

Research Article

Cite this article: van Hintum T *et al.* (2025) A proposal for genebank metrics to enhance collection management. *Plant Genetic Resources Characterization and Utilization* 1–11. <https://doi.org/10.1017/S147926212510021X>

Received: 4 April 2025

Revised: 18 July 2025




Accepted: 31 July 2025

Keywords:

ex situ conservation; genebank management; crop diversity; plant genetic resources; quality management system

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A proposal for genebank metrics to enhance collection management

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Abstract

Genebanks worldwide play a crucial role in the long-term conservation and accessibility of wide diversity of plant genetic resources (PGR). These resources are essential for addressing current and future challenges related to climate change and biodiversity loss, thereby contributing to agricultural production and sustainability. Enhancing the efficiency of genebanks requires implementing a quality management system that ensures data transparency, as well as the documentation and standardization of processes. This study proposes a set of 10 mandatory and 38 optional genebank metrics specifically designed for collections of orthodox seeds. These metrics define a set of basic parameters that are easy to calculate and collectively serve as a valuable tool for improving genebank management, enhancing performance, fostering transparency and promoting collaborations among institutions. Fourteen institutions engaged in the long-term conservation of PGR were consulted in the development of the proposed metrics. This work lays the foundation for the establishment of a widely accepted set of genebank metrics within the global genebank community. Further research and iterative development are necessary to formulate comprehensive metrics applicable to other *ex situ* conservation methods (such as cryopreservation, *in vitro* and field conservation) as well as *in situ* conservation strategies (including genetic reserves and on-farm conservation).

Introduction

The importance of conserving plant genetic resources (PGR) for future generations and their accessibility to contemporary plant scientists and breeders is widely acknowledged (King *et al.*, 2024). Genebanks, managing *ex situ* collections of PGR, play an essential role in enhancing agricultural production and sustainability (McCouch *et al.*, 2013). According to FAO (2025a), in 2022 the global genebank network conserved approximately 5.9 million accessions across 871 genebanks. Thirteen of these genebanks are international (such as those managed by the CGIAR), six are regional and the remaining 852 are national genebanks – more than half of them located in Europe. Based on the data associated with the material conserved in these genebanks, gap analyses can be conducted to identify areas where plant genetic diversity has been under-collected, enabling the establishment of targeted collecting missions and conservation programmes (Dulloo and Khoury, 2023). However, it is imperative to examine whether the material housed in genebanks is being adequately conserved and is readily accessible for utilization.

The performance of genebanks is a sensitive issue, with limited public data available regarding genebanks' efficacy in fulfilling their mandates. However, informal exchanges within



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the genebank and user communities paint a concerning picture. Considering the essential role of genebanks in safeguarding global food security, as underscored by Target 2.5 of the Sustainable Development Goals ('By 2030, maintain the genetic diversity of seeds, cultivated plants and farmed and domesticated animals and their related wild species'; UN, 2024a), assessing the reliability of these institutions is key, despite the sensitivity surrounding the issue. Recognizing effective and efficient genebanks as such and supporting less effective ones in better delivery of their fundamental activities should be prioritized. The 11th session of the FAO Intergovernmental Technical Working Group on Plant Genetic Resources for Food and Agriculture highlighted this need in their report: 'The Working Group also recommends that FAO look into options on how and which capacity-building and evaluation mechanisms could be created to support genebanks in reaching the Genebank Standards and explore the possibility for creating an acknowledgement system' (FAO, 2023). Additionally, the Plant Genetic Resources Strategy for Europe, as developed by ECPGR (2021), advocates for the establishment of a certification system for genebanks that would assure proper quality of the management of these valuable resources (see also van Hintum and Wijk, 2024).

One of the difficulties in addressing the performance and quality of a genebank is the lack of standard measures and agreed definitions of terms defining the operations. The same basic terms are not always defined in the same way in different genebanks; terms like 'accession', 'base sample' and related standards differ regarding minimum quantity of seeds per sample, regeneration, storage, safety duplication, phytosanitary tests, availability, etc. The lack of clarity regarding, e.g., what constitutes an accession within a genebank complicates assessments of the state of the collection and possible backlogs in viability testing or regeneration efforts. Often, genebanks have material with different priorities or different statuses. There can also be differences in how to determine when seeds of one accession from various regenerations need viability testing and/or regeneration. While the FAO Genebank Standards (FAO, 2014) offer a solid framework for defining terms and establishing minimum operational procedures, they are subject to interpretation, leading to inconsistencies among different genebanks and even within individual institutions.

This paper contributes to these ongoing discussions by enhancing the understanding of basic terminology employed in genebank operations. Moreover, it proposes metrics aimed at providing a more comprehensive overview of genebanks' status. The idea of the proposed metrics is to have a set of established and easy-to-calculate parameters that can inform genebank management and help focus efforts and resources. Moreover, it can be an important tool for data transparency and sharing among institutions and countries, facilitating standardization, collaboration and reporting.

Basic concepts

A genebank can be defined as an organization dedicated to the long-term conservation of PGR for the benefit of future generations of users while ensuring accessibility to the current generation. Conservation within this context can be defined as the maintenance of PGR material in accordance with established standards such as the FAO Genebank Standards (FAO, 2014). Accessibility, or availability, involves providing users with access to the conserved material under the Standard Material Transfer Agreement (SMTA) of the International Treaty on Plant Genetic Resources for Food and Agriculture or other Material Transfer Agreements (MTAs) (FAO, 2015). Availability also encompasses considerations such as

the phytosanitary status of the material, seed quantity and viability, and capacity to overcome complex and changing legal restrictions for seed movement across borders.

