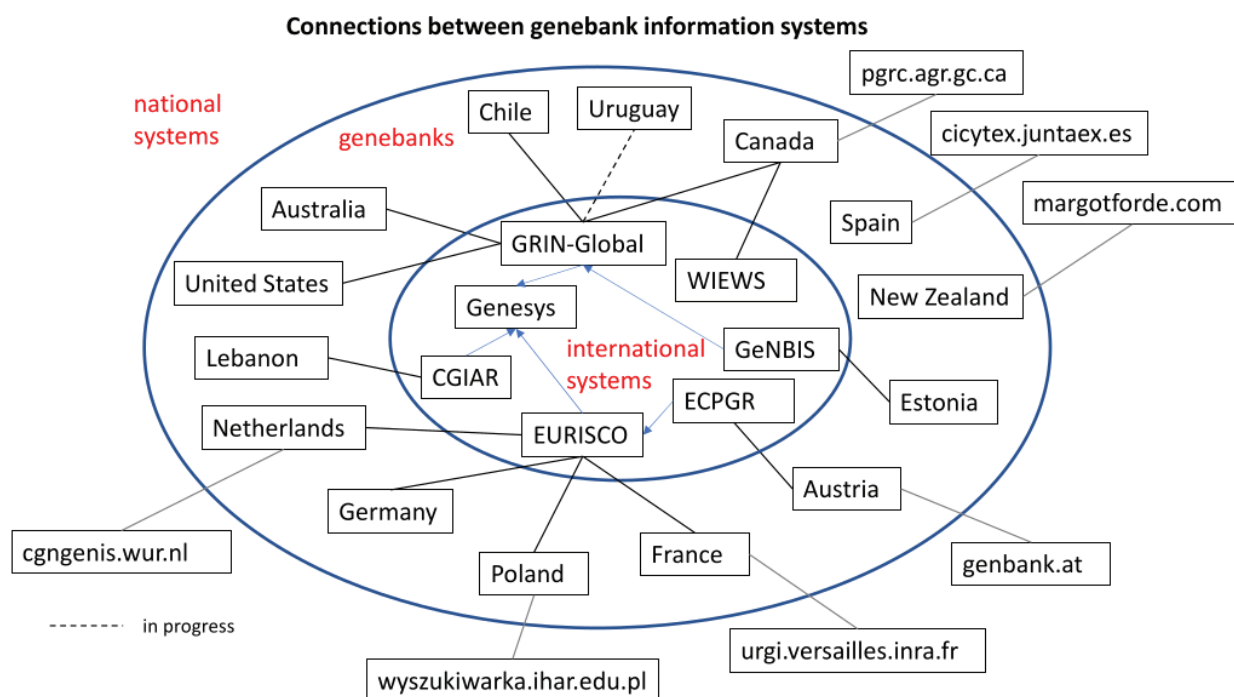


Figure 5 Use of genebank information systems by individual genebanks, based on survey responses.

4.13 Access, distribution and use of genetic resources

4.13.1 Distribution to a variety of users

Three genebank respondents did not supply information about the types of users that they distributed germplasm to, and one respondent indicated that no distributions were made. The other twelve genebank respondents indicated that they commonly received more requests for germplasm from domestic users compared with foreign users (table in Annex 9.9). Academic researchers were the most common type of recipients, followed by plant breeders in the public sector; at least half of the respondents indicated that these two groups were supplied with material several times in a year. Supply to private sector breeders, farmers, other genebanks and nongovernment organizations was less frequent. All genebanks kept records of these distributions.

4.13.2 Constraints to distribution

In the survey, all genebanks reported limits on the distribution of seed and indicated that seed supply was sometimes an issue. Only one surveyed genebank held other plant tissue types for distribution, which

was also in limited supply. Genebanks had a variety of distribution guidelines based on number or weight limits (often <100 seeds), the requirement to retain a minimum amount in storage, or the discretion of the curator for particular species or species characteristics (e.g. one distinguished between inbred and outcross species).

As noted in Section 4.6, respondents indicated that seed health was sometimes an issue hindering distribution, and that they did not have adequate procedures in place for phytosanitary certification. Some respondents commented that regulatory barriers to global seed distribution contributed to the tendency among some genebanks to support the needs of local breeders and researchers more than the needs of foreign users.

Three genebanks held a portion of their temperate forage accessions in a restricted distribution category. Otherwise, for most genebanks, the remainder of the collection was available both nationally and internationally.

In the European workshops, the issue of access to commercial lines was discussed, in terms of inconsistent regulations allowing for genebanks to store and dis-

Table 9 Gaps in collections for particular species, as identified by genebank curators. Red text indicates species in the sample set; other species identified by individual genebanks are in black.

Genebank	Type of gaps	Species identified
Australia	Climatic extremes	<i>Biserrula pelecinus</i> , <i>Medicago sativa</i> , <i>Onobrychis viciifolia</i> , <i>Trifolium subterraneum</i>
USA	Warm and cold regions	<i>Medicago sativa</i> ,
	Wild relatives	<i>Onobrychis viciifolia</i>
Chile	Genotypes and traits	<i>Biserrula pelecinus</i> , <i>Dactylis glomerata</i> , <i>Lolium perenne</i> , <i>Medicago sativa</i> , <i>Trifolium pratense</i> , <i>T. repens</i> , <i>T. subterraneum</i> , <i>Bromus</i> spp.
New Zealand	Regions of interest	<i>Biserrula pelecinus</i> , <i>Dactylis glomerata</i> , <i>Festuca arundinacea</i> , <i>Lolium multiflorum</i> , <i>Lolium perenne</i> , <i>Lotus corniculatus</i> , <i>Medicago sativa</i> , <i>Onobrychis viciifolia</i> , <i>Trifolium pratense</i> , <i>T. repens</i> , <i>T. resupinatum</i> , <i>T. subterraneum</i> , <i>Lolium</i> spp., <i>Trifolium</i> spp., <i>Festuca</i> spp., <i>Cichorium intybus</i> , <i>Plantago lanceolata</i>
Uruguay	Genotypes and traits	<i>Dactylis glomerata</i> , <i>Festuca arundinacea</i> , <i>Lolium multiflorum</i> , <i>Lolium perenne</i> , <i>Lotus corniculatus</i> , <i>Lupinus luteus</i> , <i>Medicago sativa</i> , <i>Trifolium pratense</i> , <i>T. repens</i> , <i>T. resupinatum</i> , <i>T. subterraneum</i> , <i>Cichorium intybus</i>
	Geographic areas	<i>Lupinus luteus</i> , <i>Trifolium repens</i> , <i>Vicia ervilia</i> , <i>Lathyrus cicera</i>
Lebanon	Heat and drought tolerance	<i>Hordeum spontaneum</i>
	Low ODAP content	<i>Lathyrus sativus</i>
Canada	Genotypes	<i>Festuca arundinacea</i> , <i>Lolium multiflorum</i> , <i>Lolium perenne</i> , <i>Lotus corniculatus</i> , <i>Lupinus luteus</i> , <i>Onobrychis viciifolia</i> , <i>Trifolium pratense</i> ,
	Native species	<i>T. repens</i> , <i>T. resupinatum</i> , <i>Trigonella foenum-graecum</i> , <i>Astragalus cicer</i>
France	Geographic areas	<i>Dactylis glomerata</i> , <i>Festuca arundinacea</i> , <i>Lolium perenne</i> , <i>Lupinus luteus</i> , <i>Medicago sativa</i> , <i>Onobrychis viciifolia</i> , <i>Trifolium pratense</i> , <i>T. repens</i> , <i>Festuca rubra</i> , <i>F. ovina</i> , <i>F. pratensis</i>
Netherlands	Local wild material	<i>Lupinus luteus</i> , <i>Festuca rubra</i>
Spain	Genotypes	<i>Biserrula pelecinus</i> , <i>Dactylis glomerata</i> , <i>Lolium multiflorum</i> , <i>Lolium perenne</i> , <i>Lotus corniculatus</i> , <i>Medicago sativa</i> , <i>Trifolium repens</i> , <i>T. resupinatum</i> , <i>T. subterraneum</i> , <i>T. cherleri</i> , <i>T. glomeratum</i> , <i>Medicago polymorpha</i>

tribute accessions of old varieties that were no longer on active cultivar registers.

4.13.3 Gaps in the collections

Curators' responses to the survey question about gaps in their collection varied considerably, which may indicate that the question was not well expressed. In general, their responses indicated a varying interpretation of the question (e.g. one noted trait data as a gap). The broad categories of gaps that were identified included a) ecogeographic zones, b) taxa and genotypes and c) traits and tolerances. Ten of the genebanks indicated gaps in their collections across multiple species in the initial sample set (Table 9).

Many of the genebanks noted gaps in the collections of species for which they had large collections, such as *Medicago sativa*, *Festuca arundinacea*, *Lolium perenne* and *Trifolium repens* (see Table 7), as well as those of smaller collection size. This tendency may indicate a widespread expectation for greater genetic diversity to be secured for even the most well-used forage species.

Nichols et al. (2012), writing in the context of Australian systems, suggested that key traits for temperate forages in the future include: drought resilience (especially outside of traditionally dry seasons), rainfall intensity, higher tolerance of soil acidity, higher phosphorous utilization efficiency, lower potential to produce methane emissions in grazing ruminants,

better integration into weed management strategies on mixed farms, and resistance to new pests and diseases.

In the workshops, collection gaps were recognized as an ongoing problem for securing genetic diversity, but there was general agreement that the germplasm conservation community as a whole first needed to better understand the scope of existing *ex situ* collections. This meant prioritizing better characterization of existing collections (Section 4.4), including addressing gaps in passport data and identifying redundant duplication, all of which entails a collective effort at the global scale. This work was seen as a precursor to new collection activity designed to fill gaps, especially given the multiple barriers to accessing germplasm from centers of diversity (Section 4.9). New collection initiatives should be prioritized in situations where there is a clear threat to *in situ* conservation, for those species of known value that have to date been relatively neglected.

4.14 Networks and other collaborative initiatives

In the survey, nine of the curators identified networks of collaborations, some with specific institutions and some that are general collaborations (e.g. with private companies for regeneration). The stated links are shown in Figure 6. Many of these links appear to be informal relationships between collaborating organizations, as opposed to formalized networks (i.e. those

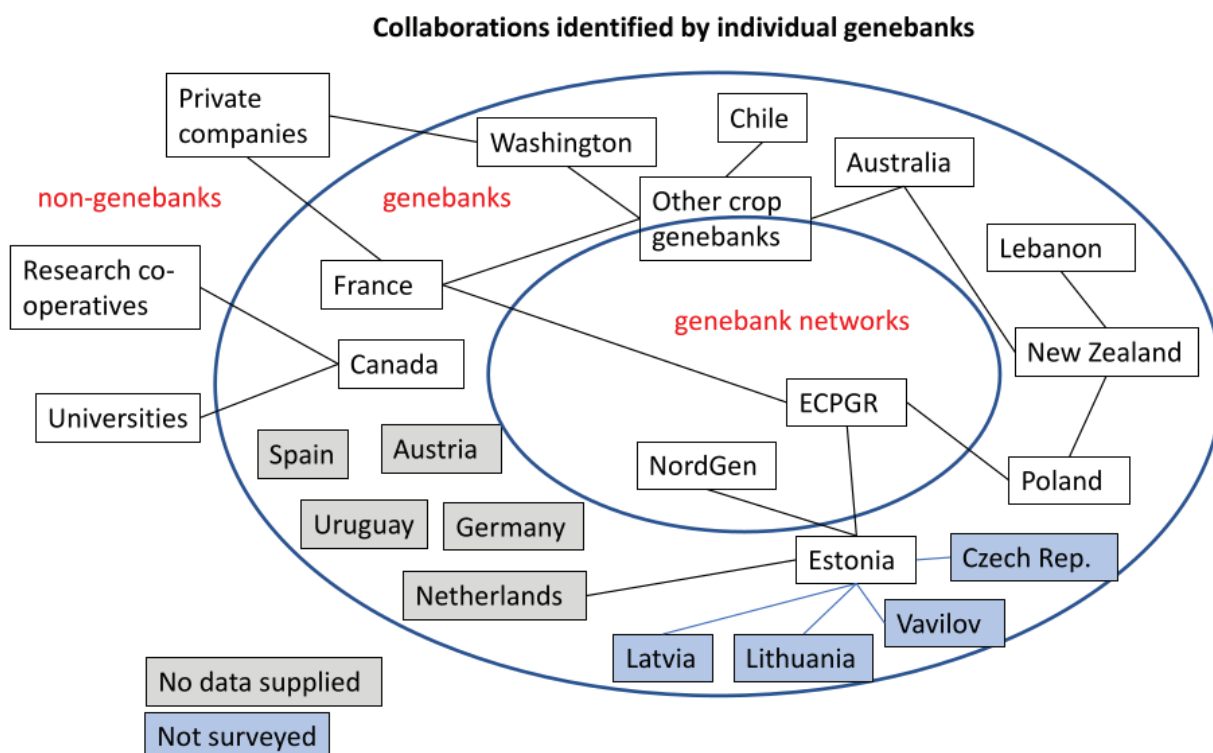


Figure 6 Collaborations with organizations or networks specifically identified in the survey by individual genebank curators.

with an administrative structure). Given that many genebanks did not respond to the survey, this is a very incomplete picture of the collaborations that exist across the genebank community.

