



**FOOD
FOREVER**

POLICY BRIEF
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Importance of Long-Term Conservation of Temperate Forages for Sustainable Livestock

Tony Conner

Key Messages



- Germplasm resources for temperate forages that support the future of sustainable livestock production contain thousands of taxa, dominated by Poaceae (grasses) and Fabaceae (legumes).
- Better coordination among genebanks in developed and developing countries via a formal network is urgently required to ensure optimal allocation of global resources.
- Global capacity and resources to ensure the conservation of temperate forage germplasm are inadequate. There is a critical need for updated interactive databases, regeneration of existing collections, and characterisation of phenotypic traits in accessions so germplasm can be utilised for pre-breeding, and targeted collections of at-risk germplasm before it is lost forever.
- A substantial 'one-off' international investment over the next decade is required to collectively address these interdependent key issues of critical importance for future sustainable livestock production.

OVERVIEW

Purpose

This policy brief highlights the crucial role temperate forage conservation plays for the long-term sustainable livestock production, especially in the context of pasture grazing versus other livestock feeding practices. It focuses on the current state of global efforts to conserve temperate forage germplasm and identifies ongoing gaps that need to be overcome to ensure that more resilient and sustainable food systems are successfully implemented in the future.

Importance of temperate forage conservation in sustainable livestock production

Grasslands form a major component of the global ecosystem by occupying 37% of the earth's terrestrial area. This is made up of natural grasslands of diverse species and sown pastures (usually involving grass and legume species) and occupies 69% of the agricultural land on the planet.

Ruminant livestock are highly efficient at converting high-cellulose plant material into protein and energy for human consumption. Grasslands and pastures make a major contribution to food security through providing the feed requirements of ruminant animals used for milk and meat production from a free-range system.

Agricultural land with good soil and water for irrigation is generally occupied by horticultural and arable crops, forcing grassland grazing onto marginal land. These marginal areas are exposed to salinization, acidification, drought escalation from ongoing climate change, and overgrazing which further escalate the problems of soil erosion and weed invasion. Consequently, many natural grasslands are in poor condition and exhibit symptoms of degradation. Conservation of grasslands and the germplasm resources within these ecosystems is crucial for future breeding efforts of forages to support sustainable livestock production.

Advantages of grazing compared to other feed practices in the livestock sector

Grazing is associated with more sustainable farming systems and the restoration of ecosystem balance. Manure from ruminant livestock provides nutrients and organic matter for promoting soil health and restoring soil microbial diversity which make the land more resilient to flooding and drought. Resilient grasslands and pastures help to reduce greenhouse gas emissions through carbon sequestration in the living soil.

Pasture-fed and grain-fed ruminant livestock, especially cattle, are responsible for considerable greenhouse gas emissions. Improving the quality and management of the feed supply can contribute to more efficient practices and reduced emissions. Germplasm resources offer opportunities to breed forages with reduced emissions, and along with grazing management, contribute to creating carbon sinks to help offset livestock sector emissions.

Social acceptability and public perceptions demand that food is produced from more natural environments. For the livestock sector this represents grazing on grasslands and pastures which mimics the grazing of ruminants in the way they evolved in nature. Provided animals are protected from extreme weather events, grazing provides a more humane agricultural system generally recognised as providing better health, welfare, and wellbeing of animals.

Pasture-fed ruminants grazing on quality forage produce food with higher concentrations of antioxidants and some vitamins than grain-fed ruminants. The resulting meat and milk have lower saturated fats and contain more omega-3 fatty acids and conjugated linoleic acid. These are all linked to health benefits for humans.

CURRENT STATE OF TEMPERATE FORAGE CONSERVATION

Temperate forages include a wide range of species naturally found in temperate grasslands latitudinally between 30° and



60° around the globe. These species are dominated by two plant families: Poaceae (the grasses) and Fabaceae (the legumes). Less than 20 key temperate forage species are primarily used across the global livestock sector. Within these species, plant breeders have selected and bred new cultivars that are commercially traded by the global seed industry. In addition, many more species have been partially domesticated and are cultivated in localised regions for livestock production. Coupled with related species that can be hybridised with cultivated temperate forages, potentially thousands of taxa make up the germplasm resource of new genetic variation for breeders of forage species.

