European
Cooperative
Programme
for Plant
Genetic
Resources
ECP/GR

METRICS DESCRIPTION

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Prague 24/02/2026

ICARDA

Basic concepts

- **Accession**: 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.
- This **does not include material 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 not fully managed anymore** (e.g. historical or partially curated and archived accessions).

Basic concepts

CIMMYT

- **Base sample**: it 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.
- **Active sample**: it is the seed **material** of an accession **used for distribution and research** and may be stored under medium-term storage conditions (MTS).
- It is important to note that **not all genebanks distinguish between ‘active’ and ‘base’ collections.**
- **These metrics focus on base samples.**

Basic concepts

Genebank Standards
for Plant Genetic Resources
for Food and Agriculture

FAO

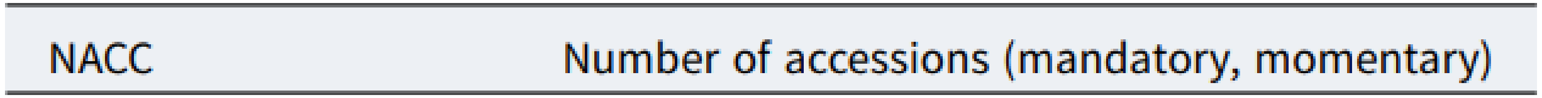
- The metrics presume that the **genebank has implemented protocols and procedures** for its operations: Standard Operating Procedures (**SOPs**).
- **They do not** inherently **reflect the quality of the SOPs** of an institution. Ideally, these SOPs adhere to internationally recognized standards such as 'FAO Genebank Standards'.
- The proposed metrics **can be calculated on any level of aggregation**: the entire collection, per crop or even per accession.

I. Size and composition of the collection

CIMMYT

This category of metrics is **based on the definition of accession**, materials that are not yet or no longer fully included in the collection are not considered.

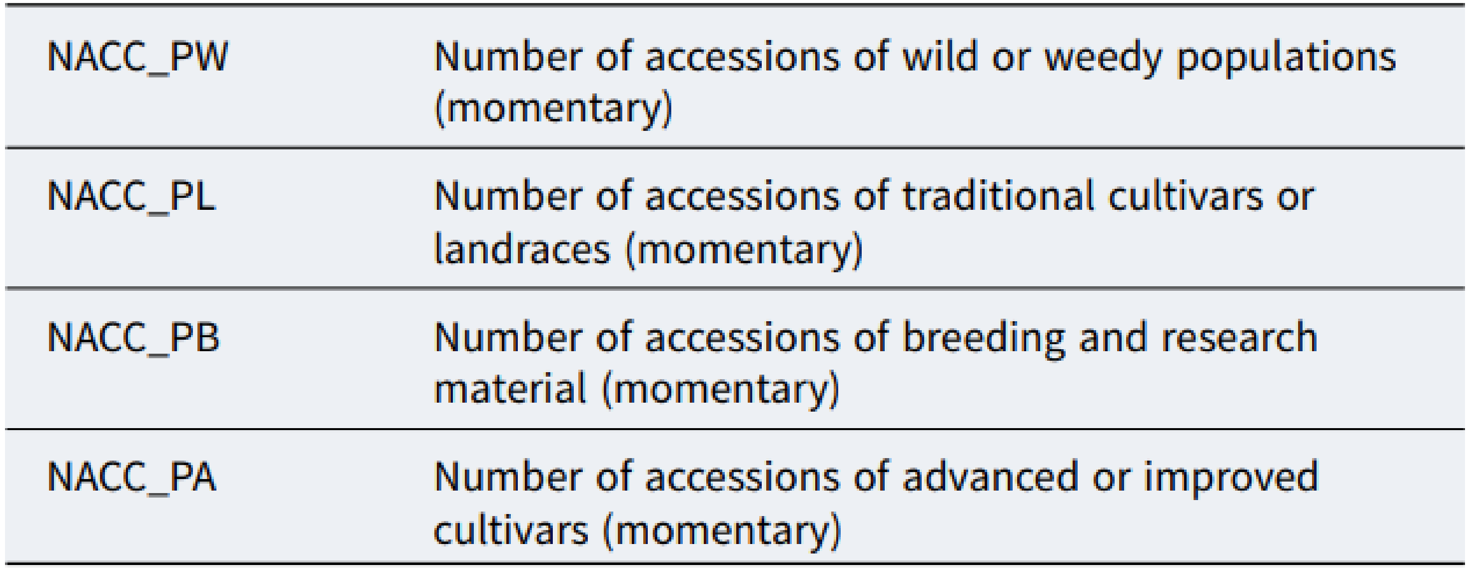
I. Size and composition of the collection