4.14.1 Global networks

The only formal global network identified was the participation of ICARDA, as one of the 15 centers (including 11 genebanks) in the CGIAR. This network is not specifically focused on temperate forages, although the development of standards and procedures that CGIAR undertakes would be relevant to temperate forage germplasm conservation.

4.14.2 Regional networks

The European Cooperative Programme for Plant Genetic Resources (ECPGR) is a collaborative program among 31 European countries. The program includes a Forages Working Group, active since 1984. In addition to the Central Crop Databases, the working group manages a Germplasm Collecting Mission database. Regular meeting reports up until 2010 covered implications of the Convention on Biological Diversity (CBD), database developments, the status of national collections, accession duplication, research reports and collection activities (Maggioni et al. 2000) and regeneration guidelines (Sackville Hamilton et al. 1998a).

NordGen (Nordic Genetic Resource Center) is the joint genebank and knowledge center for genetic resources in the Nordic countries (Iceland, Denmark, Finland, Sweden, Norway) and is one of the partners responsible for managing the Svalbard Global Seed Vault. It is guided by the Kalmar Declaration (2004), and its governing board is accountable to the Nordic Council of Ministers. NordGen has a forages working group in its Plants department.

At one of the curator workshops conducted for this strategy (Expert online consultation meeting, 17 September 2020), the South American participants identified some well-regarded historical network activity, including 1) a Southern Cone regional network, REF-COSUR (Red de Forrajas del Cono Sur), that operated in the 1980s and 1990s; 2) the REGENSUR project (a PROCISUR subprogram for plant genetic resources) supported by the Inter-American Institute for Cooperation on Agriculture (IICA); 3) an older project, REPAAN (Red de Pastizales Alto Andinos), funded by the Canadian International Development Research Centre (IDRC/CIID); and 4) the LOTASSA project supported by the European Commission. However, there were no currently active regional networks.

4.14.3 National networks

Most countries had more than one genebank, including those devoted to other crops, which were part of national networks (e.g. Australian Grains Genebank). Following are two more networks identified in the curator survey.

The National Plant Germplasm System (NPGS) is a US collaborative effort, managed by the USDA Agricultural Research Service (ARS), to safeguard *ex situ* in genebanks the genetic diversity of agriculturally important plants. Many of these genebanks are co-located with State Land Grant Universities. Administrative oversight is provided by ARS line management and the ARS Office of National Programs. Coordination and communication of best curatorial practices are facilitated by the NPGS Plant Germplasm Operations Committee, composed of NPGS genebank managers and curators. Technical input regarding optimal approaches and priorities for managing the germplasm of individual crops or crop groups is provided by Crop Germplasm Committees (e.g. alfalfa, clover), which are composed of public sector and private technical experts and customers/stakeholders

The Chilean Genetic Resources Network, managed by Instituto de Investigaciones Agropecuarias (INIA), includes four “phytogenetic banks,” one of which holds forages. Accessions are searchable via GRIN-Global.

4.14.4 Specific genebank collaborations

Some genebank curators identified specific genebanks in other countries that they were collaborating with. These connections offer a potential route to including these genebanks in future network activities.

- Czech Republic genebank, part of the Crop Research Institute, Division of Crop Genetics and breeding connected to GRIN-Global.
- Vavilov Institute All-Russian Institute of Plant Genetic Resources. Includes divisions for Legumes, Perennial Feed Grasses, Genebank (241,000+ records in online database), Information systems and Agrobotany & *In Situ* Conservation. The genebank includes collections of legumes (42,000 spp.) and forage crops (20,000 spp.)
- The Genetic Resources Centre (GRC) of Latvia, founded in 2006 under the administration of Latvijas Valsts Mežzinātnes Institūts “Silava”. Database records are held in the Nordic Baltic Genebanks Information System (GENBIS), hosted by NordGen.
- The Lithuanian Plants Gene Bank, established in 2004 and governed by the Ministry of Environment.

Forages come under the oversight of the Agricultural (field) Plant Coordination Centre of the Lithuanian Institute of Agriculture. Database records are held within their Augalų Genų Bankas GRIN-Global Platform.

Views expressed in the workshops varied with regard to the value of a new global network. In principle, participants recognized the benefits, in terms of improvements to collaboration, access to data and germplasm, genebank rationalization, backup security opportunities, technical support, training and awareness of collection activity. However, in the context of human resource capacity constraints, it was pointed out that participation would require additional investment and greater time availability for curators. Many curators have their collaborative needs met through existing formal (e.g. ECPGR, USA Crop Germplasm Committees, CGIAR, professional societies) or informal networks. For individual genebanks, the benefits of cooperation must clearly outweigh the additional time costs, to justify their involvement. Any additional operational costs from such involvement (e.g. travel) would have to be met from external investment, given tight national genebank budgets and their priority objectives (see Annex 9.8).

4.15 Key observations on the temperate forage germplasm sector

A key feature of the temperate forage germplasm conservation community that provides an underpinning rationale for the global strategy is simply the number and diversity of participants: hundreds of genebanks in dozens of countries are supplying the needs of countless users in the research and development community worldwide. With most curators being expected to “do more with less,” collaboration and coordination is a sensible pathway. A recurring theme was the need to rationalize activity within existing collections by focusing on regeneration priorities and characterization data, in order to free up limited resources for the addition of new germplasm that was identified as high priority, through robust processes such as core collections.

Following are other key observations.

- Collections of relevant material are held in more than 160 organizations across more than 70 countries worldwide. The material is widespread, but potentially redundant duplication is hard to identify and poorly quantified.
- An estimated 80% of accessions are held by 19 genebanks, based on a Genesys search of the sample set of 11 temperate forage genera. This suggests that collaborative activity to assess germplasm representativeness in *ex situ* collections could be led by relatively few organizations.

- An estimated 51 species comprise 80% of the total number of accessions, and nine species comprise 50% of the total accessions (*Lolium perenne*, *Dactylis glomerata*, *Lathyrus sativus*, *Trifolium pratense*, *T. repens*, *Festuca pratensis*, *T. subterraneum*, *F. arundinacea* and *Lupinus albus*), according to a Genesys search of the sample set of 11 temperate forage genera.
- Most genebanks are government-owned facilities with a strong germplasm conservation imperative, although in most cases the curator has a high degree of influence on genebank activity.
- Most genebanks surveyed have well-established core facilities, policies and processes for secure storage and distribution. This reflects their focus on core functions as outlined in policy documents.
- Characterization activity varied greatly across species and genebanks, and was more common among genebank users. It is not clear whether there is a significant flow of characterization data from users back to germplasm databases. Developing consistent optimal descriptor lists and putting meticulous effort into improving characterization data were highly valued and seen as a priority step that had multiple benefits. There is a strong desire to use more cost-effective methods.
- Effective regeneration of accessions is a common concern for genebank curators. This limitation is mainly related to personnel/budget constraints, but also in some cases arises from the need for effective isolation of outcrossing species, land area and technical challenges with seed multiplication. A number of genebank curators noted that rationalizing activity within their existing collections was a priority due to their inability to keep up with regeneration requirements.
- Germplasm gap-filling was recognized as important but seen as a lower priority and dependent upon a robust case following improved data curation of existing collections. This view is also partly influenced by the multiple challenges in accessing and distributing new wild collections.
- Most genebanks have effective electronic information management systems, but the degree to which these databases are globally connected varies considerably.
- There is no formal global network for temperate forage germplasm conservation. One long-standing regional network is active (ECPGR), although activity appears to have waned in recent decades. Other former networks appear to be largely inactive (e.g. South America). Most collaborative support for germplasm conservation appears to be based around within-country networks across crop groups (e.g. USA, Australia, Chile, Germany).



5 GLOBAL STRATEGY FOR THE *EX SITU* CONSERVATION OF TEMPERATE FORAGE GENETIC RESOURCES

5.1 Mission

The mission behind this strategy is to maximize the diversity and utility of germplasm in secure mid- to long-term storage and to improve global accessibility of germplasm and associated passport and characterization data, for those temperate forages of proven or demonstrated potential value to the sustainability of the international temperate livestock sector.

We distinguish here from the goal of pure germplasm conservation for the sake of preservation of global plant diversity, which is the role of other organizational initiatives (e.g. Millennium Seed Bank, national indigenous flora genebanks).

5.2 Vision of the strategy

We envisage an international network of genebanks and germplasm users with high levels of open exchange of the full diversity of temperate forage germplasm and of comprehensive passport and characterization data.

It may be useful to consider a very simple but powerful existing vision statement from the VIR (slightly modified): "To bring the best plant resources of the world to the service of *sustainable* agriculture."

5.3 Core values

A global strategy should achieve broad acceptance among all stakeholders of a set of core values. The following values are suggested:

- Genetic diversity: the widest possible genetic and phenotypic diversity is captured.
- Utilitarianism: the focus is on species, genes and traits of demonstrable value to agriculture.
- Data quality: data on germplasm accessions are considered to be as valuable as the accessions themselves.
- Accessibility: germplasm and the associated passport and characterization data should be available to any bona fide interested party globally.

5.4 Core elements

The basic elements required for successful germplasm conservation, as outlined in national policy documents that mandate germplasm conservation, include:

1. Long-term security of diverse germplasm: the actual plant material.
2. Information systems and data: information about the plant material held.
3. Human resources: time, skills and knowledge to curate the germplasm and the data.
4. Infrastructure: facilities for storage, regeneration and distribution.

Supporting these core elements are governance structures, documented processes and relevant scientific research (botanical, taxonomic, genomic, etc.).

For this global-scale strategy, it is assumed that the infrastructure, governance and human resource requirements are the responsibility of national administrations, and that relevant scientific activity is the responsibility of the global research community. Hence, the recommendations in this strategy focus on elements 1 and 2 and relevant parts of 3.

5.5 Scope of the strategy

The strategy covers the following, with specific exclusions noted:

- Species (and subordinate taxa) used for grazing livestock forages collected from or used within the temperate zone. The exact definition is necessarily vague. For example, subtropical taxa are commonly used in temperate grazing systems but are covered in a previous strategy.
- *Ex situ* conservation activities (i.e. excluding *in situ* initiatives).
- Herbaceous forages (i.e. excluding woody forage species).

- Plant material (i.e. excluding symbiotic organisms such as rhizobia and endophytes).

5.6 Exclusions

It is important not only to identify strategic objectives, but also to identify the elements for which a strategy is not responsible, principally in terms of addressing issues at national or regional scales.

- National human resources capacity: this is fundamentally a national priority and should not be usurped by global intervention.
- Genebank infrastructure: issues related to storage facilities and land area for regeneration are for national self-determination.
- Taxa priority at the national level: coordination between countries may be encouraged but no attempt should be made to rearrange national priorities.
- Existing national networks: a strategy may recommend leveraging existing regional networks (e.g. ECPGR, NPGS) at the global level, but may not call for new networks at the national level.

5.7 Externalities

There are some important barriers to progress in germplasm conservation that are not unique to temperate forages, and that operate at higher levels than germplasm conservation networks. These should be recognized and considered in any initiatives, but effective change to these drivers is clearly beyond the influence of this strategy.

- Political: conflict zones and national policies that restrict the flow of germplasm, data and people.
- Commercial: intellectual property rights held by commercial entities resulting from their germplasm development activities.

6 RECOMMENDATIONS FOR THE GLOBAL STRATEGY

For this strategy, four high-level strategic actions are proposed.

A. Taxa categorization and prioritization

Given the wide range of taxa, which are used to varying degrees across many ecogeographic zones and held by many genebanks, an important first step is to categorize and prioritize the temperate forage group. Categorization may involve the following considerations:

- Degree of development, in terms of collection status and global relevance. That is, some taxa have well-recognized value based on decades of research and use and have been extensively collected and developed into many cultivars. Others have shown potential for use, sometimes for specific characteristics, but have been subject to much less research and cultivar development. The value of many others is virtually unknown.
- Ecogeographic zone. The temperate zone may be divided into subzones based on dominant climatic influences, for example, Mediterranean, cool temperate and cold temperate. Priorities will differ for different parts of the temperate forage sector depending on how these zones align with their local zones of interest. If the global strategy is to engage the whole sector, the priority taxa list must include species of both global and regional interest.
- Type of use. Within livestock systems, types of use include *in situ* grazing systems, cut-and-carry systems and ecological restoration of grazed ecosystems. Valued uses outside of livestock systems include biofuel, crop support, direct human consumption and medicinal uses. As noted above, priorities for different parts of the temperate forage sector will vary depending on the intended use.