Temperate forage germplasm is at risk from the usual threats to biodiversity. These include loss of habitats in the centres of origin and diversity, land use changes, political conflicts, urbanisation, and lack of resources in genebanks for further collections. For temperate forage germplasm, this is exacerbated by overgrazing of natural grasslands and conversion of natural grasslands to intensive grazing systems using introduced species.

Collections of temperate forage germplasm are held in >160 organisations across >70 countries, which substantiates the global recognition that conservation of these species is important. Many of these collections are relatively small, with 19 key genebanks holding approximately 80% of all temperate forage accessions. Nine species dominate these collections and account for about half of all temperate forage accessions. Other key species are only poorly represented in genebanks, with the situation being even more dramatic for related species as germplasm resources of new genetic variation forage breeders.

Emerging challenges

Phytosanitary requirements are becoming increasingly important for the international distribution of seed. Such requirements are put in place to protect territories from the inadvertent introduction of weeds, pests and diseases that may impact on agriculture, with certification requirements varying between countries. Recent updates to biosecurity requirements in some countries are placing more stringent conditions on germplasm introductions, and in some cases require the evaluation of germplasm accessions within quarantine facilities. This involves not just the host plant, but also any associated endogenous symbiotic microbes such as endophytic *Epichloë* fungi of grasses or rhizobia in legumes. Meeting phytosanitary requirements is placing additional demands on genebanks when attempting to screen germplasm accession for traits of interest for genetically improving forage species.

Biosecurity regulations that underpin phytosanitary requirements are generally based on taxa at the species level. For the international exchange of germplasm accession between genebanks and the release of germplasm to next users such as forage breeders, it is important that consistent taxonomic nomenclature is used. The status of plant taxonomy presents a major challenge for the characterisation of germplasm resources, especially for unique outlier accessions. Ongoing taxonomic revisions, while essential, cause intermittent confusion for identifying redundant duplications within and between genebank databases. Adoption of a standard nomenclature across genebanks, especially for the grass (Poaceae) and legume (Fabaceae) families, would provide greater clarity for interactions among genebanks.

Genomic tools offer new opportunities to assess genetic diversity within and between populations (and species) in a rapid and efficient manner. Estimates of genetic relatedness of individuals based on large data sets of single nucleotide polymorphisms can be easily derived from new methodologies such as genotyping-by-sequencing coupled with data assemblage workflows and statistical tools. This provides a powerful new tool for characterisation of germplasm. It allows accurate assessment of redundancy and biases in collections, as well as validating that the full genetic diversity has been captured and maintained during regeneration of accessions.

Future Scenarios

Future proofing advances in science and utilisation of germplasm resources would be facilitated by genebanks undertaking two additional activities with respect to accessions: depositing herbarium specimens and establishing DNA banks, with the details added to passport data associated with accessions.

Depositing herbarium specimens for each accession in national herbaria provides a huge study resource for taxonomists and aligns taxonomic studies and revisions of nomenclature to accessions in genebanks. This would mitigate the ongoing issues that curators face when assigning taxonomic status to accessions and facilitate the alignment of data base records between genebanks.

Likewise, given the opportunities provided by genomics to efficiently investigate genetic variation within and between populations (and species), a DNA bank of accessions in genebank collections would be immensely valuable. Applying



genomic tools will provide assurance that the full genetic diversity is captured and maintained; this will also allow identification of duplications and biases within and between genebanks.

The preparation of herbarium specimens at the time of collecting seed of wild accessions would be cumbersome. The best practice would be to undertake this task at the time accession are regenerated. However, DNA isolation should be done as soon as seeds have arrived from the collecting missions to ensure the originality is captured and changes in DNA makeup during storage or regeneration are avoided. Establishment and adoption of standard operating protocols across genebanks would be important. The transfer of herbarium specimens and DNA samples will help to satisfy the needs of some users when phytosanitary requirements for importation of seed across international borders creates an issue.

Depositing herbarium specimens in national herbaria and establishing DNA banks will demand additional resources for genebanks and/or collaborative links to other funded organisations with similar aspirations.