These conservation and availability concepts also involve other important practical aspects for genebank management. Further elaboration and refinement of these definitions are essential to address potential disputes and complexities. Establishing common definitions and standards will require much discussion and collaboration across multiple stakeholders. The metrics outlined below will build upon the previously formulated definitions and presume that the genebank has implemented protocols and procedures for its operations, often referred to as Standard Operating Procedures (SOPs). For instance, a metric like the 'number of accessions requiring germination testing' presupposes the existence of a protocol outlining which accessions need testing, while the 'number of performed germination tests' also assumes that these tests were carried out in accordance with an SOP. It is important to note that while metrics provide quantifiable data, they do not inherently reflect the quality of the SOPs of an institution. Ideally, these SOPs adhere to internationally recognized standards such as the aforementioned 'FAO Genebank Standards'.

The proposed metrics align with the framework outlined by Lusty *et al.* (2021), who describe a 'Performance Management System for Long-Term Germplasm Conservation' within the CGIAR context. The quantitative key performance indicators formulated by the Global Crop Diversity Trust and presented in the paper correspond closely to the metrics proposed here, insofar as they pertain to accessions. Broader targets, such as the implementation of a Quality Management System, extend beyond the scope of these metrics. Notably, all accession-based statistics required for the CGIAR's online reporting tool (ORT) can be derived from the proposed metrics. The proposed metrics can thus be seen as a formalization of the metrics used in the ORT. However, clear community-based definitions for fundamental concepts such as 'accession' and 'base sample', also adopted outside the CGIAR community, can be expected to improve consistent online reporting within and outside the CGIAR system. Defining terms like 'accession' and 'base sample' is essential for clarity and consistency within the context of genebank operations. An accession can be defined as a PGR unit corresponding to a sample of a cultivated variety, landrace or wild population that is managed according to a protocol that aims at its long-term conservation and timely availability for distribution to users. Ideally, genebanks should aim to conserve their accessions in perpetuity and assure they are available for immediate distribution. This definition does not include material that is on the waiting list to become an accession but not yet fully part of the collection (e.g. material recently collected or acquired that has still to complete all the processes of documentation and seed processing to be considered an accessions), or material that used to be in the collection but is, for whatever reason, not fully managed anymore (e.g. historical or partially curated and archived accessions, *sensu* Hanson *et al.*, 2024). Several genebanks conserve more than one seed sample per accession; oftentimes, these samples are conserved under different storage conditions and are meant for a different use. The 'base sample' is the material of an accession that is stored under long-term storage conditions (LTS) and regularly monitored, according to the relevant protocols, and that will be used ultimately for regenerating the new base sample of this accession (FAO, 2014), i.e., it is the 'life-line' of the accession. The 'active sample' is the seed material of an accession used for distribution and research and may be stored under medium-term storage conditions (MTS) (FAO, 2014). It is important to note that

not all genebanks distinguish between ‘active’ and ‘base’ collections (i.e. in many genebanks, all seed samples and accessions are stored under LTS conditions). Recent scientific research on seed longevity in different genebanks demonstrated that conservation under LTS conditions significantly increases seed longevity when compared to MTS conditions of dry seeds (see, e.g., Hay *et al.*, 2013; van Treuren *et al.*, 2018; Guzzon *et al.*, 2021). Conservation of samples of the same accession under LTS and MTS temperature conditions can therefore be counterproductive, significantly diverting resources and activities that should be dedicated to seed conservation at optimal temperature conditions (LTS) to maximize seed longevity and minimize the need for regeneration and viability testing (Guzzon *et al.*, 2021). For these reasons, we are focusing these metrics on ‘base’ collections.

Other technical genebank terms will be elucidated within the definitions of the metrics below.

Principles of proposed genebank metrics

Genebank metrics aim to describe the status of a genebank collection and the activities in the genebank. They do not describe generic institutional aspects such as funding and number of staff. The status of a genebank generally relates to a specific moment in time, e.g. the number of accessions. On the other hand, activities often relate to specific intervals of time, e.g. number of newly added accessions. When calculating these metrics, it is crucial to clearly specify both the moment of measuring and the period covered. A default period commonly utilized is a five-year timeframe. For momentary metrics, the end of the reporting period typically serves as the default moment for calculation. However, if a different moment or period is utilized, it should be explicitly indicated to ensure transparency and clarity in reporting.

Apart from the distinction between the metrics related to a moment and those related to a period, some metrics can be considered basic, possibly even mandatory. On the other hand, others can be regarded as optional, as they are further elaborations of the basic ones. An example of a mandatory metric is the number of accessions. This is a fundamental metric, whereas, e.g., the number of landraces or accessions originating from Asia can be considered optional elaborations – important but not as essential as the basic ones.

Genebank metrics should meet several criteria to allow for wide acceptance and adoption. First, they should capture fundamental concepts applicable to all genebanks, ensuring relevance and universality. Secondly, calculating the metrics should be relatively straightforward and feasible for any well-organized genebank, minimizing complexity and technical barriers. Additionally, the value of the metrics should ideally be derived from digitized data available in most genebank databases. This facilitates automation through the development of scripts or algorithms that can be written once and executed whenever needed. Once the script is established, users would only need to input parameters such as the reporting period and moment, streamlining the generation of metric values. This standardized approach not only facilitates monitoring and evaluation of genebank developments internally but also enables consistent reporting to funding agencies and international organizations like the FAO for initiatives such as the ‘State of the World’ reports (see, e.g., FAO, 2019, 2025b).