Prioritization will require consideration, within the above categories, of which taxa should be focused on and the specific needs for those taxa. Important considerations include the following:

- Urgency of collection: where there is an imminent threat of local extirpation due to climate, land development or political conflict. Determining

this need would involve mapping exercises, incorporating the origins of existing material, climate change projections and conflict zones.

- Underrepresented traits: where a species currently in widespread use would benefit from exploration of diversity for a specific trait, perhaps to improve mitigation of environmental impacts.
- More research required to understand the value of the taxa: where a species has only limited evidence of potential (e.g. as a methanogenesis suppressant) and hence germplasm conservation activity should be “parked” at this point.

A key step in prioritization would be the identification of a lead agent (or agents) with an organizational mandate to focus on the conservation of that taxon. The most likely candidates would be those organizations with existing strong collections of particular taxa. However, as noted in Section 4.14, existing networks such as ECPGR (Europe) and NPGS (USA) have already appointed crop database coordinators, who would be the obvious first choice for such leadership roles.

B. Improvement of data curation

It is clear that the passport and characterization data associated with the species already in *ex situ* genebanks around the world vary in quality. In many cases, the data are incomplete, relative to current FAO standards. For many taxa, standard descriptors are dated or absent. For many descriptors, measurement standards vary, having been adopted by diverse providers. The process of addressing these various issues is likely to involve intensive work, with database specialists collaborating with individual germplasm curators and supported by taxonomists. Given the almost universal feedback from curators that they are under-resourced in terms of staff capacity, the investment for this activity will need to be externally sourced. As such, this initiative would also go some way to the development of human resources (Strategic action D) within individual genebanks—and this represents the *quid pro quo* value proposition for them to engage.

The following steps would be worthwhile:

- Update or develop new standardized descriptors for the prioritized species in Strategic action A.
- Engage database specialists and taxonomists to work with curators.
- Work with curators, perhaps using short-term secondments of specialists from the lead agencies identified in Strategic action A, to collate data and transfer the data to global databases.
- Incorporate user-generated data in accessible databases where there is no commercial restriction.

This step is considered a priority initiative ahead of Strategic action C, given that any assessment of genetic resource rationalization for a given taxon must begin with analysis of the characterization data on accessions already held. It is therefore a necessary step both for minimizing redundancy and for filling gaps.

C. Germplasm activity rationalization

In a context of limited resources (in terms of people's time, storage space and regeneration capacity), two major tasks emerge, as follows:

1. To minimize redundant activity within the global collection of any given taxon. An example of redundant activity is the regeneration of duplicate accessions by different genebanks, which would represent a waste of staff time and facility resources. This is distinct from the need to maintain sufficient quantities of viable seed for distribution to users, and distinct from the need for safety backup duplication, normally within a separate facility. Neither should it be confused with elimination of any germplasm deemed to be redundant; this is not contemplated by any curator. Identifying redundancy appears to be a difficult problem even at the level of individual genebanks, let alone at a global level (given extensive historical germplasm exchange). Modern, high-throughput characterization techniques can help, but meticulous collation and analysis of existing data are a necessary prerequisite (Strategic action B).
2. To fill gaps in the global collection of any given taxon, to best represent the true diversity of the species. Generally, efforts to collect temperate forages appear to have declined over the past few decades, for a number of reasons, including travel costs, biosecurity restrictions on germplasm importation (or, more specifically, the risk of transferring associated pathogens), political obstruction and the ongoing investment required to maintain and regenerate new accessions. Therefore, any future collection activity must be strategic and clearly demonstrate strong benefits, that is, a demonstrable, critical germplasm gap identified

as a result of robust analysis of existing global accessions. Successful collection missions will thus require prior multinational collaboration to establish the benefit case, to undertake the mission, and to coordinate responsibility for germplasm maintenance.

Methods such as core collections and FIGS (Focused Identification of Germplasm Strategy) have been used for identifying redundancy and gaps in collections. These germplasm rationalization approaches have already been undertaken for temperate forages (e.g. core collections for *Medicago sativa*, *Trifolium subterraneum* and FIGS for *Lathyrus*), although some collections are regional only (e.g. *Dactylis glomerata* core collection) and others are in progress (e.g. *T. repens*, *Lolium perenne* core collections). The prioritization exercise in Strategic action A would identify future worthy candidate taxa.

D. Human resource development

Human capacity was almost universally cited as a major constraint to progress in global collaboration and coordination. Curators and staff are already fully occupied with attending to their core genebank functions of storage, regeneration and distribution. However, all respondents saw value in collaboration and coordination at a wider scale. Collaborative goodwill appears to be a feature of the temperate forage conservation community, with participants citing the following benefits:

- Access to wider knowledge and skills pertinent to their taxa of interest, methods and processes.
- Opportunities for duplicate backup.
- Rationalization of collections to reduce local costs.
- Collective action to reduce global policy or commercial barriers to exchange.
- Enhanced biosecurity through collective compliance.
- Recognition of individual countries' contribution to the benefits derived from germplasm development.

At the global scale, initiatives in this regard should initially focus on support for data curation (Objective B) with associated needs for database and taxonomic skills. In addition, support for wider participation in existing regional networks or the establishment of regional networks would be valuable (some existed previously, but activity has waned, e.g. in South America). The aim would be to increase the engagement of those countries less connected to global networks. Russia and Ukraine, in particular, appear to be important holders of temperate forage germplasm. It may be that, in the presence of political impediments to engagement, the global strategy can support regional clusters of "like-minded nations" as a trust-building exercise and an encouragement to eventual participation at the global level.

7 ACRONYMS

Table 10 Abbreviations and acronyms used in the report (see Annex 9.1 for three letter ISO3 country codes)

CBD	Convention on Biological Diversity
CGIAR	Consultative Group on International Agricultural Research
ECPGR	European Cooperative Programme for Plant Genetic Resources
EURISCO	European Search catalogue for Plant Genetic Resources
FAO	Food and Agriculture Organization of the United Nations
FIGS	Focused Identification of Germplasm Strategy
GENBIS	Nordic Baltic Genebanks Information System
GRIN	Genetic Resources Information Network
IBPGR	International Board for Plant Genetic Resources (now Bioversity International)
ICARDA	International Center for Agricultural Research in the Dry Areas
ILDIS	International Legume Database and Information System
IHSG	International Herbage Seed Group
IICA	Inter-American Institute for Cooperation on Agriculture
IPK	Leibniz-Institut Für Pflanzengenetik und Kulturpflanzenforschung
ISO3	International Organization for Standardization Alpha-3 country codes
ITPGRFA	International Treaty on Plant Genetic Resources for Food and Agriculture
MLS	Multilateral System
LOTASSA	Resources for Adaptation and Sustainable Production of forage Lotus species
NordGen	Nordic Genetic Resource Center
NPGS	National Plant Germplasm System
POTW	Plants of the World
PROCISUR	Programa Cooperativo para el Desarrollo Tecnológico Agroalimentario y Agroindustrial del Cono Sur
REFCOSUR	Red de Forrajas del Cono Sur
REPAAN	Red de Pastizales Alto Andinos
RH	relative humidity
TSW	thousand seed weight
USDA-ARS	United States Department of Agriculture – Agricultural Research Service
VIR	N.I. Vavilov Research Institute of Plant Industry
WIEWS	World Information and Early Warning System

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9 ANNEXES

9.1 Country list

Table 11 Countries within the temperate zone (30–60° latitude) and their ISO3 country codes used in tables.

Northern Hemisphere							
Afghanistan	AFG	Albania	ALB	Armenia	ARM	Austria	AUT
Azerbaijan	AZE	Belarus	BLR	Belgium	BEL	Bosnia & Herzegovina	BIH
Bulgaria	BGR	Canada	CAN	China	CHN	Croatia	HRV
Cyprus	CYP	Czech Republic	CZE	Denmark	DNK	Estonia	EST
France	FRA	Georgia	GEO	Germany	DEU	Greece	GRC
Hungary	HUN	Iran	IRN	Iraq	IRQ	Ireland	IRL
Israel	ISR	Italy	ITA	Japan	JPN	Jordan	JOR
Kazakhstan	KAZ	Kyrgyzstan	KGZ	Latvia	LVA	Lebanon	LBN
Lithuania	LTU	Luxembourg	LUX	Malta	MLT	Moldova	MDA
Mongolia	MNG	Morocco	MAR	Montenegro	MNE	Netherlands	NLD
N Korea	PRK	N Macedonia	MKD	Norway	NOR	Pakistan	PAK
Poland	POL	Portugal	PRT	Romania	ROU	Russia	RUS
Serbia	SRB	Slovakia	SVK	S Korea	KOR	Slovenia	SVN
Spain	ESP	Sweden	SWE	Switzerland	CHE	Syria	SYR
Tajikistan	TJK	Turkey	TUR	Tunisia	TUN	Turkmenistan	TKM
Ukraine	UKR	United Kingdom	GBR	United States	USA	Uzbekistan	UZB
Southern Hemisphere							
Australia	AUS	Argentina	ARG	Chile	CHL	New Zealand	NZL
Lesotho	LSO	South Africa	RSA	Uruguay	URY		

A number of non-temperate zone countries also hold temperate forage germplasm, listed in Table 17 of Annex 9.7. Additional country codes noted in text and tables include: Chile (CHL), Ethiopia (ETH), Peru (PER).

9.2 Survey Respondents

Table 12 Genebank curators and users who responded to the survey

Genebank	Respondent	User	Respondent
G01	Wilhelm Graiss, HBLFA, Austria	U01	Alan Stewart, PGGW, New Zealand
G02	Alan Humphries, SARDI, South Australia	U02	Hai-Chun Jing, CAS, China
G03	Brian Irish, USDA-ARS, Washington	U03	Sachiko Isobe, Kasuza, Japan
G04*	Mauricio Köpp, Embrapa, Brazil	U04*	Kelly Craven, Noble, Oklahoma
G05	Rodrigo Diaz Cea, INIA, Chile	U05	Michael Trammell, Noble, Oklahoma
G06	Barbara Hellier, USDA-ARS, Washington	U06	Michael Casler, UW, Wisconsin
G07	Michelle Williamson, AgR, New Zealand	U07	David Kopecky, UEB-CAS, Czech Republic
G08	Federico Condón, INIA, Uruguay	U08	Charlie Brummer, UC, California
G09	Küllli Annamaa, ETKI, Estonia	U09	Metin Tuna, NKU, Turkey
G10	Michael Udvardi, Noble, Oklahoma	U10*	Megan Perales, Forage Genetics, USA
G11	Grzegorz Gryziak, IHAR, Poland	U11	Phillip Nichols, UWA, Australia
G12	Ali Shehadeh, ICARDA, Lebanon	U12	Mark Smith, S&W, Idaho
G13	Axel Diederichsen, AA-FC, Canada	U13	Unidentified, Utah
G14	Jean-Paul Sampoux, INRAE, France	U14	Eric von Wettberg, UVM, Vermont
G15	Chris Kik, WUR, The Netherlands	U15	Maria Monteros, Noble, Oklahoma
G16	Andreas Börner, IPK, Germany	U16	Annie Claessens, AA-FC, Canada
G17	Francisco Gragera, IIAFLO, Spain	U17	Marty Faville, AgR, New Zealand
		U18	Xuefeng Ma, Noble, Oklahoma
		U19	Stig Andersen, AarhusUni, Denmark
		U20	Bill Biliget, USASK, Canada

9.3 Additional taxa

Table 13 List of additional temperate¹ forage germplasm taxa identified by genebank curators, or users (light blue rows), or both (dark blue rows), with descriptive information.