CRITICAL ISSUES TO RESOLVE FOR CONSERVATION OF TEMPERATE FORAGES

Key issue 1: Genebank databases and passport/characterisation data

- Genebank databases aim to record:
- passport data that relate to the origin of each accession;
 - crop descriptor data that document morphological characteristics of relevance to taxonomy and genetic diversity;
 - data from the characterisation of phenotypic traits of importance for genetic improvement of forages.

The screening of germplasm accessions for traits of interest is generally undertaken by the next users of genebanks (e.g. geneticists and breeders). This presents a challenge of ensuring that characterisation data is subsequently provided back to the genebank for documentation. While this is more achievable for government funded breeders, this data is often regarded as proprietary information by seed company breeders.

Generic crop descriptor lists used to characterise legumes and grasses urgently need updating to clarify the key traits to be documented and the standardisation of trait information. This will provide consistency across genebanks and should incorporate



contemporary methods for both phenomic and genomic characterisation.

Some germplasm material is widespread across various genebanks, but redundancy and duplication are difficult to identify and poorly quantified. The completeness of passport data and trait information varies markedly among genebanks, further complicated by limited connectivity and transfer of information between the independent databases of genebanks. Updating passport data with improved coordination among genebanks will allow the identification of duplications and gaps across collections. A coordinated programme of regeneration can then be allocated to collaborating genebanks, with subsequent sharing of multiplied accessions. This will improve seed availability that is often limited by the lack of accession regeneration.

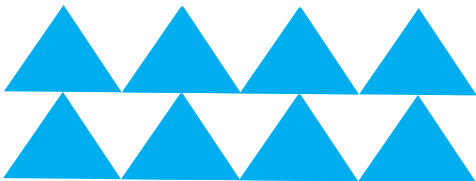
Key Issue 2: Regeneration of genebank accessions

Regeneration/replenishment of existing accessions in genebanks is critical before the loss of seed viability. This places a huge demand on the resources of genebanks, with the need to prevent cross-contamination between accessions for the many outcrossing temperate forage species. When regeneration is undertaken, it is usually at the cost of making further collections. Determining which accessions to prioritise for regeneration/replenishment is further complicated by the undetermined duplication between genebanks.

Regeneration/replenishment is especially challenging for temperate forage species due to the extensive number of taxa involved and a poor understanding of the biology of many species. Outside the major cultivated species there is a paucity of information on the pollination systems, seed dormancy, germination requirements, plant growth needs and flowering requirements. This lack of knowledge can result in regeneration being based on seed production from a few chance individuals that just happen to grow and set seed. This presents a major risk for severe bottlenecks to genetic diversity within accessions resulting from genetic drift or the unconscious selection for plants that survive better under the conditions of replenishment. The lack of biological knowledge for many taxa can lead to the unintended loss of potentially valuable allelic variants of genes and the inadvertent reduction in biodiversity.

Key Issue 3: Characterisation of germplasm accessions

The most successful temperate forage species in terms of breeding commercial cultivars has involved white clover (*Trifolium repens*, with over 250 cultivars) and perennial ryegrass (*Lolium perenne*, with over 100 cultivars). Despite this commercial success,



genomic tools have recently estimated that less than 10% of the genetic diversity available in these species has been accessed to date by plant breeders. A vast genetic resource remains to be characterised and utilised for improved production in the livestock sector. The situation is even more extreme for other temperate forage species.

The conservation of temperate forage germplasm only serves a purpose if the resource is used to support sustainable livestock production. The effective utilisation of germplasm requires accessions to be screened for traits of interest for pre-breeding. Such germplasm characterisation has received little attention from genebanks to date. The increasing threat of climate change demands greater emphasis on screening for tolerances to abiotic and biotic stresses, which are further exacerbated by grazing grasslands and pastures being forced onto more marginal land. Traits such as tolerance to drought, salt, acid soils, water logging, and temperate extremes, as well as resistance to a changing spectrum of pests and diseases, are becoming increasingly important to maintain productive pastures for ruminants. Additional traits involving phytochemical composition will be critical for mitigating greenhouse gas emissions from ruminants, nutritive value for healthy animals, and healthy milk and meat from these animals for human consumption. Thorough characterisation of germplasm accessions will identify traits to help forage breeders produce temperate forages for resilient and sustainable food systems.