NACC	Number of accessions (mandatory, momentary)

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.**

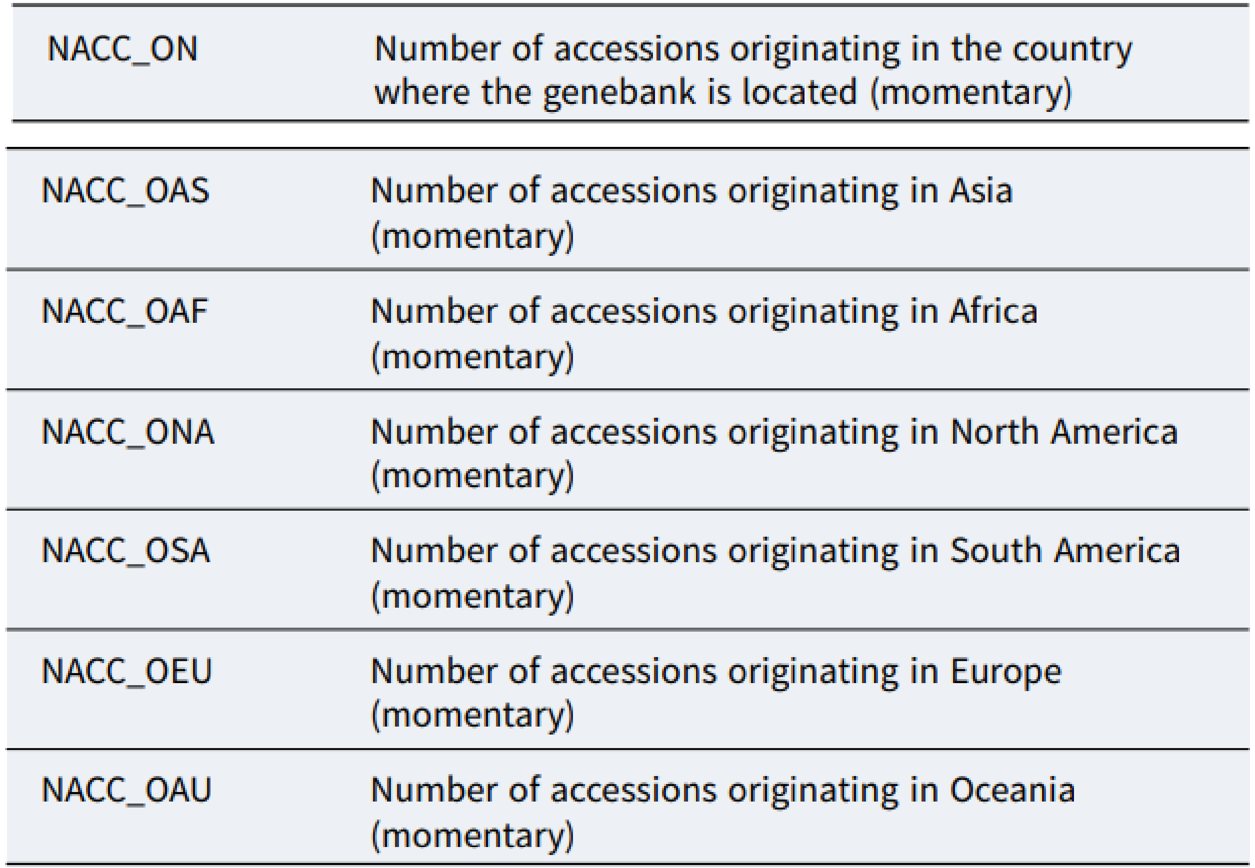
I. Size and composition of the collection



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)

Biological status of the accession, based on FAO/Bioversity Multi Crop Passport Descriptors; The difference between the sum of these four metrics and the tot. number of accessions indicates the number of accessions without a known biological status

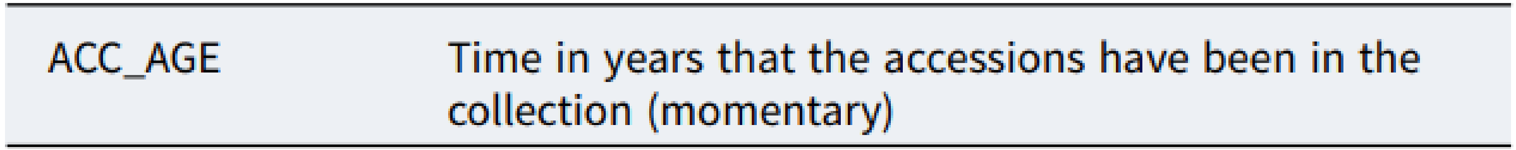
I. Size and composition of the collection



NACC_ON	Number of accessions originating in the country where the genebank is located (momentary)
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)

Geographical origin of the accessions, based on the United Nations geoscheme.