Species name	Country noted	Common name(s)	Family	Indigenous	Introduced	Habit
<i>Agropyron cristatum</i> (L.) Gaertn.	Turkey Utah	Crested wheatgrass	Poaceae	Europe Eurasia Persia Asia	N America	Caespitose perennial up to 60 cm
<i>Agropyron desertorum</i> (Fisch. ex Link) Schult.	Utah	Desert wheatgrass	Poaceae	Eurasia Asia	Europe N America	Caespitose perennial up to 50 cm
<i>Agropyron fragile</i> (Roth) P.Candargy*	Utah	Siberian wheatgrass	Poaceae	Eurasia Asia	N America	Caespitose perennial up to 80 cm
<i>Anthyllis vulneraria</i> L.*	USA	Common kidneyvetch	Fabaceae	N Europe Scandinavia Eurasia	N America Australia	Non-climbing perennial forb
<i>Arachis hypogaea</i> L.*	China	peanut	Fabaceae			Annual up to 30 cm
<i>Astragalus cicer</i> L.	USA Canada	Chickpea milkvetch Cicer milkvetch	Fabaceae	Europe Eurasia	Scandinavia North America	Non-climbing, rhizomatous perennial forb up to 90cm
<i>Avena sativa</i> L.	China	Oat	Poaceae			Annual up to 120 cm
<i>Bromus auleticus</i> Trin. Ex Nees*	Uruguay		Poaceae	S America		Caespitose perennial up to 120 cm

Species name	Country noted	Common name(s)	Family	Indigenous	Introduced	Habit
<i>Bromus catharticus</i> Vahl*	Turkey	Rescue grass grazing brome	Poaceae	S America	N America Africa Europe Eurasia Asia Australia	Caespitose perennial up to 100 cm
<i>Bromus inermis</i> Leys.*	Turkey	Smooth brome	Poaceae	Europe Eurasia Asia Persia	N & S America S Africa Australia	Rhizomatous perennial up to 100 cm
<i>Bromus riparius</i> Rehmann*	Turkey Canada	Asian meadow brome	Poaceae	S Europe Eurasia	E Asia	Caespitose perennial up to 60 cm
<i>Cichorium intybus</i> L.*	New Zealand	Chicory	Asteraceae	Europe Scandinavia Mediterranean Eurasia Persia	Asia N, C & S America Arabia S Africa Australasia	Perennial herb up to 120 cm
<i>Elymus</i> spp.*	USA		Poaceae			
<i>Festuca ovina</i> L.	France	Sheep's fescue	Poaceae	Northern hemisphere		Caespitose perennial up to 60 cm
<i>Festuca pratensis</i> Huds. ²	Wisconsin France	Meadow fescue	Poaceae	Europe Eurasia Persia N Asia	China E Asia Australasia N & S America	Caespitose short-rhizome perennial up to 150 cm
<i>Festuca rubra</i> L. ³	Estonia France Netherlands	Red fescue	Poaceae	Northern hemisphere	Australasia S America	Caespitose perennial up to 90 cm
<i>Festulolium</i> Asch. & Graebn.*	California Czech Republic		Poaceae	Europe		Caespitose perennial or annual
<i>Hordeum stenostachys</i> Godr.	Uruguay		Poaceae	S America S Africa		Caespitose perennial up to 150 cm
<i>Lathyrus cicera</i> L.	Lebanon	Red pea	Fabaceae	Mediterranean Eurasia Persia	N & S America Europe	Annual climbing herb
<i>Lotus corniculatus</i> subsp. japonicus (Regel) H.Ohashi	Japan		Fabaceae	E Asia		Perennial herb
<i>Medicago littoralis</i> Rohde ex Loisel.*	Australia	Strand medic	Fabaceae	Mediterranean	Australia	Annual herb
<i>Medicago polymorpha</i> L.*	Australia Spain	Bur clover	Fabaceae	Europe; Mediterranean; Persia; Eurasia	SE Asia Australasia S Africa N & S America	Annual herb up to 60 cm
<i>Medicago truncatula</i> Gaertn.	Australia	Barrel medic	Fabaceae	Mediterranean	Australia S America	Annual herb up to 60 cm
<i>Melilotus officinalis</i> (L.) Lam.*	Canada	Yellow sweet clover	Fabaceae	Europe Eurasia N Asia	Scandinavia N Africa E Asia Australasia N & S America	Annual or perennial herb
<i>Ornithopus compressus</i> L.*	Australia	Yellow serradella	Fabaceae	Mediterranean	Australasia	Annual herb
<i>Phalaris aquatica</i> L.	California	Canary grass	Poaceae	Mediterranean	N & S America S Africa Australasia	Caespitose perennial up to 150 cm
<i>Phleum pratense</i> L.	California Canada Netherlands	Timothy	Poaceae	Europe Scandinavia Persia Eurasia Asia	E Asia Australasia N & S America	Caespitose perennial up to 150 cm

Species name	Country noted	Common name(s)	Family	Indigenous	Introduced	Habit
<i>Plantago lanceolata</i> L.*	New Zealand	Ribgrass	Plantaginaceae	Europe Scandinavia Mediterranean Arabia Eurasia Persia Asia	N & S America E & S Africa E Asia Australasia	Perennial herb up to 50 cm
<i>Poa pratensis</i> L.	Estonia Netherlands	Kentucky bluegrass	Poaceae	Northern hemisphere	Australasia S America S Africa	Caespitose perennial up to 90 cm
<i>Secale cereal</i> L.	Oklahoma	Rye	Poaceae	Turkey	Mediterranean Persia Eurasia Asia N & S America Australasia	Caespitose annual up to 150 cm
<i>Thinopyrum intermedium</i> (Host) Barkworth & D.R. Dewey ^{4*}	Turkey Utah	Intermediate wheatgrass	Poaceae	Europe Eurasia Persia	N America	Perennial
<i>Thinopyrum obtusiflorum</i> (DC.) Banfi ^{5*}	California	Tall wheatgrass	Poaceae	E Europe Eurasia	W & N Europe N America	Caespitose perennial up to 200 cm
<i>Trigonella foenum-graecum</i> L.*	Canada	fenugreek	Fabaceae	Persia	Europe Eurasia Africa S Asia	Annual herb
<i>Trifolium alexandrinum</i> L.	California	Berseem clover	Poaceae	Persia	Europe N Africa SE Asia Australasia	Annual herb
<i>Trifolium cherleri</i> L.*	Spain	Cupped clover	Fabaceae	Mediterranean	Australasia	Annual herb
<i>Trifolium glomeratum</i> L.*	Spain	Clustered clover	Fabaceae	Mediterranean	Australasia S Africa S America	Annual or perennial herb
<i>Trifolium michelianum</i> Savi*	Australia	Balansa clover	Fabaceae	Mediterranean	Australasia	Annual herb up to 60 cm
<i>Trifolium vesiculosum</i> Savi	Australia	Arrowleaf clover	Fabaceae	Mediterranean	Australasia	Annual herb
<i>Vicia ervilia</i> L. Willd.	Lebanon	Bitter vetch	Fabaceae	S Europe Eurasia	N Europe N Africa	Annual forb
<i>Vicia sativa</i> L.	Lebanon	Common vetch	Fabaceae	Europe Asia N Africa	Australia N & S America S Africa	Scrambling annual forb up to 120 cm
<i>Vicia villosa</i> Roth	Oklahoma	Hairy vetch Fodder vetch	Fabaceae	Europe Mediterranean Eurasia Persia	Scandinavia Asia S Africa Australasia N&S America	Annual herb
<i>x Triticosecale</i> Wittm. Ex A.Camus	Oklahoma	Triticale	Poaceae	Artificial hybrid		Caespitose annual up to 100 cm

¹ Additional subtropical species identified as being adapted to the temperate zone included *Cynodon dactylon* (L.) Pers. (Bermuda grass) for Oklahoma; *Sorghum bicolor* (L.) Moench (sweet sorghum) for China; and *Paspalum notatum* Flügge, *Paspalum dilatatum* Poir. and *Paspalum urvillei* Steud. for Uruguay.

² Now accepted as *Lolium pratensis* (Huds.) Darbysh.

³ Identified as *Festuca glaucescens*

⁴ Identified as *Agropyron intermedium*

⁵ Identified as *Thinopyrum ponticum*

* Not specifically named in Annex I of the International Treaty on Plant Genetic Resources for Food and Agriculture

Table 14 List of additional temperate¹ forage germplasm taxa and the rationale for inclusion, as identified by both curators and users (dark blue rows) or users (light blue rows).

Additional species name	Significance	Activity	Reasoning
<i>Agropyron cristatum</i> (L.) Gaertn.	Global (2)	Breeding	Rangeland forage (USA)
<i>Agropyron desertorum</i> (Fisch. ex Link) Schult.	Global	Breeding	Rangeland forage (USA)
<i>Agropyron fragile</i> (Roth) P.Candargy	Global	Breeding	Rangeland forage (USA)
<i>Arachis hypogaea</i> L.	Global	-	Crop rotation (CHN)
<i>Avena sativa</i> L.	Global	-	Short-term growth
<i>Bromus catharticus</i> Vahl	Global	Breeding	Coastal-adapted species (TUR)
<i>Bromus inermis</i> Leyss.	Global	Breeding	Well-adapted native (TUR)
<i>Bromus riparius</i> Rehmman	Global	Breeding	Well-adapted native (TUR)
<i>Cichorium intybus</i> L.	Global	Breeding	Commercial use
<i>Festuca pratensis</i> Huds. ²	Global	Research	Freezing tolerance
<i>Festuca rubra</i> L.	Global	Research	
<i>Festulolium</i> Asch. & Graebn.	Global (2)	Research	Quality/yield/persistence
<i>Lotus corniculatus</i> subsp. japonicus (Regel) H.Ohashi	Global	Research	Model legume (JPN)
<i>Medicago polymorpha</i> L.	Regional	Research	Widely sown (AUS)
<i>Medicago truncatula</i> Gaertn.	Global	Research	Widely sown (AUS)
<i>Ornithopus compressus</i> L.	Regional	Research	Adapted to poor soils
<i>Phalaris aquatica</i> L.	Global	Research	Widely adapted
<i>Phleum pratense</i> L.	Global	Research/Breeding	Hay crop
<i>Plantago lanceolata</i> L.	Regional	Breeding	Commercial use (NZL)
<i>Secale cereal</i> L.	Global	Breeding	Cool season annual
<i>Thinopyrum intermedium</i> (Host) Barkworth & D.R. Dewey	Global (2)	Breeding	Rangeland forage (USA)
<i>Thinopyrum obtusiflorum</i> (DC.) Banfi	Global	Research	Widely adapted stress tolerant
<i>Trifolium alexandrinum</i> L.	Global	Breeding	High yield alfalfa alternative
<i>Trifolium michelianum</i> Savi	Global	Breeding	Widely sown (AUS)
<i>Trifolium vesiculosum</i> Savi	Global	Breeding	Range expansion potential
<i>Vicia villosa</i> Roth	Global	Breeding	Soil cover
<i>x Triticosecale</i> Wittm. Ex A.Camus	Global	Breeding	Cool season annual

Table 15 Relative size and activity of additional temperate forage taxa collections identified by curators, in order of total number of accessions from 16 responding genebanks.

Taxa name	Number of genebanks with accessions	Relative collection size ¹	Total accessions	Number of genebanks with expanding collection	Number of genebanks with regular requests	Number of genebanks gathering data
Other <i>Trifolium</i> spp.	2	5	15615	1	1	2
Other <i>Lolium</i> spp.	1		6291	1	1	1
<i>Medicago polymorpha</i>	2	5	6073	1	1	2
<i>Medicago truncatula</i>	1		5681	1	1	1
Other <i>Festuca</i> spp.	3	13	4670	1	3	4
<i>Vicia sativa</i>	1	5	2945	1	1	1
<i>Medicago littoralis</i>	1		2885	1	1	1
<i>Elymus</i> spp.	1	5	2648		1	1
<i>Poa</i> spp.	1	9	2524	1	1	2
<i>Plantago</i> spp.	1		564	1	1	1
<i>Cichorium</i> spp.	1		516	1	1	1
<i>Bromus</i> spp.	2		472	1		
<i>Melilotus officinalis</i>	1	5	375			1
<i>Vicia ervilla</i>	1	4	340	1	1	1
<i>Lathyrus cicera</i>	1	4	199	1	1	1
<i>Astragalus cicer</i>	2	6	180			1
<i>Phleum pratense</i>	1	4	108			1
<i>Glycyrrhiza</i> spp.	1	4	60			
<i>Trigonella foenum-graecum</i>	1	2	58			1
<i>Anthyllis vulneria</i>	1	4	44			
<i>Hordeum stenostachys</i>	1		39	1		

¹The survey used four categories and a score was assigned to each category: a. Whole collection of diverse geographic origins (score 4); b. Core collection (score 3); c. Subset collection of restricted origin (score 2); d. Small incidental collection (1). No respondent indicated a core collection for any species. Some respondents did not provide this data.

9.4 Forage seed production data

Table 16 Global seed production data from Danish Seed Council (1993–2006 data published in the proceedings of the 2007 IHSO). Survey sample set species in red text.