Key Issue 4: Future collections to encapsulate full genetic diversity

Ensuring that genetic diversity is secured requires collection gaps to be identified. This is very difficult with only poor or incomplete passport data recorded for many accessions. Some urgency is required to identify collection gaps in eco-geographical zones representing climatic, edaphic and altitudinal extremes. Biodiversity in many ecosystems from such zones is under threat from loss of habitats, land use changes, political conflicts, urbanisation. This is exacerbated by the ongoing threat of climate change resulting in extreme weather events that place immense survival pressure on taxa in natural habitats. The consequences are a changing spectrum of abiotic and biotic stresses on grassland and pasture ecosystems that place germplasm diversity at risk of extinction before it is secured in a genebank.

Core collections aim to encapsulate the full genetic diversity of a species in a minimal number of accessions based on global ecological, geographical, environmental, edaphic, micro-climatic, genomic and phenotypic data. To date these have only been established for a limited number of forage species with varying degrees of reliability. The core collection of subterranean clover (*Trifolium subterraneum*) is a unique example of a carefully developed resource based on a range of data. There is a pressing need to expand this activity to other temperate forage species.

Associated symbiotic organisms play a critical role for the effective use and performance of temperate forages. This is especially important for endophytic fungi of grasses (e.g. *Epichloë* species) and nitrogen fixing bacteria of legumes (e.g. *Rhizobium*). Equal attention needs to be placed on collecting and conserving genetic diversity of these microbial symbionts as their host plants, especially given their role in increasing abiotic and/or biotic stress tolerance in their forage hosts.

POLICY RECOMMENDATIONS

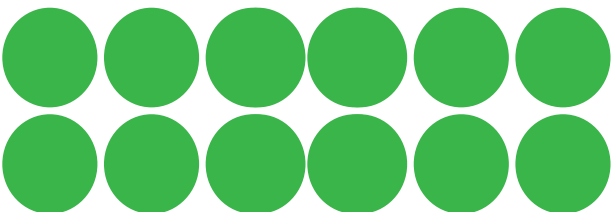
The resources of genebanks are currently so limited that many curators need to severely prioritise activities. They struggle to keep up with regeneration requirements and data curation of existing collections. This means that while germplasm gap-filling is recognised as critically important, collecting and curating new wild germplasm is generally put on hold. This is a major risk due to the ongoing loss of habitats in centres of origin, land use changes, political conflicts, urbanisation, and degradation of natural grasslands exacerbated by overgrazing. Given that most genebanks are government-owned facilities with public good aspirations, it is critical that the importance of ongoing adequate funding for genebanks is advocated to key governments.