In defining genebank metrics, terms or concepts are often derived from the FAO/IPGRI Multi Crop Passport Descriptors (Alercia *et al.*, 2015), a generally adopted list of ‘passport descriptors’ describing origin and identity of the accession. However, it is

important to acknowledge that certain concepts, like ‘country of origin’, may present conceptual challenges (that extend beyond the scope of this paper). Addressing such conceptual challenges might require broader discussions and consensus-building efforts within the genebank community.

Finally, the metrics outlined in this paper primarily pertain to genebanks conserving orthodox seeds (e.g. seeds that can tolerate drying to low moisture content and subsequent freezing; Li and Pritchard, 2009), which currently represent the most common form of PGR conservation. Adapting the metrics for use with field-, *in vitro*- or cryo-collections or for *in situ* conservation projects will necessitate some adjustments to account for the unique characteristics and challenges associated with these conservation methods. This may involve collaborating with experts in each respective field and drawing upon established best practices to develop comprehensive and meaningful metrics for assessing the status and activities of genebank collections conserving recalcitrant species and/or clonal crops as well as *in situ* conservation programmes.

Validation process

Earlier versions of the list of genebank metrics originally developed by the Centre for Genetic Resources, The Netherlands (CGN) were shared with colleagues (genebank curators and database managers) from 14 institutions (13 genebanks and the Global Crop Diversity Trust; Table 1) for further development and validation of the metrics. Genebank curators and database managers filled in the metrics with the data of the genebank they manage and provided additional feedback on (1) the usefulness of this tool, (2) metrics that were not clear, (3) important metrics that were missing and (4) metrics considered redundant. After these iterations and inclusion of the feedback received, the initial list of metrics was amended into the version presented in this paper.

The genebank metrics

Genebank management encompasses a wide array of activities and aspects, which can be grouped in various ways depending on the focus and objectives of the assessment. Here, the following thematic groups are considered: (1) size and composition of the collection, (2) data and documentation, (3) conservation, (4) availability and (5) distribution. For each category, the proposed metrics have been given coded names, complete names and brief descriptions. It is also indicated if the metrics are periodic (e.g. referred to a specific period of time or reporting interval) or momentary (reflecting the current status of the collection), and whether they should be considered mandatory (e.g. covering fundamental aspects for the genebank management, metrics that should be readily available to the curators) or optional (covering further elaborations of mandatory metrics). See ‘Supplementary material 1’ for an overview of the genebank metrics proposed in this paper.

Size and composition of the collection

Many of the metrics relate to properties of the seed accessions. An accession in this context should be seen as the basic unit of conservation of the PGR collection, representing, as mentioned, a sample of a cultivated variety, landrace or wild population. It is an integral part of the collection and thus should be conserved and made available following the procedures highlighted in the SOPs of the genebank. In this context, material that is not yet or no longer fully included in the collection is not considered accessions. This refers, for instance, to new introductions that have not yet been

Table 1. Institutions that reviewed and validated the genebank metrics. FAO WIEWS codes are provided for all genebanks. IPK genebank collections are conserved in three different stations, each with its own WIEWS code. The column country refers to the country where the headquarter and/or main genebank for each institution is located (for institutions that operate in multiple countries)

Institution	Country	FAO WIEWS codes
Austrian Agency for Health and Food Safety	Austria	AUT001
Banca del Germoplasma Vegetale dell'Università di Pavia	Italy	ITA411
Centre for Genetic Resources, The Netherlands	Netherlands	NLD037
Czech Agrifood Research Center	Czechia	CZE122
Genebank, Leibniz Institute of Plant Genetics and Crop Plant Research, Germany	Germany	DEU146, DEU159, DEU271
Global Crop Diversity Trust	Germany	
John Innes Centre	UK	GBR011
National Centre for Biodiversity and Gene Conservation	Hungary	HUN003
Nordic Genetic Resource Center	Sweden	SWE054
Plant Breeding and Acclimatization Institute	Poland	POL003
ProSpecieRara	Switzerland	CHE063
Scientific Centre of Vegetable and Industrial Crops	Armenia	ARM008
Walloon Centre of Agricultural Research, Life Sciences Department – Potato	Belgium	BEL023
World Vegetable Center	Taiwan	TWN001

fully accessioned as part of the collection or archived or historical accessions. Once the total number of accessions is known, it might be interesting to know more about the nature of these accessions: the biological status (variety, landrace, wild, etc.), the continent or country of origin and possibly how long the accessions have been in the collection, etc.

NACC	Number of accessions (mandatory, momentary)
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The number of accessions in the collection, conserved under the SOPs of the genebank. This metric is the basis of all metrics in this category. It is the only mandatory metric in this first category of 'Size and composition of the collection'.

NACC_PW	Number of accessions of wild or weedy populations (momentary)
NACC_PL	Number of accessions of traditional cultivars or landraces (momentary)
NACC_PB	Number of accessions of breeding and research material (momentary)
NACC_PA	Number of accessions of advanced or improved cultivars (momentary)

These four metrics are further specifications of NACC and are all calculated similar to NACC, only with the added requirement of the biological status (based on the FAO/Bioversity Multi Crop Passport Descriptors: '100', '110', '120' or '200' for wild or weedy populations, '300' for traditional cultivars or landraces, '410', '411', '412', '413', '414', '415', '416', '420', '420', '421', '422' and '423' for breeding and research material and '500' for advanced or improved cultivars; Alercia *et al.*, 2015). The difference between the sum of these four metrics and the number of accessions obviously indicates the number of accessions without a known biological status or with another that is not included in these metrics.

NACC_ON	Number of accessions originating in the country where the genebank is located (momentary)
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A further specification of NACC, calculated similarly to NACC, only with the added requirement that the accession originates in the country where the genebank is located. An accession is considered as originating in a specific country when it was collected (in case of wild or weedy populations and traditional varieties or landraces) or it was developed (in case of breeding and research material and advanced cultivars). This metric indicates the level at which the genebank is oriented towards national material.