Species	Area grown for seed (ha)			Seed production (tons per annum)		
	1993	2006	growth (% p.a.)	1993	2005	growth (% p.a.)
<i>Lolium perenne</i>	121179	187250	4	143549	233357	5
<i>Lolium multiflorum</i>	84674	102565	2	120327	141195	1
<i>Festuca arundinacea</i>	37586	77437	8	51326	110369	10
<i>Poa pratensis</i>	51049	73361	3	27572	51669	7
<i>Festuca rubra</i>	53656	57349	1	35213	54921	5
<i>Phleum pratense</i>	25956	34713	3	7511	7870	0
<i>Trifolium repens</i>	20159	28125	3	5943	8109	3
<i>Trifolium pratense</i>	30650	27740	-1	7325	7522	0
<i>Dactylis glomerata</i>	14786	14690	0	9804	11103	1
<i>Festuca pratensis</i>	8483	14149	5	4188	6535	5
Hybrid ryegrass	3515	9453	13	3208	8772	14
<i>Festuca ovina</i>	3932	4671	1	1846	2714	4
<i>Agrostis</i> spp.	7989	4544	-3	3279	2144	-3
<i>Festulolium</i>	211	3762	129	102	1854	143
<i>Poa trivialis</i>	645	1178	6	456	1302	15

9.5 Taxonomic resources

- [International Plant Names Index \(IPNI\)](#)
- [Tropicos](#)
- [International Legume Database & Information Service \(ILDIS\)](#)
- [Grassbase](#)
- [USDA Plants database](#)
- [GRIN Global](#)
- [Plants of the World \(POTW\)](#)
- [The Plant List \(TPL\)](#)
- [Euro+Med PlantBase](#)

9.6 Trifolium diversity tree

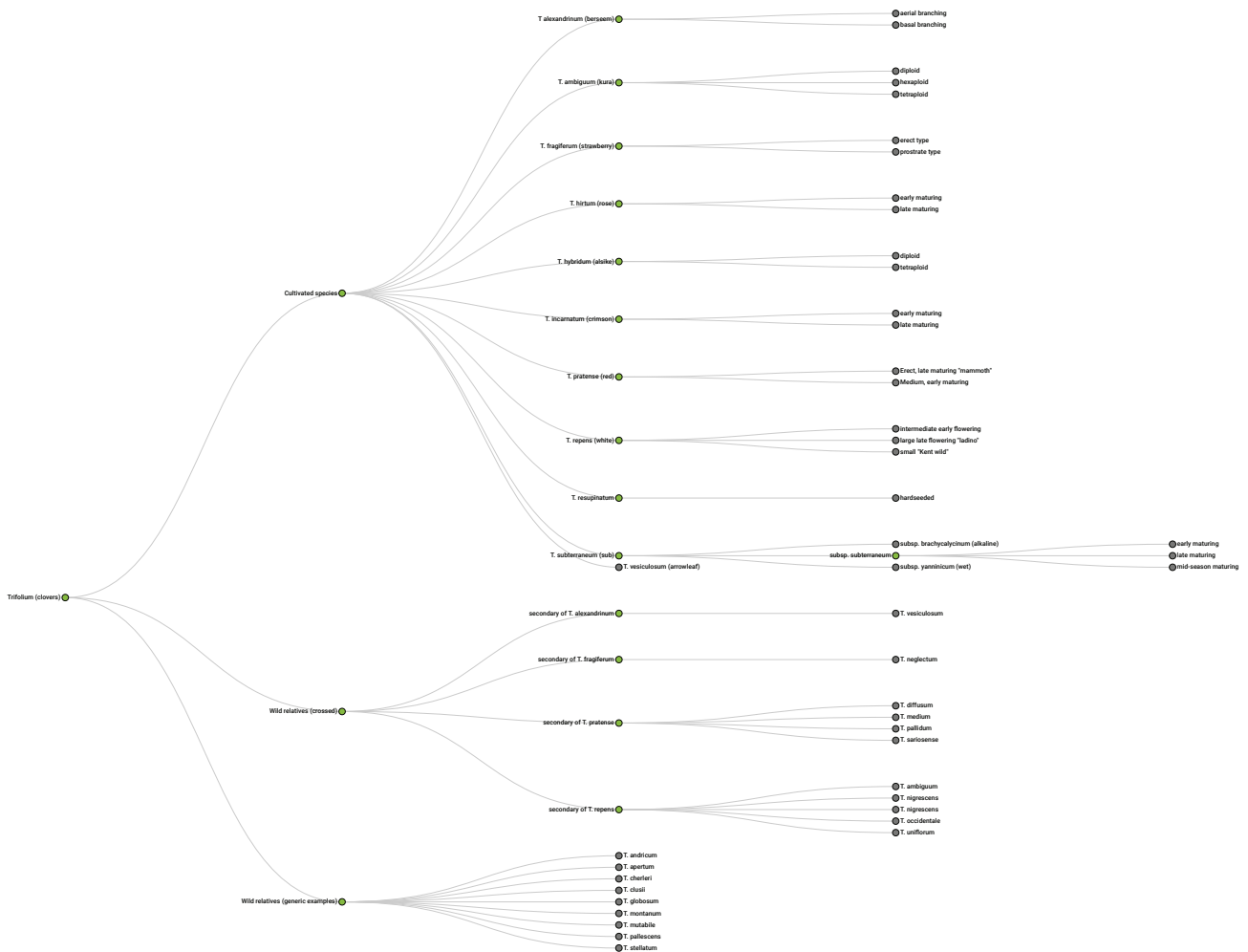


Figure 7. Initial draft diversity tree for *Trifolium*, based on information in Taylor (1985) and Ellison et al. (2006)

9.7 Temperate forage genebanks

Table 17 Genebanks identified from Genesys/WIEWS database search as holding accessions of the sample list genera (*Astragalus*, *Biserrula*, *Bromus*, *Dactylis*, *Hedysarum*, *Lathyrus*, *Lolium*, *Lupinus*, *Medicago*, *Onobrychis* and *Trifolium*), in order of total number of accession for those genera. Those providing survey responses identified in red text.

Name	Location	Country	Code	Storage Type	Institute Type	Number of accessions
Australian Pastures Genebank	Adelaide	Australia	AUS167	Long	Gov	57218
Western Regional Plant Introduction Station	Pullman	United States	USA022	Long	Gov/Uni	24586
International Centre for Agricultural Research in Dry Areas	Beirut	Lebanon	LBN002	Long	CGIAR	22774
Margot Forde Forage Germplasm Centre	Palmerston North	New Zealand	NZL001	Medium	Gov	22077
N.I. Vavilov Research Institute of Plant Industry	St. Petersburg	Russia	RUS001	Long	Gov	17887
Plant Breeding and Acclimatization Institute	Blonie	Poland	POL003	Long	Gov	15870
Genetic Resources Unit	Aberystwyth	Wales	GBR016	Long	Gov/Uni	15605
NARO Genebank	Tsukuba-shi	Japan	JPN183	Long	Gov	10435
External Branch North of the Department Genebank, IPK	Malchow	Germany	DEU271	Long	Gov	9197
Centro de Investigació Agraria Finca La Orden	Badajoz	Spain	ESP010	Medium	Gov	8018
Leibniz Institute of Plant Genetics and Crop Plant Research	Gatersleben	Germany	DEU146	Long	Gov	5271
Australian Grains Genebank	Horsham	Australia	AUS165	NS	Gov	5013
Centre Régional de la Recherche Agronomique de Settat	Settat	Morocco	MAR088	Long	Gov	4847
Millennium Seed Bank Project	Ardingly	England	GBR004	Long	Govt	4344
Institute for Agrobotany	Tápiósele	Hungary	HUN003	Long	Govt	4289
Banco Activo INIA Carillanca	Temuco	Chile	CHL150	Medium	Govt	3754
National Bureau of Plant Genetic Resources	New Delhi	India	IND001	Long	Govt	3676
Gene bank	Prague	Czech Republic	CZE122	Long	Govt	3462
Institute for Plant Genetic Resources	Sadovo	Bulgaria	BGR001	Long	Govt	3282
Centro di Ricerca Zootecnia e Acquacoltura	Lodi	Italy	ITA394	Long	Govt	3139
Portuguese Bank of Plant Germplasm	Braga	Portugal	PRT001	Long	Govt	3070
Banque national de gènes de Tunisie	Tunis	Tunisia	TUN029	Long	Govt	2782
Dipartimento di Biologia Applicata	Perugia	Italy	ITA363	Long	Govt	2684
Plant Genetic Resources Conservation Unit	Griffin	United States	USA016	Medium	Govt/Uni	2643
Plant Biology and Breeding, INRA	Montpellier	France	FRA041	Long	Govt	2457
Nordic Genetic Resource Center	Alnarp	Sweden	SWE054	Long	Regional	2446
Ustymivka Experimental Station of Plant Production	Poltava	Ukraine	UKR008	Long	Govt	2418
Plant Gene Resources of Canada	Saskatoon	Canada	CAN004	Long	Govt	2362
International Livestock Research Institute	Addis Ababa	Ethiopia	ETH013	Long	CGIAR	2133
Estación Experimental Agraria Santa Ana	Huancayo	Peru	PER029	Long	Govt	1786
Genetic Resources Research Institute	Kikuyu	Kenya	KEN212	Long	Parastatal	1607
Bangladesh Agricultural Research Institute	Gazipur	Bangladesh	BGD003	Long	Govt	1561
INIA La Estanzuela	La Estanzuela	Uruguay	URY003	Long	Govt	1543
Suceava Genebank	Suceava	Romania	ROM007	Long	Govt	1204
Centro de Investigaciones Agrarias de Mabegondo	Mabegondo	Spain	ESP119	Medium	Govt	977
Ethiopian Biodiversity Institute	Addis Ababa	Ethiopia	ETH085	Long	Govt	976
Republican Unitary Enterprise	Zhodino	Belarus	BLR011	NS	Govt	972

Name	Location	Country	Code	Storage Type	Institute Type	Number of accessions
Institute of Agriculture	Kyiv	Ukraine	UKR004	NS	Govt	948
Israel Gene Bank for Agricultural Crops	Bet Dagan	Israel	ISR002	Long	Govt	927
Greek Genebank, Agricultural Research Center of Macedonia and Thrace	Thermi	Greece	GRC005	Long	Govt	871
Plant Production Research Center Piestany	Piestany	Slovakia	SVK001	Long	Govt	854
Centre for Genetic Resources	Wageningen	Netherlands	NLD037	Long	Govt	849
National Agricultural Research and Development Institute	Calarasi	Romania	ROM002	NS	Govt	817
Departamento Nacional de Recursos Fitogenéticos	Quito	Ecuador	ECU023	Long	Govt	802
Unité de Recherche Pluridisciplinaire Prairies et Plantes Fourragères	Lusignan	France	FRA001	Long	Govt	726
Centro Nacional de Recursos Fitogenéticos	Alcalá de Henares	Spain	ESP004	Long	Govt	688
Oak Park Research Centre	Carlow	Ireland	IRL001	Long	NGO	651
Departamento de Botânica e Engenharia Biológica	Lisboa	Portugal	PRT018	Long	Govt	648
Genetic Resources Institute	Baku	Azerbaijan	AZE015	Long	Govt	610
International Center for Biosaline Agriculture	Dubai	United Arab Emirates	ARE003	Long	International	575
National Gene Bank	Giza	Egypt	EGY087	Long	Govt	536
Plant Variety Protection Office	Washington	United States	USA158	NS	Govt	529
Lithuanian Institute of Agriculture	Akademija	Lithuania	LTU001	Long	Govt	525
National Seed Storage Laboratory	Fort Collins	United States	USA005	Long	Govt	511
Latvian State Forest Research Institute	Salaspils	Latvia	LVA009	Long	Govt	504
Agricultural Research Service		Jordan	JOR015	NS	Govt	445
Before-Carpathian Branch	Lviv	Ukraine	UKR084	NS	Govt	444
National Agricultural Research Center	Baqa'	Jordan	JOR105	Long	Govt	443
Research and Development Institute for Meadows Brasov	Brasov	Romania	ROM003	Long	Govt	421
Desert Legume Program	Tucson	United States	USA971	NS	Govt	414
Chernihiv Institute of Agroindustrial Production	Chernihiv	Ukraine	UKR099	NS	Govt	411
Plant Genetic Resources Program	Islamabad	Pakistan	PAK001	Long	Govt	397
Institute of Botany	Yerevan	Armenia	ARM005	Medium	Govt	349
Agroscope Reckenholz	Zurich	Switzerland	CHE002	Short	Govt	332
Institute of Forages	Vinnytsia	Ukraine	UKR020	NS	Govt	313
Embrapa Pecuária Sul	Bagé	Brazil	BRA144	Long	Govt	280
Embrapa Clima Temperado	Pelotas	Brazil	BRA020	Medium	Govt	247
Clover Collection, University of Kentucky	Lexington	United States	USA134	NS	Govt/Uni	242
Agricultural and Education Center Raumberg-Gumpenstein	Irdning	Austria	AUT060	Long	Govt	240
Istituto di Bioscienze e Biorisorse	Bari	Italy	ITA436	Long	Govt	240
Institute of Agriculture of the Southern Region	Kherson	Ukraine	UKR006	NS	Govt	227
Lebanese Agricultural Research Institute	Zahle	Lebanon	LBN020	Short	Govt	220
Banco Base INIA Quilamapu	Chillán	Chile	CHL099	Medium	Govt	210
National (CYPARI) Genebank	Nicosia	Cyprus	CYP004	Medium	Govt	197
Crops and Seed Production Department	Ljubljana	Slovenia	SVN019	Long	Govt	188
Estonian Crop Research Institute ²	Jõgeva	Estonia	EST019	Long	Govt	173
Embrapa Recursos Genéticos e Biotecnologia	Brasilia	Brazil	BRA003	Long	Govt	163
Faculty of Agriculture, University of Zagreb	Zagreb	Croatia	HRV041	Medium	Govt/Uni	156