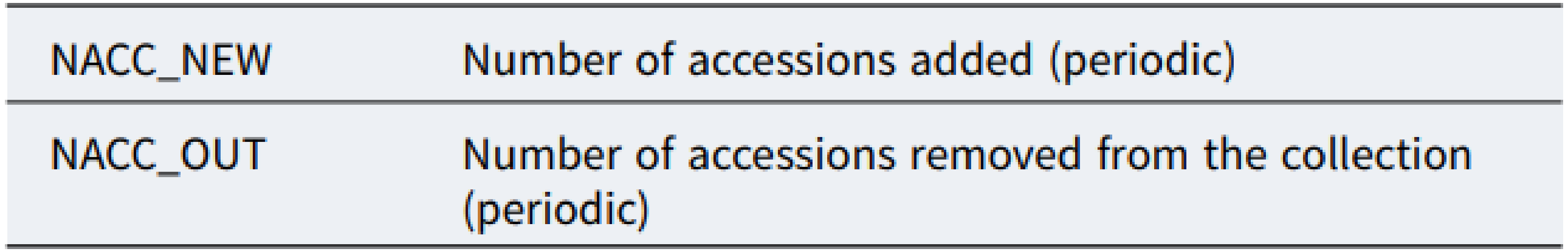
I. Size and composition of the collection



ACC_AGE	Time in years that the accessions have been in the collection (momentary)

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.**

I. Size and composition of the collection



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**. Accessions classified as archived or historical in the reporting period should also be considered as removed from the collection.

I. Size and composition of the collection

Discussion points

- What do you think about the basic definitions (accession and base sample)?
- Are we missing additional metrics?
- Are the biological status categories clear and complete (wild/ weedy, landrace, breeding material, improved cultivar)?
- Does the geographical grouping make sense?
- Would you be able to calculate the ‘time in years in the collection’?
- What is your opinion on the metric ‘number of accessions removed from the collection’?

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II. 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.

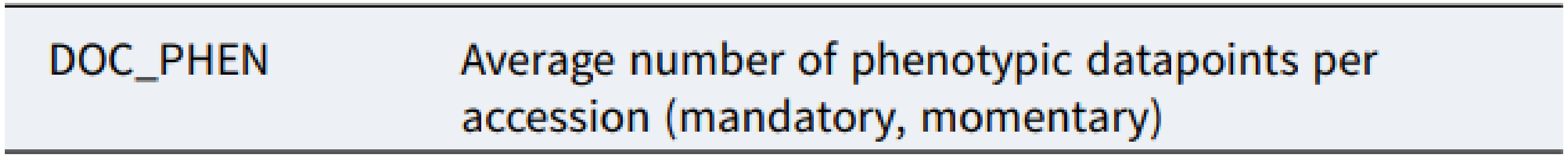
It is difficult to formalize phenotypic and genotypic data into a metric indicating the number of datapoints that comply with a proper standard.

II. Data and documentation

DOC_PDCI	Average PDCI of the accessions (mandatory, momentary)

The calculation of the **Passport Data Completeness Index** (PDCI) is done per accession and requires a simple script based on **van Hintum et al.** (2011). The value has a maximum of 10, which indicates complete passport documentation. It can be also automatically **retrieved from Genesys**.

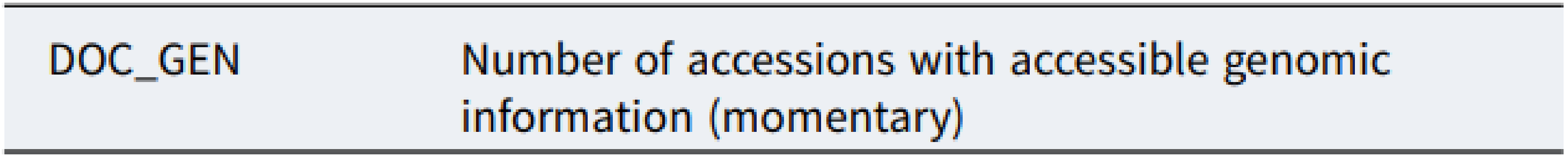
II. Data and documentation



DOC_PHEN	Average number of phenotypic datapoints per accession (mandatory, momentary)

The **average number of characterization and/or evaluation datapoints** per accession of the collection, which are readily available in an information system.