NACC_OAS	Number of accessions originating in Asia (momentary)
NACC_OAF	Number of accessions originating in Africa (momentary)
NACC_ONA	Number of accessions originating in North America (momentary)
NACC_OSA	Number of accessions originating in South America (momentary)
NACC_OEU	Number of accessions originating in Europe (momentary)
NACC_OAU	Number of accessions originating in Oceania (momentary)

These six descriptors are further specifications of NACC, calculated similarly to NACC, only with the added requirement that the origin country is located in a specific continent. A continent division of the (origin-)countries is required to calculate these metrics. The classification of the United Nations geoscheme (UN, 2024b) should be used, where all continents are distinguished except for North America and South America. North America can be considered to consist of the regions 'Northern America', 'Central America' and the 'Caribbean' and South America of the Region 'South America' (see Supplementary Material 2).

ACC_AGE	Time in years that the accessions have been in the collection (momentary)
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The only metric in this category with a time dimension. Per accession, the year of entering the genebank collection (becoming an accession) is subtracted from the year of the moment of reporting.

NACC_NEW	Number of accessions added (periodic)
NACC_OUT	Number of accessions removed from the collection (periodic)

The only two metrics in this category measured over a period of time. The first is a specification of NACC, calculated similarly to NACC, only with the added requirement that the moment of entering the genebank collection (becoming an accession) falls in the reporting period. The second metric, the number of accessions removed from the collection, is of a slightly different nature as it is not a property of the accessions in the collection. Accessions can be removed from the collection for various reasons, e.g., because they appear to be duplicates of other accessions in the collection. Accessions classified as archived or historical in the reporting period should thus be considered as removed from the collection.

Data and documentation

The quality of the documentation of the accessions is challenging to measure. Regarding passport data, simply counting the datapoints does not yield relevant information. In the case of passport data, for example, a vernacular name is very important for traditional varieties and landraces, but irrelevant for wild populations, whereas the location of collecting is crucial for a wild population and less relevant for a modern variety. For passport data, this issue was addressed with the introduction of the Passport Data Completeness Index (PDCI), which weighs the importance of certain datapoints depending on the biological status of the accession (van Hintum *et al.*, 2011). As a result, the PDCI gives a good indication of the completeness of passport data, but it says nothing about the reliability of these data. Regarding the phenotypic data, often referred to as characterization and evaluation data in the genebank community, it is more difficult, and possibly a simple count of the number of datapoints of this type is the best that can be done. Hopefully, in the coming years, this can be formalized into a metric indicating the number of datapoints that comply with a proper standard for this type of information, such as MIAPPE (Papoutsoglou *et al.*, 2020), but that has not yet been achieved. Many genebanks are generating genomic data, which can greatly increase the usability of the accessions (e.g. allowing genome-wide association studies, allele mining and predictive breeding) and improve the genebank management (e.g. by defining core-collections or subsets, Sansaloni *et al.*, 2020). A metric is proposed to indicate how many accessions have genomic data that are accessible to users (either in public repositories or upon request to the genebank curators). An additional option that can easily be added is the number of accessions that received a Digital Object Identifier (DOI). The DOIs were introduced as a standard to increase the possibility of univocally identifying genebank accessions, linking information sources and monitoring the flow of PGR (Alercia *et al.*, 2018). Finally, all these data should (at least in principle) be publicly available to be reported, as access to data is the first step towards

access to the material – this should be part of an SOP and is not reflected in a metric.

DOC_PDCI	Average PDCI of the accessions (mandatory, momentary)
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The calculation of the PDCI is done per accession and requires a simple script based on the paper about this metric (van Hintum *et al.*, 2011). The value has a maximum of 10, which indicates complete passport documentation. For genebanks that contribute data to Genesys, this index can be automatically retrieved from this information system (Genesys, 2024). Supplementary Material 3 provides guidance in calculating the PDCI.

DOC_PHEN	Average number of phenotypic datapoints per accession (mandatory, momentary)
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This metric refers to the average number of characterization and/or evaluation datapoints per accession of the collection, which are readily available in an information system. This obviously depends on the number of digitally stored and accessible datapoints (observations), which could miss the historical data stored on paper or otherwise.

DOC_GEN	Number of accessions with accessible genomic information (momentary)
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This metric refers to the number of accessions for which genomic data were generated and are accessible internally (to the genebank) and externally by users (via public repositories or upon request to the genebank). For genebanks holding diverse genomic data, further specifications of this metric can be included, e.g. number of accessions with genomic marker data and number of accessions with genomic sequence data.

DOC_DOI	Number of accessions with a DOI (momentary)
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The DOI, a unique identifier of the accession, helps to link the information about accessions from different sources. DOIs are assigned by the secretariat of the ITPGRFA or other providers (Alercia *et al.*, 2018).

Conservation

As mentioned before, accessions in a PGR collection should be managed following the SOPs of the genebank. If these SOPs comply with the international standards (FAO, 2014), proper conservation should be assured. However, it is essential to monitor the conservation status by indicating the level of activity regarding viability tests and regenerations, and to provide information on seed quality, available seed quantities and the status of the safety back-up of the accessions.

CON_NGER	Number of completed germination/viability tests on base samples (mandatory, periodic)
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This metric is calculated only on data collected from base samples (i.e. one sample per accession intended for long-term conservation), indicating if the base sample has been tested in the reporting period. Tests on active samples (e.g. intended for

short- to medium-term conservation and/or distribution) can also be counted here, provided that they give a direct estimate of the viability of the base sample.