Name	Location	Country	Code	Storage Type	Institute Type	Number of accessions
Instituut voor Landbouw- en Visserijonderzoek	Melle	Belgium	BEL094	Long	Govt	155
National Agricultural Research Institute	Asmara	Eritrea	ERI003	Long	Govt	141
Poltava State Regional Agricultural Experimental Station	Poltava	Ukraine	UKR093	NS	Govt	140
Banco de Germoplasma - Universidade da Madeira	Funchal	Portugal	PRT102	Long	Govt/Uni	133
Plant Science Agricultural Research and Training Institute	Darkhan Uul	Mongolia	MNG030	Long	Govt	132
Faculty of Agriculture, University Ss. Cyril and Methodius	Skopje	Macedonia	MKD001	NS	Govt/Uni	130
Laboratory of Plants Gene Pool and Breeding	Yerevan	Armenia	ARM035	Short	Govt	123
Estación Experimental de Toralapa	Tiraque	Bolivia	BOL317	Long	Govt	119
Plant Genetic Resources Department	Izmir	Turkey	TUR001	Long	Govt	114
Instituto Canario de Investigaciones Agrarias	Puerto de la Cruz	Spain	ESP117	Botanical	Govt	102
Banco Nacional de Germoplasma Vegetal	Edo	Mexico	MEX006	Long	Parastatal	101
National Agriculture Genetic Resources Centre-Genebank	Lalitpur	Nepal	NPL069	Long	Govt	100
Institute of Experimental Botany of the National Academy of Sciences of Belarus	Minsk	Belarus	BLR014	Long	Govt	99
Institute of Agriculture & Cattle-breeding of the Western Region	Lviv	Ukraine	UKR007	NS	Govt	99
Plant Genetic Resources Center	Tirana	Albania	ALB026	Long	Govt	94
Research Institute of Forage, Meadows and Pastures	Baku	Azerbaijan	AZE006	Short	Govt	86
Genetic Resources Institute	Banjaluka	Bosnia and Herzegovina	BIH039	Long	Govt/Uni	83
University of Agricultural Sciences and Veterinary Medicine Timisoara	Timisoara	Romania	ROM023	NS	Govt/Uni	73
Botanical Garden of the University of Osnabrück	Osnabrück	Germany	DEU502	Long	Govt/Uni	70
Centro de Conservación de la Biodiversidad Agrícola de Tenerife	Tacoronte	Spain	ESP172	NS	Govt	55
National Bank for Plant Genetic Resources	Tripoli	Libya	LBY006	Medium	Govt	55
Botanical Garden Berlin-Dahlem	Berlin	Germany	DEU022	Long	Govt	50
Botanical Garden of Plant Breeding and Acclimatization Institute	Jezdziecka	Poland	POL022	Medium	Govt	43
Pädagogische Hochschule Karlsruhe	Karlsruhe	Germany	DEU626	Long	University	42
National Clonal Germplasm Repository	Corvallis	United States	USA026	Long	Govt	42
Research Institute of Crop Husbandry	Baku	Azerbaijan	AZE003	Medium	Govt	41
Botanischer Versuchs- und Lehrgarten der Universität Regensburg	Regensburg	Germany	DEU515	Long	Govt/Uni	41
Government Plant Breeding Station	Merelbeke	Belgium	BEL094	NS	Govt	39
Centro de Investigación de Zamadueñas	Valladolid	Spain	ESP109	Medium	Govt	39
Corporación Colombiana de Investigación Agropecuaria Tibaitata	El Dorado	Colombia	COL017	Long	Govt	33
Banco Base de Germoplasma	Hurlingham	Argentina	ARG1342	Long	Govt	31
Myronivka Institute of Wheat	Myronivka	Ukraine	UKR003	NS	Govt	30
OSEVA PRO Ltd. Grassland Research Station	Zubri	Czech Republic	CZE082	NS	Private	29
Armenian Botanical Society	Yerevan	Armenia	ARM010	NS	NGO	26
Escuela Técnica Superior de Ingenieros Agrónomos. Banco de Germoplasma	Madrid	Spain	ESP003	Long	Govt	26
Bangladesh Institute of Nuclear Agriculture	Mymensingh	Bangladesh	BGD028	Short	Govt	25

Name	Location	Country	Code	Storage Type	Institute Type	Number of accessions
Agricultural Plant Genetic Resources Conservation and Research Centre	Wad Medani	Sudan	SDN002	Long	Govt	25
Instituto Nacional de Ciencias Agrícolas	San Jose de las Lajas	Cuba	CUB005	Long	Govt	24
Fruit Laboratory, ARS Plant Germplasm Quarantine Office	Beltsville	United States	USA148	NS	Govt	24
Research Station of Medicinal Crops	Vinnytsia	Ukraine	UKR019	NS	Govt	23
Institute of Agriculture	Podgorica	Montenegro	MNE001	NS	Govt	22
Austrian Agency for Health and Food Safety / Seed Collection	Linz	Austria	AUT001	Long	Govt	18
Banco Activo de Germoplasma de La Consulta	La Consulta	Argentina	ARG1350	Medium	Govt	15
Federal Plant Variety Office (Bundessortenamt)	Hannover	Germany	DEU101	Long	Govt	15
National Crop Variety Testing Centre	Leixlip	Ireland	IRL029	NS	Govt	15
Phytotechnie tropicale et Horticulture	Gembloux	Belgium	BEL002	Long	Govt	13
Norddeutsche Pflanzenzucht Hans-Georg Lembke KG	Holtsee	Germany	DEU005	Long	Private	13
Institute of Rose and Essential-oil Plants, Ministry of Agriculture	Kazanlak	Bulgaria	BGR005	NS	Govt	12
Arche Noah Association	Schiltern	Austria	AUT046	NS	NGO	10
Banco de Germoplasma de Horticolas	Zaragoza	Spain	ESP027	Long	Govt	10
Agricultural Institute Osijek	Osijek	Croatia	HRV021	NS	Govt	10
Centro di Ricerca Orticoltura e Florovivaismo	Pontecagnano	Italy	ITA391	Long	Govt	9
Research Institute of Horticulture	Skierniewice	Poland	POL101	Long	Govt	8
Scientific Center of Agrobiotechnology	Echmiadzin	Armenia	ARM059	Long	Govt	7
Institute for Seed and Seedlings	Osijek	Croatia	HRV053	Long	Govt	7
Centro Internacional de Agricultura Tropical	Cali	Colombia	COL003	Long	CGIAR	6
World Vegetable Center	Tainan	Taiwan	TWN001	Long	NGO	5
National Arboretum-Germplasm Unit	Washington	United States	USA151	NS	Govt	5
National Tree Seed Laboratory	Dry Branch	United States	USA476	NS	Govt	5
Centro Agronómico Tropical de Investigación y Enseñanza	Turrialba	Costa Rica	CRI001	Long	International	4
Kyiv Experimental Station	Kyiv	Ukraine	UKR053	NS	Govt	4
Institute of Botany	Baku	Azerbaijan	AZE004	NS	Govt	3
Estación Central de Pastos y Forrajes de Sancti Spiritus	Sancti Spiritus	Cuba	CUB126	NS	Govt	3
Fiompiana Fambolena Malagasy Norvéziana	Antsirabe	Madagascar	MDG038	Long	Govt	3
Centro Nacional de Recursos Genéticos	Tepatitlán de Morelos	Mexico	MEX208	Long	Govt	3
Institut for forage crops Krusevac	Kruševac	Serbia	SRB062	Short	Govt	3
Seed Savers Exchange	Decorah	United States	USA974	NS	NGO	3
SADC Plant Genetic Resources Centre	Lusaka	Zambia	ZMB030	NS	Regional	3
Banco de Germoplasma de Papa	Valdivia	Chile	CHL071	Medium	University	2
Estación Experimental de Pastos y Forrajes Indio Hatuey	Perico	Cuba	CUB010	NS	Govt	2
Niko Ketskhoveli Institute of Botany	Tbilisi	Georgia	GEO013	Medium	Govt	2
Banca del germoplasma autoctono vegetale regionale	Udine	Italy	ITA368	NS	Govt	2
Argotti Botanic Gardens & Resource Centre	Floriana	Malta	MLT001	Botanic	Govt	2
Plant Breeding Station	Wiatrowo	Poland	POL033	Medium	Govt	2

Name	Location	Country	Code	Storage Type	Institute Type	Number of accessions
Institute of Plant Production n.a. V.Y. Yurjev of UAAS	Kharkiv	Ukraine	UKR001	Long	Govt	2
Institute of Breeding and Genetics	Odesa	Ukraine	UKR002	NS	Govt	2
Estación Experimental Agropecuaria Chubut	Trelew	Argentina	ARG1221	Long	Govt	1
The Polesye Institute of Plant Growing	Knychny	Belarus	BLR026	Long	Parastatal	1
Banco de Germoplasma de la Universidad Técnica Particular de Loja	Loja	Ecuador	ECU167	Medium	Private	1
Consejo Superior de Investigaciones Científicas. Misión Biológica de Galicia	Salcedo	Spain	ESP009	Long	Govt	1
Instituto Murciano de Investigación y Desarrollo Agrario y Alimentario	Murcia	Spain	ESP133	Long	Govt	1
Institut de recerca i formació agrària i pesquera	Palma de Mallorca	Spain	ESP200	Long	Govt	1
Lieberman Germplasm Bank	Tel-Aviv	Israel	ISR003	Medium	Govt/Uni	1
Botanical Garden	Vilnius	Lithuania	LTU010	Long	Govt/Uni	1
Instituto de Investigación y Capacitación Agropecuaria, Acuicola y Forestal	Metepec	Mexico	MEX194	Long	Regional	1
Krasnohrad Experimental Station	Kharkiv	Ukraine	UKR068	NS	Govt	1
Ornamental Plant Germplasm Center	Columbus	United States	USA956	NS	Govt/Uni	1
National Plant Genetic Resources Centre	Chilanga	Zambia	ZMB048	Long	Govt	1

¹NS, Not Specified

²Note that the Jõgeva Plant Breeding Institute (EST001) has merged with the Estonian Crop Research Institute (EST019), accession numbers for these were added.

9.8 Summary of guiding documents for genebanks, available online

G-01 Austria

European Commission Directive 2010/60/EU

Directive allows for the collection, marketing and distribution of seed mixtures intended for preservation of the natural environment (grasslands in this case) and conservation of genetic diversity, even if some of the components of those seed mixtures do not meet other seed marketing requirements. Such mixtures should be accompanied by identification of component species and source of origin.

G-03 Washington (USA)

Management of Temperate-adapted Forage Legume Genetic Resources and Associated Information

- Objective 1: Efficiently and effectively acquire temperate-adapted forage legume genetic resources; maintain their safety, genetic integrity, health and viability; and distribute them and associated information worldwide. Sub-objectives include gap filling, regeneration, screen for glyphosate resistance.
- Objective 2: Develop more effective genetic resource maintenance, characterization and evaluation methods and apply them to priority genetic resources of temperate-adapted forage legumes. Record and disseminate evaluation and characterization data and digital images via GRIN-Global and other data sources. Sub-objectives include generating and providing access to characterization data, estimating genetic diversity & redundancy.
- Objective 3: With other NPGS genebanks and Crop Germplasm Committees, develop, update, document, and implement best management practices (particularly for alfalfa with genetically engineered traits) and Crop Vulnerability Statements for temperate-adapted forage legume genetic resource and information management.