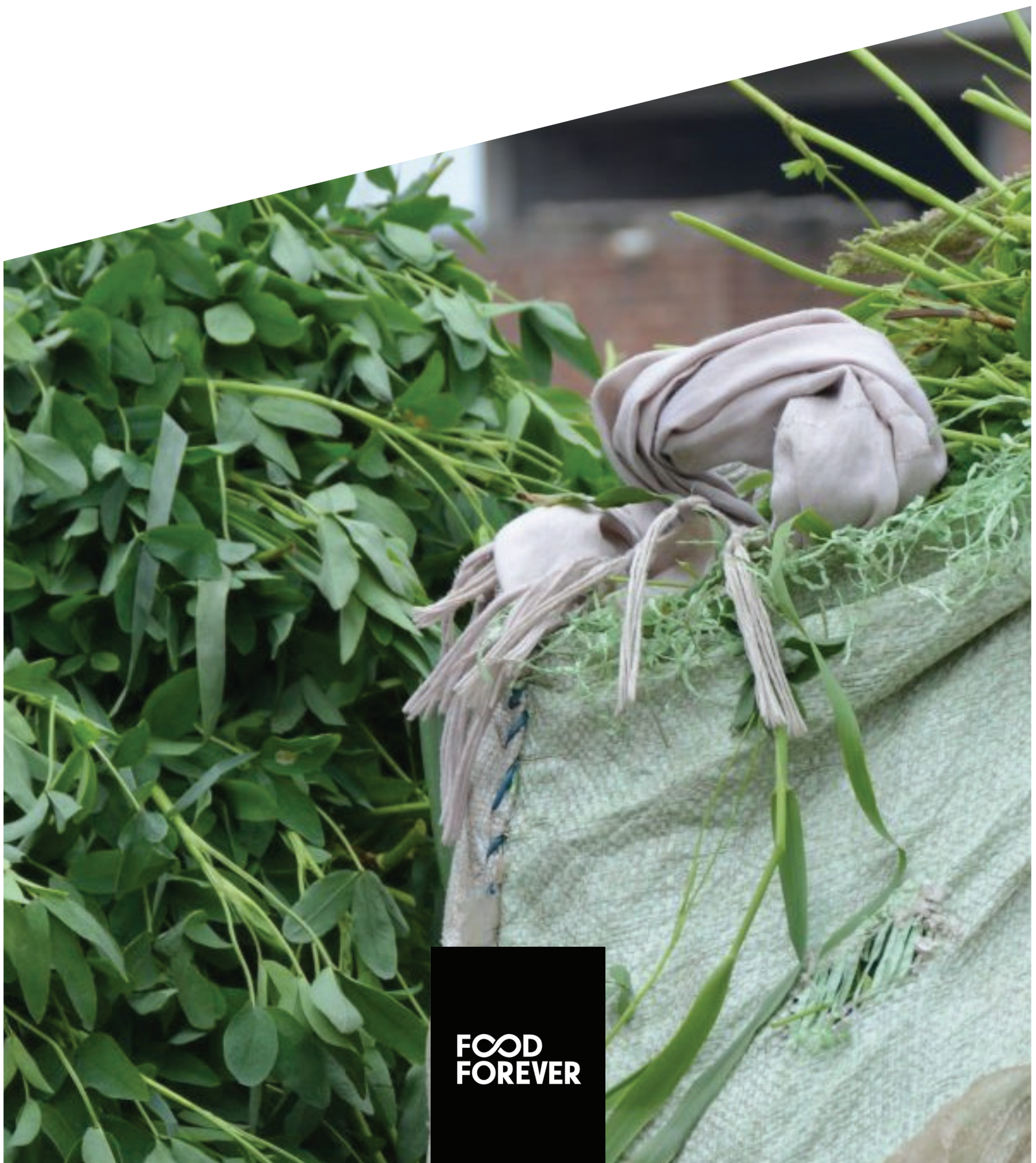
There is no formal global network for temperate forage germplasm conservation. There is an urgent need for better coordination among genebanks to ensure optimal allocation of global resources for documentation of key information in databases, regeneration of accessions, characterisation of accessions, and identifying gaps in collections. With limited resources to support the conservation of existing accessions, this coordination is critical to avoid duplicated effort on a limited pool of germplasm at the expense of other accessions. A formal network for temperate forage genebanks with an appropriate philanthropic focused governance/leadership structure will facilitate greater collaboration, the exchange of germplasm, appropriate backup of collections, interconnectedness of databases, and adoption of consistent operating standards and nomenclature of taxa.

This document has identified **four key issues that need urgent attention** to ensure future successful and long-term conservation of temperate forages for resilient and sustainable food systems from livestock production. These involve:

- 1. *accurate up-to-date databases of passport/characterisation information on accessions;*
- 2. *regeneration of existing accessions before seed viability is lost;*
- 3. *the characterisation of phenotypic traits in accessions so they can be utilised for pre-breeding; and*
- 4. *further collections of at-risk germplasm before it is lost forever.*

These four issues are all interdependent and need to be addressed as a collective to maintain productive pastures for ruminant grazing and contribute to sustainable livestock production. It will require a substantial ‘one-off’ international investment over the next decade to mitigate the risk from these four key issues. In parallel, national governments must continue to maintain their respective genebanks. On-going guidance from a formal global network for temperate forage genebanks will be essential to ensure optimal allocation of resources across these genebanks.





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