CON_NREG	Number of accessions for which newly regenerated seeds were stored (mandatory, periodic)
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This metric relates to any regeneration of the accession (including also non-base samples) in the reporting period, indicating if new seeds of the accession have been produced.

CON_AGE	Average storage time in the base collection (momentary)
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This metric indicates the average age of the base sample per conserved accession, i.e. the difference in years between the year of storage of the sample and the year of reporting.

CON_GER	Number of accessions that need a germination test (mandatory, momentary)
CON_REG	Number of accessions that need to be regenerated (mandatory, momentary)

These two metrics entirely depend on the SOPs of the genebanks that identify the time intervals for viability testing, the viability thresholds and the minimum seed quantity per sample that trigger regeneration activities. The comparison with the other Conservation metrics, indicating the number of viability tests and regenerations done, gives an overview of potential backlogs in the genebank operations.

CON_LGER	Number of accessions that are below the standard germination level as defined in the SOP (momentary)
CON_LSEE	Number of accessions that have less than the standard amount of seeds as defined in the SOP (momentary)

Two metrics further specify the previous metric (which gives the number of regenerations needed). They provide an overview of the needs for regeneration. These two metrics also entirely depend on the SOPs of the genebanks that identify the viability thresholds and the minimum seed quantity per sample that trigger regeneration activities.

CON_NSAP	Number of accessions that are safety duplicated (mandatory, momentary)
CON_NDUP	Number of accessions that are safety duplicated to another genebank (momentary)
CON_NTRI	Number of accessions that are safety duplicated to the Svalbard Global Seed Vault (momentary)

These metrics indicate the level of safety backup (e.g. duplication of accessions in an external genebank) and the nature of this backup. Internal duplication (e.g. the same accessions conserved in both active and base collections in the same location by the genebank) is, in general, not considered as safety duplication and is not included in the framework of this metric. If accessions are

duplicated under long-term storage conditions in at least one different location (including another genetic resources centre of the same institution in a different location), this is considered safety duplication and can be reported in these metrics. The first metric, indicating that an accession is either duplicated in another genebank or location, and as a second level of safety, in the Svalbard Global Seed Vault (see Asdal, 2025), is mandatory.

Availability

In principle, all accessions in the genebank collection should be available for distribution. However, this is not always the case; even if the SOPs are followed, it is possible that genebank accessions are (temporarily) not available for distribution to users. A genebank can run out of seeds for some accessions because of a sudden increased demand for specific material, a sudden decrease in viability of the seeds or simply mistakes in the operations. However, it is also possible that due to a new phytosanitary issue, some materials cannot be distributed until retested. For this reason, metrics, indicating the number of accessions that are not available with an indication of the reason for non-availability, can be very useful.

This is a problematic category since availability usually depends also on some characteristics of the requestor; legal or phytosanitary reasons can make it impossible to distribute material to specific countries or users. However, strict interpretation of these terms should be used.

AVA_AVA	Number of accessions that are readily available for distribution (mandatory, momentary)
AVA_NLEG	Number of accessions not available due to legal reasons (such as unresolved ownership) (momentary)
AVA_NPHY	Number of accessions not available due to phytosanitary reasons (momentary)
AVA_NMAT	Number of accessions not available due to lack of quality seeds (momentary)

The first metric, the only mandatory metric in this category, indicates that seeds of the accession are ready for distribution under SMTA or other MTAs in terms of seed amount and quality, phytosanitary requirements and legal status. The other three metrics explore the reasons for the unavailability of accessions and specify how many accessions are not available due to various issues.

Legal unavailability implies that material cannot be distributed under an SMTA or other MTAs. Phytosanitary unavailability implies that it cannot be moved according to phytosanitary regulations in the country of the genebank. The final, lack of quality seeds, implies that the accession does not have sufficient seeds. Moreover, some genebanks do not distribute seed samples if accessions do not reach the viability threshold for distribution established by the SOP of the genebank describing the distribution process.

Distribution

Even if the material is available, that does not mean it is actually requested, distributed and finally used. Defining use for genebank accessions is complex; therefore, the most straightforward interpretation of 'number of samples distributed from the genebank' can be used as a proxy to clarify the utilization of the collections. This includes 'internal use' of the genebank for routine genebank operations, e.g. germination testing, regeneration and safety duplication. It is essential that this component of internal use is separately

quantified. Other metrics indicating the amount and type of use are relevant, such as the number of times accessions have been distributed per year they were in the collection, or metrics indicating the type and location of the users.

DIS_EVER	Number of distributed samples ever (momentary)
DIS_EEXT	Number of distributed samples ever excluding internal genebank use (momentary)
DIS_EXT	Number of distributed samples excluding internal genebank use in the reporting period (mandatory, periodic)

These metrics indicate the total use of material in the genebank. The third metric, the only mandatory metric in this category, shows the external distribution numbers in the reporting period. Only the first metric in this category includes internal use; internal use refers to the use of the genebank material for the management of the genebank, i.e. germination testing, regeneration and characterization. The use of accessions in scientific research or breeding activities done by the genebank or associated programmes in the same institution is not considered as internal use. The first two metrics refer to the distributions carried out by the genebank across its history to indicate the level at which the accession has been used in the past. As several genebanks have a long history encompassing several decades of activity and early distribution accounts might not be available or digitized, a later starting date from the beginning of the genebank operations can be proposed.

DIS_SAYE	Average number of times an accession is distributed per year it was in the collection (momentary)
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This metric, excluding internal genebank use, indicates the 'popularity', as a rate of distribution across time, of the genebank accessions over time. This is calculated by dividing the number of times each accession was distributed by the number of years this same accession has been part of the collection. As mentioned above for genebanks that do not have a complete historical record of all their distribution, a later starting date from the beginning of the genebank operations or a specific reporting period can be proposed.