G-05 Chile

Policy access to Genetic Resources of INIA

The general objective of this policy is to provide an institutional framework under which INIA will deal with requests for genetic material collected and/or maintained in its germplasm banks, and the terms and conditions under which it may grant access to these materials.

Specific objectives

- To establish and have institutional rules and procedures for processing access requests to germplasm held by INIA.
- To promote protection, research and sustainable use of genetic resources incorporated in the Bank Network.
- To secure an immediate but properly controlled access to the germplasm held by INIA.

G-07 New Zealand

Nationally Significant Collections and Databases

Objectives as implied by key performance indicators include:

- Improved accessibility and prompt distribution of accessions to users (nationally and internationally)
- Increasing the number of accessions held by the genebank
- Improving the quality of passport data for existing and new accessions
- Development of global core collections, primarily for white clover and ryegrass

G-11 Poland

The National Centre for Plant Genetic Resources serves as the National Coordinator for Plant Genetic Resources Programme, with the objective of conservation of genetic variability of crop plants endangered with genetic erosion in Poland.

Objectives:

- collection of populations and cultivated varieties of crop and wild plants threatened with genetic erosion,
- description and evaluation of collected materials,
- maintenance of seed samples and clones in viable state and in genetic purity,
- documentation of collected materials, exchange of samples with other gene banks and botanical gardens worldwide,
- providing of initial plant materials for breeding and research programs.

G-12 Lebanon (ICARDA)

CGIAR Genebank Platform, four outcomes

- Disease-free, viable, documented germplasm made available

- More effective access and use of germplasm enabled
- Policy engagement and compliance ensured
- Crop diversity conserved in a rational and effective global system

Targets – by 2022

- Availability: 90% of accessions healthy and available for immediate distribution
- Security: 90% of samples safety duplicated in two locations by 2022
- Information: 90% of accessions have minimum passport or characterization data online
- Quality Management System: agreed elements of QMS in place at all genebanks

G-12 Canada

AAFC/STB Sector Strategy Biodiversity and Collections

Key activities relevant to agricultural germplasm conservation include

- Enhancing crop productivity, quality and resiliency by providing sources of genetic variability for genetic improvement
- Providing authoritative identification of species and enhancing the understanding of beneficial organisms (biocontrol agents, symbionts, pollinators, etc.), biotic competitors and pests that affect the sector's productive capacity
- Enhancing the understanding and use of crop and livestock genetic diversity to support sustainable agricultural production
- Providing research, knowledge and sources of genetic variability to improve the attributes of Canada's agricultural commodities and to support new opportunities for food and non-food uses
- Mitigating genetic erosion of production systems through the enhancement and conservation of crop and farm animal genetic diversity

G-13 France

Charte pour la gestion des ressources génétiques des fourrages et des gazons ("Charter for the management of genetic resources of fodder and turf")

G-14 Netherlands

Bronnen van ons bestaan ("Sources of our existence"), conservation and sustainable use of genetic diversity

G-16 Spain

Programa Nacional de Conservación y Utilización Sostenible de los Recursos Fitogenéticos para la Agri-

cultura y la Alimentación ("National Programme for the Conservation and Sustainable Use of Plant Genetic Resources for Food and Agriculture").

Objectives of the first plan of Action (2018-2022)

- To ensure the long-term conservation of plant genetic resources whose genetic potential makes them susceptible to use in agriculture and food;
- Guarantee their viability and good health
- Encourage its use by research and the productive sector
- Optimize the use of resources for their conservation and utilization and encourage the participation of the responsible Administrations
- Improve the competitiveness of the agricultural sector, establish synergies between all sectors with interests in plant genetic resources, and promote European cooperation and international in this area

Ex situ Conservation Actions. The following permanent shares are considered preferred:

- Maintenance of the Network of Collections of the National Program, both of the species conserved by seeds and those of vegetative reproduction maintained in the field or in vitro, including the conservation, multiplication and regeneration of the material, guaranteeing its good sanitary status and viability.
- Primary characterization of the active collections, which will be fundamentally an agro/morphological characterization based on internationally agreed descriptor lists.
- Duplication in the base collection of the Center for Plant Genetic Resources (CRF) of the National Institute for Agricultural and Food Research and Technology (INIA) of the orthodox seed collections of the Network of Collections of the National Program that have not yet been deposited in the CRF.
- Duplication of the active collection of cereals and legumes of the INIA Plant Genetic Resources Center that currently shares facilities with the base collection.
- In addition, the prospecting and collection of traditional plant genetic resources, autochthonous or of socio-economic or environmental importance of agricultural species, in particular those of minor and disused species and those existing in marginal areas for their cultivation, is considered as a specific action, as well as its associated traditional knowledge. Likewise, special attention will be paid to related wild species, at risk of extinction, not yet collected.

9.9 Numbers of genebanks distributing temperate forage germplasm to various types of user groups.

Numbers of genebanks (total 12 respondents) distributing temperate forage germplasm to various types of user groups.

User Group	Multiple times per year	Once per year	Occasionally	Never
Domestic users	10		1	1
Academic researchers and students	8	2	1	
Foreign users	7	1	2	1
Plant breeders – public sector	6	3	2	
Farmers or farmer organizations	5		5	1
Plant breeders – private sector	5	1	5	
Non-government organizations	4	1	5	
Other genebank curators	3	2	6	

9.10 Selected metrics for forage crops and maize (as comparison)

This annex was written by Dr. Felix Frey, International Consultant, Global Crop Diversity Trust

Khoury et al. (2021) compiled a comprehensive dataset as part of a project funded by the [International Treaty on Plant Genetic Resources for Food and Agriculture](#) and 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 for use 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. (2021) 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.

To put numbers into context, we compare temperate forage crops with maize (Table 1). Both crops / crop groups are produced on a global scale and are used for animal feed. Temperate forage crops span 11 genera including 49 species (Tables 2 and 3a and 3b). Genus and species names of maize are *Zea* and *Zea mays*, 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. 2021). The respective metrics are not always reported for all temperate forage crops independently as e.g. for maize, where FAOSTAT reports separate metrics. With respect to production and trade of

temperate forage crops, FAOSTAT reports values for grasspea within the category “Pulses, nes”, among other crops, thus numbers for these crops cannot be disaggregated. However, lupins are reported in its own category “Lupins”. For the rest of the temperate forage crops no data for production is available from FAOSTAT. 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). We must note that most forage crops are not used for human consumption and thus, food supply values are not available or do not reflect their actual use as feed. Nevertheless, we present numbers reported for some of the forage crops in the following. With respect to food supply, FAOSTAT summarizes various crops into categories, independently from production. The reported temperate forage crops fall into two groups. Grasspea and lupins are reported, among other crops, within the category “Pulses, Other”. Although food supply numbers are not reported separately for “Pulses, Other”, Khoury et al. (2021) inferred the food supply values for this group from the combined metrics reported for “Lupins” and “Pulses, nes”. They first calculated the weight of “Lupins” within “Pulses, Other” by global production. For this the global annual production of “Lupins” was divided by global annual production of “Pulses, Other”, resulting in the weight within the group. To finally calculate food supply for “Lupins”, they segregated the “Pulses, Other” food supply value by the weight of “Lupins”. For the case of grasspea this couldn’t be done, as data for both production and food supply is reported in aggregated categories, thus summarized numbers can be hugely overestimated. The global production of temperate forage crops is about 1.7 million tons

Table 1 Selected metrics collected by Khoury et al. (2021) for temperate forage crops and maize, subdivided by indicator domain

Metric	Temperate forages (Sum/Range)	Maize	Temperate forages / maize
Crop use			
Global production [tons] (Across all temperate forages species)	1,710,238	917,517,036	0.2%
Food supply (Amount consumed) [g/capita/day] (Across all temperate forage species)	1	49	2.0%
Percentage of countries producing crop * (Range across all temperate forage species)	12–50%	81%	
Percentage of countries consuming (being supplied with) crop *	93%	99%	94.2%
Quantity exported globally [t] (Across all temperate forage species)	1,402,268	120,837,238	1.2%
Number of publications between 2009–2019, including patents and citations, searching title of publication (Google scholar search hits) for genus ** (Across all temperate forage species)	25,965	16,400	158.3%
Number of publications between 2009–2019, including patents and citations, searching title of publication (Google scholar search hits) for species *** (Across all temperate forage species)	8,668	16,300	53.2%
Interdependence			
Interdependence of global production from germplasm from primary centers of diversity [0–1] **** (Range across all temperate forage species)	89–94%	97%	
Interdependence of global food supply from germplasm from primary centers of diversity [0–1] **** (Range across all temperate forage species)	96%	89%	107.9%
Demand			
Accessions distributed from genebanks (Annual average 2014–2017) (Across all temperate forage species)	13,992	49,148	28.5%
Variety releases in 5 years (2014–2018) (Across all temperate forage species)	41,674	126,232	33.0%
Supply			
Number of accessions in <i>ex situ</i> collections of genus ** (Across all temperate forage species)	316,183	213,337	148.2%
Number of accessions in <i>ex situ</i> collections of species *** (Across all temperate forage species)	245,941	208,062	118.2%
Accessions of the genus ** available through Multilateral System (MLS) directly noted in databases [%] (Range across all temperate forage species)	8–45%	20%	
Accessions of the species *** available through Multilateral System (MLS) directly noted in databases [%] (Range across all temperate forage species)	8–45%	20%	
Accessions of the genus ** available through Multilateral System (MLS) indirectly by matching institute countries with party status [%] (Range across all temperate forage species)	66–84%	69%	
Accessions of the species *** available through Multilateral System (MLS) indirectly by matching institute countries with party status [%] (Range across all temperate forage species)	65–83%	69%	
Security			
Accessions of genus ** safety duplicated in Svalbard Global Seed Vault [%] (Range across all temperate forage species)	5–27%	15%	
Accessions of species *** safety duplicated in Svalbard Global Seed Vault [%] (Range across all temperate forage species)	6–43%	15%	
1-GINI index for equality of production across the world [0–1] ***** (Range across all temperate forage species)	0.01–0.06	0.03	
1-GINI index for equality of food supply across the world [0–1] *****	0.15	0.15	100%

* 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)

** Temperate forages: Genus names, Table 2; Maize: *Zea*

*** Temperate forages: Species names, Table 2; Maize: *Zea mays*

**** 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

annually, which is only 0.2% of the global maize production (about 917 M t). The quantity of food supply by temperate forage crops, i.e. the average global consumption, is about 1 g/cap/day representing about 2% of global maize supply as food source (49 g/cap/day). As stated before, data for production and food supply of temperate forages can be hugely overestimated, as it can't be disaggregated. The percentage of countries in the world producing temperate forage crops ranges from 12 (lupins) to 50% (grasspea).

Maize is produced in 81% of countries in the world. Temperate forage crops consumption takes place in 93% (grasspea and lupins) of the world's countries, where maize is consumed in 99% of the world's countries. Export of temperate forage crops is relatively more important than export of maize. About 50% of produced temperate forage crops are exported (1,440,276 t), where only 13% of produced maize (120,837,238 t) is exported. This being said, it must be taken into account that information for the metrics

Table 2 Temperate forage crops, corresponding genus, species, FAOSTAT category and origin