DIS_COU	Number of distributed samples within the country where the genebank is located (including the institution of the genebank; excluding internal distributions) (periodic)
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A further specification of DIS_EXT, to indicate the (inter-)national orientation of the genebank distributions. This metric excludes internal genebank use.

DIS_DAS	Number of samples distributed to Asia (periodic)
DIS_DAF	Number of samples distributed to Africa (periodic)
DIS_DNA	Number of samples distributed to North America (periodic)
DIS_DSA	Number of samples distributed to South America (periodic)
DIS_DEU	Number of samples distributed to Europe (periodic)
DIS_DAU	Number of samples distributed to Oceania (periodic)

Further subdivisions of DIS_EXT. These metrics exclude internal genebank use. To calculate these metrics, a continent division of the countries of the users is needed. The classification of the United Nations geoscheme can be used, where all continents are distinguished except for North America and South America (UN, 2024b). North America can be considered to consist of the regions 'Northern America', 'Central America' and the 'Caribbean' and South America of the Region 'South America' (see Supplementary Material 2).

DIS_COM	Number of samples distributed to private companies (periodic)
DIS_PUB	Number of samples distributed to public institutions (periodic)
DIS_NGO	Number of samples distributed to non-governmental organizations (NGOs) (periodic)
DIS_IND	Number of samples distributed to private individuals (periodic)

Further subdivisions of DIS_EXT. No formal categorization of users exists, and we are proposing the following subdivisions: private companies, public institutions, NGOs and private individuals. Public institutions include universities, public research centres and public genebanks.

Calculation, analysis and presentation

The proposed metrics can be calculated on any level of aggregation: the entire collection, per crop or even per accession. When done per accession, for example, the 'number of accessions' (NACC) is obviously 1, and for a landrace, the 'number of accessions of wild or weedy populations' (NACC_PW) will be 0. This approach allows for an aggregation that can be decided later; it can be aggregated per crop, per population type, per continent of origin or any other aggregation. The only complication when choosing this accession-wise approach is the metric 'Number of accessions removed from the collection' (NACC_OUT) since this metric cannot be calculated with the information about the material currently in the collection.

Once the proposed metrics have been determined, they can be analysed and presented in various forms and for multiple purposes. They can be tabulated in a spreadsheet, transforming absolute numbers into percentages. Examples are given in Figures 1 and 2 and in Supplementary Material 4.

In Figure 1, it is, among others, immediately visible that relatively many germination tests were done in the reporting period of five years, given that the normal frequency of germination testing per stored seed sample at CGN is once every ten years. It can also be seen that most of the regeneration needs are due to low germination. The Cruciferae and *Allium* collections have relatively large regeneration needs – these crops are difficult to regenerate and might deserve extra attention to avoid bottlenecks in the future.

Figure 2 shows the 'popularity' of the crops and the destination of the material. It becomes, for example, immediately clear that despite the small size of the spinach collection, its popularity has been extremely wide – this might call for expansion of this collection.

This type of data presentation provides important information for the curators and the genebank manager, as described in the examples above, which provides the business intelligence of a genebank. Having a more dynamic presentation of the data

3 apr 2025 Period 2020-2024		CONSERVATION															
Cnr Crop	# accessions	age base (yrs)	base germination 2020-2024		regeneration 2020-2024		base germination needs		base regeneration needs		low germination low seed amount		safety duplicated		colleague genebank Svalbard		
1 wheat	4919	30.9	2406	49%	303	6%	235	5%	339	7%	312	38	4919	100.0%	4919	4441	
2 barley	2671	28.4	1362	51%	362	14%	68	3%	242	9%	227	29	2671	100.0%	2671	2457	
3 flax	954	26.0	858	90%	18	2%	8	1%	7	1%	4	3	951	99.7%	934	951	
4 peas	1039	33.1	550	53%	29	3%	66	6%	22	2%	3	20	1014	97.6%	1014	918	
5 oat	403	30.6	181	45%	21	5%	10	2%	11	3%	6	9	403	100.0%	403	384	
6 lettuce	2584	32.8	734	28%	21	1%	232	9%	7	0%	4	3	2555	98.9%	2554	2437	
7 cruciferae	1803	30.6	1102	61%	204	11%	297	16%	140	8%	88	52	1796	99.6%	1796	1692	
8 maize	487	34.7	246	51%	24	5%	25	5%	13	3%	8	8	487	100.0%	487	454	
12 faba beans	724	29.7	439	61%	42	6%	71	10%	37	5%	6	32	720	99.4%	720	550	
14 lolium	398	27.3	240	60%	19	5%	5	1%	16	4%	16		398	100.0%	398	333	
15 clover	263	29.2	161	61%	1	0%	1	0%	5	2%	5		263	100.0%	263	166	
16 spinach	541	27.5	128	24%	30	6%	65	12%	36	7%	2	34	541	100.0%	541	341	
17 allium	437	22.0	115	26%	32	7%	11	3%	46	11%	36	15	432	98.9%	432	356	
34 timothy	108	31.1	84	78%			19	18%	1	1%	1		108	100.0%	108	48	
35 cocksfoot	42	22.4	2	5%					2	5%	2		42	100.0%	42	29	
36 lupin	68	25.2	33	49%	6	9%	2	3%	10	15%	9	2	68	100.0%	68	57	
37 tomato	1337	31.2	703	53%	1	0%	62	5%	18	1%	7	11	1337	100.0%	1337	1053	
38 pepper	1177	23.6	362	31%	39	3%	5	0%	25	2%	13	12	1177	100.0%	1177	989	
39 eggplant	516	31.8	206	40%	7	1%	9	2%	3	1%	3		515	99.8%	514	475	
40 cucumber	924	27.1	528	57%					5	1%	5		924	100.0%	924	736	
41 potato	1479	28.1	681	46%	42	3%	138	9%	96	6%	86	10	1471	99.5%	1471	640	
42 meadow grass (P	135	19.3					43	32%	1	1%	1		135	100.0%	135	128	
43 fescue	78	23.4					2	3%	1	1%	1		78	100.0%	78	63	
44 caraway	23	10.9	11	48%									23	100.0%	23	23	
45 agrostis	11	23.0											11	100.0%	11		
48 melon	79	16.1	3	4%	1	1%			1	1%	1		79	100.0%	79	78	
49 lily	40	24.0							6	15%	1	5	40	100.0%	40		
50 carrot	125	8.8	111	89%	3	2%	7	6%					14	11.2%	14	14	
51 black salsify	34	12.4	1	3%									34	100.0%	34	34	
52 lamb's lettuce	47	14.1	6	13%	1	2%							47	100.0%	47	45	
53 asparagus	49	8.3	15	31%	9	18%							27	55.1%	27	13	
54 common bean	27	5.3	27	100%	21	78%							4	14.8%	4		
55 cichorium	20	4.7	20	100%	13	65%											
CGN collection	23542	29.3	11359	48%	1249	5%	1381	6%	1090	5%	847	283	23284	98.9%	23265	19905	

Figure 1. Small part of a screen dump of the spreadsheet that presents the genebank metrics for the CGN collection (see Supplementary Material 4 for the full spreadsheet) focusing on the base sample management of several crops. The columns are calculated based on the values (the absolute numbers) or a combination of values (the percentages) of the metrics aggregated on the crop level.

would be even more interesting. As the information systems used by genebanks differ, it would always be useful to have an interface allowing the user to drill down to more detailed aggregation levels, for example, starting at the collection level, going to the agricultural/horticultural crop level, the crop level within the horticultural crops, the crop types within the lettuce collection and the geographical origins of the butterhead lettuce (for an illustration of such a hierarchical structuring of PGR collections, see van Treuren *et al.*, 2009). At each level, the metrics could generate important insights, for example, the division between the use by commercial versus private users, or the popularity in Asia. Such dynamic interfaces could create insights into the status and use of collections that are otherwise very difficult to obtain.

Keeping records of the metrics over time would furthermore allow an analysis of developments of the collection and allow better planning of activities such as regeneration and viability testing. More importantly, easy visualization and presentation of germplasm utilization trends would allow better strategic planning of the genebank operations, such as prioritization of the acquisition of new material, funding, staffing and infrastructure needs. A finalized and agreed list of genebank metrics could be incorporated in the major information systems used by genebanks (e.g. GRIN-Global), as well as public PGR information repositories (e.g. EURISCO and Genesys), to facilitate automatic calculation of the metrics and ease data transparency and reporting, thus enhancing the appreciation of genebanking, improving

3 apr 2025 Period 2020-2024		DISTRIBUTION														
Cnr Crop	# accessions	# ever distributed	# ever distr. out	# distr. / yr in coll	# out 2020-2024	#out to NL	% to Asia	% to Africa	% to N. America	% to S. America	% to Europe	% to Oceania	% to commercial	% to public	% to NGO's	% to persons
1 wheat	4919	20635	13072	0.08	1227	236	19%	3%			97%		15%	66%	18%	1%
2 barley	2671	9374	4573	0.05	837	224	27%	2%			98%		11%	73%	15%	1%
3 flax	954	2195	1070	0.04	333	3	1%				100%		84%	16%		
4 peas	1039	5152	3553	0.10	425	109	26%	10%			90%		68%	27%	3%	2%
5 oat	403	1968	1228	0.09	576	167	29%				100%		75%	1%	24%	
6 lettuce	2584	40867	34897	0.44	3760	504	13%	63%	4%	33%			75%	24%	1%	0%
7 cruciferae	1803	27017	23489	0.39	3063	433	14%	56%	0%	7%	37%		43%	55%	1%	2%
8 maize	487	1266	504	0.03	32	2	6%				100%		9%		91%	
12 faba beans	724	2735	1813	0.08	743	370	50%		0%		100%		6%	93%	1%	
14 lolium	398	709	276	0.02	6	4	67%				100%		50%	50%		
15 clover	263	1068	719	0.10	30	9	30%				100%			97%	3%	
16 spinach	541	17976	15514	1.00	2291	867	38%	13%	1%	36%	50%		55%	45%	0%	
17 allium	437	6504	5161	0.46	562	178	32%	40%	13%		48%	0%	60%	39%		1%
34 timothy	108	151	31	0.01	1	1	100%				100%			100%		
35 cocksfoot	42	49	33	0.03	9						100%		100%			
36 lupin	68	417	309	0.14	116	15	13%	13%			87%		11%	70%	19%	
37 tomato	1337	10824	7653	0.20	575	229	40%	2%	3%	1%	94%		38%	57%	5%	
38 pepper	1177	17845	14690	0.51	1170	506	43%	11%	8%	1%	80%		50%	49%	1%	
39 eggplant	516	3974	3471	0.28	789	36	5%	64%	6%		31%		25%	74%	0%	
40 cucumber	924	7351	6229	0.27	837	198	24%	22%	6%		72%		64%	33%	2%	0%
41 potato	1479	9921	7883	0.20	392	242	62%				100%		25%	75%		
42 meadow grass (P	135	192	61	0.02	1	1	100%				100%			100%		
43 fescue	78	37	2	0.00	2						100%		50%	50%		
44 caraway	23	114	49	0.18	28	27	96%				100%		86%	14%		
45 agrostis	11	3	2	0.01	1	1	100%				100%			100%		
48 melon	79	598	512	0.45	126	15	12%	57%	10%		33%		46%	54%		
49 lily	40	155	155	0.22	84	40	48%				100%		48%	52%		
50 carrot	125	417	68	0.05	29	15	52%	48%			52%		97%	3%		
51 black salsify	34	113	15	0.04	1						100%			100%		
52 lamb's lettuce	47	340	226	0.46	115	93	81%				100%		23%	72%		4%
53 asparagus	49	224	34	0.15	34	28	82%				100%		82%	18%		
54 common bean	27	31	27	0.45	5	2	40%	60%			40%			100%		
55 cichorium	20	2		0.00	0											
CGN collection	23542	190224	147319	0.21	18200	4555	25%	31%	2%	7%	61%	0%	49%	47%	4%	1%