Crop	Genus	Species	FAO stat category	Origin
Alfalfa	<i>Medicago</i>	<i>Medicago sativa</i> , <i>Medicago arborea</i> , <i>Medicago falcata</i> , <i>Medicago scutellata</i> , <i>Medicago rigidula</i> , <i>Medicago truncatula</i>	NA*	Central Asia and West Asia
Clovers	<i>Trifolium</i>	<i>Trifolium repens</i> , <i>Trifolium pratense</i> , <i>Trifolium alexandrinum</i> , <i>Trifolium alpestre</i> , <i>Trifolium ambiguum</i> , <i>Trifolium angustifolium</i> , <i>Trifolium arvense</i> , <i>Trifolium agrocicerum</i> , <i>Trifolium hybridum</i> , <i>Trifolium incarnatum</i> , <i>Trifolium pratense</i> , <i>Trifolium repens</i> , <i>Trifolium resupinatum</i> , <i>Trifolium rueppellianum</i> , <i>Trifolium semipilosum</i> , <i>Trifolium subterraneum</i> , <i>Trifolium vesiculosum</i>	NA*	Central Asia, South Asia, West Asia, South and East Mediterranean, North Eastern Europe, South Eastern Europe, North Western Europe and South Western Europe
Dactylis	<i>Dactylis</i>	<i>Dactylis glomerata</i>	NA*	Central Asia, South Asia, West Asia, South and East Mediterranean, North Eastern Europe, South Eastern Europe, North Western Europe and South Western Europe
Fescue	<i>Festuca</i>	<i>Festuca arundinacea</i> , <i>Festuca gigantea</i> , <i>Festuca heterophylla</i> , <i>Festuca ovina</i> , <i>Festuca pratensis</i> , <i>Festuca rubra</i>	NA*	Central Asia, South Asia, West Asia, South and East Mediterranean, North Eastern Europe, South Eastern Europe, North Western Europe and South Western Europe
Grasspea	<i>Lathyrus</i>	<i>Lathyrus sativus</i>	Pulses, nes (production/trade**) / Pulses, Other (food supply)	West Asia
Lolium	<i>Lolium</i>	<i>Lolium hybridum</i> , <i>Lolium xhybridum</i> , <i>Lolium multiflorum</i> , <i>Lolium perenne</i> , <i>Lolium rigidum</i> , <i>Lolium temulentum</i>	NA*	Central Asia, South Asia, West Asia, South and East Mediterranean, North Eastern Europe, South Eastern Europe, North Western Europe and South Western Europe
Lotus	<i>Lotus</i>	<i>Lotus corniculatus</i> , <i>Lotus subbiflorus</i> , <i>Lotus uliginosus</i>	NA*	Central Asia, East Asia, South Asia, West Asia, South and East Mediterranean, North Eastern Europe, South Eastern Europe, North Western Europe and South Western Europe
Lupins	<i>Lupinus</i>	<i>Lupinus mutabilis</i> , <i>Lupinus albus</i> , <i>Lupinus angustifolius</i> , <i>Lupinus luteus</i>	Lupins (production/trade**) / Pulses, Other (food supply)	Andean South America, South and East Mediterranean, South Eastern Europe and South Western Europe
Onobrychis	<i>Onobrychis</i>	<i>Onobrychis viciifolia</i>	NA*	South Eastern Europe and South Western Europe
Phleum	<i>Phleum</i>	<i>Phleum pratense</i>	NA*	Central Asia, East Asia, South Asia, West Asia, South and East Mediterranean, North Eastern Europe, South Eastern Europe, North Western Europe and South Western Europe
Poa	<i>Poa</i>	<i>Poa alpina</i> , <i>Poa annua</i> , <i>Poa pratensis</i>	NA*	Central America and Mexico, North America, Central Asia, East Asia, South Asia, West Asia, South and East Mediterranean, North Eastern Europe, South Eastern Europe, North Western Europe and South Western Europe

*Forage so not in food supply data

**Not clearly in trade data

“Global production”, “Food supply”, “Percentage of countries producing crop” and “Percentage of countries consuming crop” information was only available for grasspea and lupins, while for the metric “Quantity exported globally” information was only available for alfalfa (Table 3).

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. 2021). Search hits on Google Scholar indicate the level of scientific interest in a crop. The genus names of the different temperate forage crops (Table 2) are found in 25,965 publication titles, which is about 58% higher than the publication titles including the maize genus *Zea* (16,400). However, we must take into account that temperate forages encompass 11 genera compared

to only one of maize. Publication numbers including the species names of temperate forage crops and maize are more relatable. The scientific names of the temperate forage crops (Table 2) appear in 8,668 publication titles, led mainly by alfalfa with 3,230, where *Zea mays* appears in 16,300 publication titles. Temperate forage crops research at the species level is 53% of maize’s research. If related to the comparison of production between both crops presented previously, temperate forage crops research is highly overrepresented when compared to maize research. However, research is not evenly distributed among temperate forage crops, as scientific species names of *Poa*, *Phleum* and *Onobrychis* are present in only 11, 230 and 242 publication titles, respectively.

Khoury et al. (2021) defined interdependence as a measure for the degree of dependence of the global cultivation and use of a certain crop from germplasm

Table 3a Table of indicator values for species within temperate forage crops

Metric	Phleum	Poa	Lolium	Lotus	Fescue
Crop use					
Global production [tons]	NA	NA	NA	NA	NA
Food supply (Amount consumed) [g/capita/day]	NA	NA	NA	NA	NA
Percentage of countries producing crop *	NA	NA	NA	NA	NA
Percentage of countries consuming (being supplied with) crop *	NA	NA	NA	NA	NA
Quantity exported globally [t]	NA	NA	NA	NA	NA
Number of publications between 2009–2019, including patents and citations, searching title of publication (Google scholar search hits) for genus **	293	1,410	3,190	6,270	1,790
Number of publications between 2009–2019, including patents and citations, searching title of publication (Google scholar search hits) for species ***	230	11	1,660	435	602
Interdependence					
Interdependence of global production from germplasm from primary centers of diversity [0–1] ****	NA	NA	NA	NA	NA
Interdependence of global food supply from germplasm from primary centers of diversity [0–1] ****	NA	NA	NA	NA	NA
Demand					
Accessions distributed from gene banks (Annual average 2014–2017)	75	379	1,366	631	NA
Variety releases in 5 years (2014–2018)	1,463	2,979	20,280	323	NA
Supply					
Number of accessions in <i>ex situ</i> collections of genus **	10,665	12,908	28,711	10,597	NA
Number of accessions in <i>ex situ</i> collections of species ***	9,898	9,692	26,522	5,879	NA
Accessions of the genus ** available through Multilateral System (MLS) directly noted in databases [%]	42%	26%	30%	32%	NA
Accessions of the species *** available through Multilateral System (MLS) directly noted in databases [%]	45%	33%	31%	22%	NA
Accessions of the genus ** available through Multilateral System (MLS) indirectly by matching institute countries with party status [%]	66%	72%	76%	73%	NA
Accessions of the species *** available through Multilateral System (MLS) indirectly by matching institute countries with party status [%]	65%	71%	77%	67%	NA
Security					
Accessions of genus ** safety duplicated in Svalbard Global Seed Vault [%]	15%	12%	15%	6%	NA
Accessions of species *** safety duplicated in Svalbard Global Seed Vault [%]	16%	15%	16%	10%	NA
1-GINI index for equality of production across the world [0–1] *****	NA	NA	NA	NA	NA
1-GINI index for equality of food supply across the world [0–1] *****	NA	NA	NA	NA	NA

present at the primary centers of diversity of the respective 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 the 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 centers of diversity and thus also higher than the global mean. Therefore, interdependence with respect to food supply can be above 100%. Primary centers of diversity of temperate forage crops are located in Asia, Europe and the Americas (Table 2). Grasspea is mainly produced in India (FAOSTAT 2021A), having its primary center of diversity in West Asia. However, as production for grasspea is not reported separately, interdependence cannot be

Table 3b Table of indicator values for species within temperate forage crops

Metric	Lupins	Grasspea	Alfalfa	Clovers	Dactylis	Onobrychis
Crop use						
Global production [tons]	1,138,257	571,981	NA	NA	NA	NA
Food supply (Amount consumed) [g/capita/day]	1	0	NA	NA	NA	NA
Percentage of countries producing crop *	12%	50%	NA	NA	NA	NA
Percentage of countries consuming (being supplied with) crop *	93%	93%	NA	NA	NA	NA
Quantity exported globally [t]	NA	NA	1,402,268	NA	NA	NA
Number of publications between 2009–2019, including patents and citations, searching title of publication (Google scholar search hits) for genus **	2,320	983	5,870	2,720	531	588
Number of publications between 2009–2019, including patents and citations, searching title of publication (Google scholar search hits) for species ***	456	537	3,230	767	498	242
Interdependence						
Interdependence of global production from germplasm from primary centers of diversity [0–1] ****	89%	94%	NA	NA	NA	NA
Interdependence of global food supply from germplasm from primary centers of diversity [0–1] ****	96%	96%	NA	NA	NA	NA
Demand						
Accessions distributed from gene banks (Annual average 2014–2017)	1,432	2,195	5,295	1,651	577	391
Variety releases in 5 years (2014–2018)	1,183	48	4,681	9,032	1,562	123
Supply						
Number of accessions in <i>ex situ</i> collections of genus **	28,874	23,818	81,671	92,046	22,307	4,586
Number of accessions in <i>ex situ</i> collections of species ***	21,601	14,657	39,040	95,287	21,927	1,438
Accessions of the genus ** available through Multilateral System (MLS) directly noted in databases [%]	8%	18%	43%	33%	45%	19%
Accessions of the species *** available through Multilateral System (MLS) directly noted in databases [%]	8%	19%	41%	28%	45%	35%
Accessions of the genus ** available through Multilateral System (MLS) indirectly by matching institute countries with party status [%]	74%	78%	84%	73%	80%	71%
Accessions of the species *** available through Multilateral System (MLS) indirectly by matching institute countries with party status [%]	71%	83%	80%	66%	80%	80%
Security						
Accessions of genus ** safety duplicated in Svalbard Global Seed Vault [%]	5%	11%	27%	7%	11%	6%
Accessions of species *** safety duplicated in Svalbard Global Seed Vault [%]	6%	17%	43%	7%	12%	16%
1-GINI index for equality of production across the world [0–1] *****	0.01	0.06	NA	NA	NA	NA
1-GINI index for equality of food supply across the world [0–1] *****	0.15	0.15	NA	NA	NA	NA

calculated for this crop. Interdependence with respect to production value is high for lupins (89%), Australia being its main producer (FAOSTAT 2021A), with its centers of diversity located in Andean South America, South and East Mediterranean, South Eastern Europe and South Western Europe. The interdependence value of production for maize is 97%, where primary centers of diversity are in Andean South America, Central America and Mexico, and main producers are the United States of America and China (FAOSTAT 2021A). For the case of interdependence with respect to food supply, lupins have a value of 96%, where the main consuming country is Morocco (FAOSTAT 2021B). Maize has an interdependence with respect to food supply value of 89%. For the interdependence metrics information was only available for grasspea and lupins (Table 3).

Demand for germplasm is defined by two metrics (Khoury et al., 2021): (1) the number of distributions of accessions by genebanks, as an annual average between 2014 and 2017 drawn from the Plant Treaty 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; www.upov.int). There is a relatively strong use of temperate forage crops germplasm reflected by the 13,992 accessions per year distributed by gene banks, led by alfalfa (5,295) and grasspea (2,195), which is about 28% of yearly distributions of maize accessions (49,148). A similar picture is true in relation to the development of new cultivars in a five-year period. 41,674 temperate forage crops varieties were released during a five-year period, lolium and clovers showing the higher numbers, with 20,280 and 9,032 new cultivars, respectively. This represents 33% of maize varieties released in the same time period (126,232 registered new cultivars). In relation to low global production of temperate forage crops mentioned above, germplasm conservation and cultivar development are relatively high. However, some temperate forage crops show severely low levels of accessions per year distributed in gene banks and for new cultivars developed, such as onobrychis (391 and 123, respectively) and lotus (631 and 323, respectively).

Khoury et al. (2021) 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 consid-

ering 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 316,183 accession of temperate forage crops when relating to the genus level, with clover and alfalfa having highest accession numbers, (92,046 and 81,671, respectively), and onobrychis the lowest with 4,586 accessions. The number of temperate forage crop accessions, at the genus level, is approximately 48% higher than maize's genus *Zea* (213,337 accessions), where 208,062 accessions are attributed to the species *Z. mays*. Temperate forages have a total of 245,941 accessions at the species level, where, again, clovers and alfalfa present the highest numbers (with 95,287 and 39,040 accessions, respectively) and onobrychis the lowest, with 1,438 accessions. From the crops discussed in this document, maize, lotus (species *Lotus corniculatus*, *L. subbiflorus* and *L. uliginosus*), onobrychis, phleum and poa (species *Poa alpina*, *P. annua* and *P. pratensis*) are listed in Annex I of the Plant Treaty (FAO 2009). For both the genus and species level, 8 (lupins) to 45% (dactylis, phleum only for genus level) of the temperate forage crop accessions are available under MLS, stated directly in respective databases, where 20% of maize's accessions are available directly under MLS, both at the genus (*Zea*) and species (*Z. mays*) level. However, if counting accessions available indirectly by matching institute countries with party status, at the genus level 66 (phleum) to 84% (alfalfa) of temperate forage crops accessions can be made available, compared to 69% of maize accessions with respect to both genus and species. At the species level, 65 (phleum) to 83% (grasspea) of accessions are available for temperate forage crops.

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 (see above), 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. (2021) 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, as in the case of natural disasters. At the genus level, 5 (lupins) to 27% (alfalfa) of temperate forage accessions are safety duplicated at SGSV. At the species level the values range from 6 (lupins) to 43% (alfalfa). For maize, 15% of its accessions, both at the genus and species level, are safety duplicated at SGSV. Equality of the distribution across the world's regions with respect to global production of temperate forage crops (0.01 – 0.06) is in the same range as equality of distribution for production of maize (0.03). It is relatively low for lupins (0.01), while grasspea has the highest value (0.06). Food supply of temperate forage crops has the same value as maize (0.15), meaning they are equally distributed throughout the world.

Literature

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