Figure 2. Small part of a screen dump of the spreadsheet that presents the genebank metrics for the CGN collection (see Supplementary Material 4 for the full spreadsheet) focusing on the destination of the distributed samples of several crops. The column '#out 2020-2024' indicates the number of samples distributed in this period (not for internal genebank purposes).

its global coordination and upgrading its capability for strategic planning.

Discussion

Transparency regarding the composition, management and use of genebank collections would significantly contribute to optimizing and rationalizing genebank management and operations. It could also be the basis for reporting and strengthening collaborations. The proposed metrics represent wide concepts, relevant to any genebank conserving orthodox-seeded species, and should be relatively easy to calculate by any genebank.

Agreed concepts are required for these metrics and for all communication regarding genebank composition, management and use. Basic concepts that require shared and agreed definitions are, for example, 'accession' and 'base sample'. Transparency regarding

the SOPs of the genebank is also essential for these metrics, but also for improvement of the genebank quality and, ultimately, genebank certification (van Hintum and Wijk, 2024).

The proposed list of genebank metrics is undoubtedly not the end point of the development of standardized genebank metrics but could serve as a positive step forward. The proposed metrics, which are inspired by reporting requirements for the FAO State of the World reports and the online reporting tool for CGIAR genebanks, could spark the discussion needed to facilitate a broadly accepted list of metrics within the genebank community. The metrics coordinated operations would support the management of the genebank on one hand and ease reporting and auditing to improve the communication with funders, policymakers and the user community on the other. We believe that such coordinated effort could improve the genebanks' delivery worldwide.

After its development in the CGN genebank, the metrics quickly revealed insights that improved management. Previously, less explicit issues regarding the collection's composition and use became apparent. Documentation metrics highlighted the strong focus on leafy and fruit vegetables, while usage data showed stark differences among crops – many were used less than 0.1 times per year, compared to over 0.4 for leafy and fruit vegetables, with spinach reaching 1.0. The metrics also clarified future priorities, such as addressing the significant regeneration backlog in the Cruciferae collection.

This first set of metrics was developed for orthodox seed collections in genebanks. Further discussions in the PGR community will be needed to optimize and validate metrics for the other *ex situ* conservation methodologies of PGR (i.e. *in vitro* conservation, cryopreservation and field collections) as well as community seed bank networks and *in situ* conservation (networks of genetic reserves and on-farm conservation). Clearly, the development of future metrics should be informed by the practical experiences of the communities involved. For example, the CGIAR genebank community has already implemented performance indicators for other *ex situ* conservation methodologies, which could serve as a foundation for the formulation of new, relevant metrics. From preliminary discussions held during the validation of the current metrics in the framework of the 'New AEGIS' project (<https://www.ecpgr.org/aegis/projects/new-aegis>), specific metrics for on-farm and *in vitro* conservation were mentioned. More detailed on-farm conservation specific metrics were proposed dealing with (1) the number of conservation sites per accession, (2) the type and number of 'conservation units' per accession (e.g. trees and populations) and (3) number of on-farm accessions duplicated in genebanks. For *in vitro* conservation, specific metrics should deal with (1) the number of accessions that are low in number (e.g. with a number of clones in slow growth conditions below the one recommended in the genebank's SOPs), (2) average number of subcultures per accession and (3) number of accessions duplicated in cryopreservation and/or in glasshouse/field collections. Finally, further discussions and quantitative analyses of the metrics of different genebanks could allow the identification of thresholds for some of these metrics to facilitate quality management and certification for genebanks.

It is important to acknowledge that not all genebanks worldwide are currently in a position to implement these metrics, as their operations may be less structured and often lack adequate documentation of both materials and procedures. Nevertheless, the authors contend that the establishment of a global system of collaborating genebanks necessitates a certain standard of quality. Effective conservation depends fundamentally on reliability. By defining clear metrics and promoting transparency, we aim to contribute to the ongoing improvement of genebanks in pursuit of this shared objective. We hope that this initial discussion could foster the creation of sets of metrics tailored to the different methodologies of PGR conservation to increase the integration of conservation actions, their quality management and transparency.

Supplementary material. The supplementary material for this article can be found at <https://doi.org/10.1017/S147926212510021X>.

Acknowledgements. The authors acknowledge the support of the projects PRO-GRACE (supported by the European Union's Horizon research and innovation programme under grant agreement no. 10109) and New AEGIS (funded by the Federal Ministry of Food and Agriculture, Germany, grant no. GenR 2024-1). The authors are grateful to Lorenzo Maggioni (ECPGR), Rob van Treuren (CGN), Rik Lievers (CGN) and Janny van Beem (Global Crop Diversity

Trust) for their useful comments on earlier versions of the manuscript and all other colleagues who were involved in the various discussions on the topic of genebank metrics.

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