II. Data and documentation



DOC_GEN	Number of accessions with accessible genomic information (momentary)

The **number of accessions for which genomic data were generated** and are accessible internally (to the genebank) and externally by users

II. Data and documentation

DOC_DOI	Number of accessions with a DOI (momentary)

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 Eurisco.

II. Data and documentation Discussion points

- Are you able to calculate PDCI?
- Are we missing additional metric?
- How can we better account for completeness in characterization&evaluation data in the metrics?
- Should we add additional metrics on genotypic/genomic information (e.g. e.g. number of accessions with marker data and/or number of accessions with sequence data)?
- Do you employ DOIs?

III. Conservation

It is important that SOPs comply with the **international standards** (FAO, 2014).

It is essential to **monitor the conservation status** by indicating the level of activity regarding **viability tests and regenerations**, and to provide information on **available seed quantities** and the status of the **safety back-up** of the accessions.

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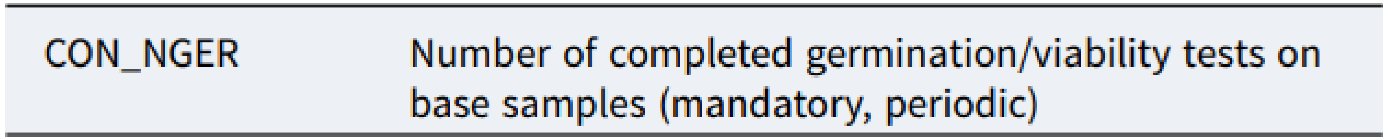
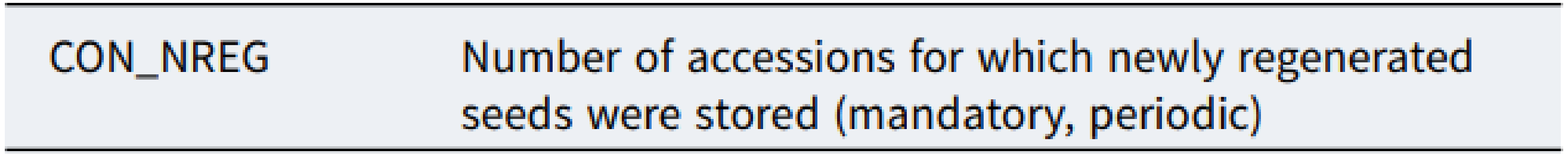
III. Conservation



CON_NGER	Number of completed germination/viability tests on base samples (mandatory, periodic)

Tests on active samples can also be counted here, provided that they give a direct estimate of the viability of the base sample.

III. Conservation



CON_NREG	Number of accessions for which newly regenerated seeds were stored (mandatory, periodic)

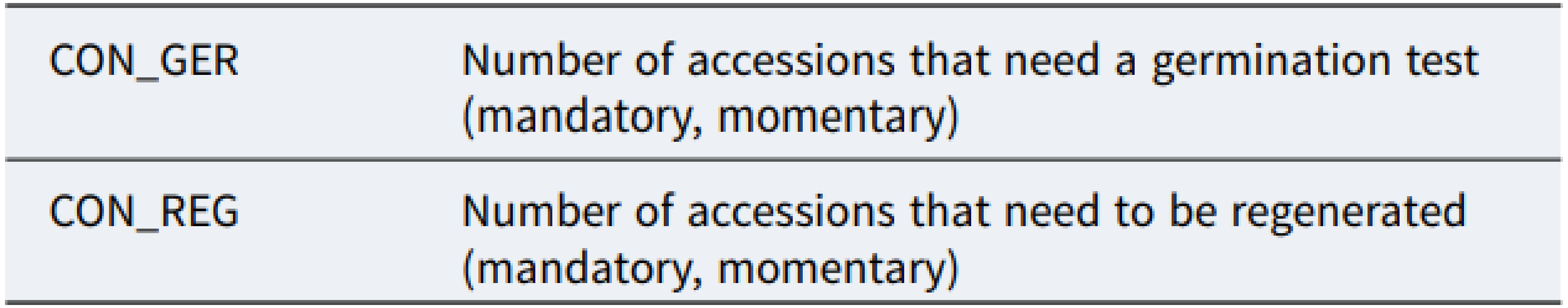
This relates to **any regeneration of the accession** (including also non-base samples) in the reporting period, indicating if new seeds of the accession have been produced and stored.

III. Conservation

CON_AGE	Average storage time in the base collection (momentary)

This **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.

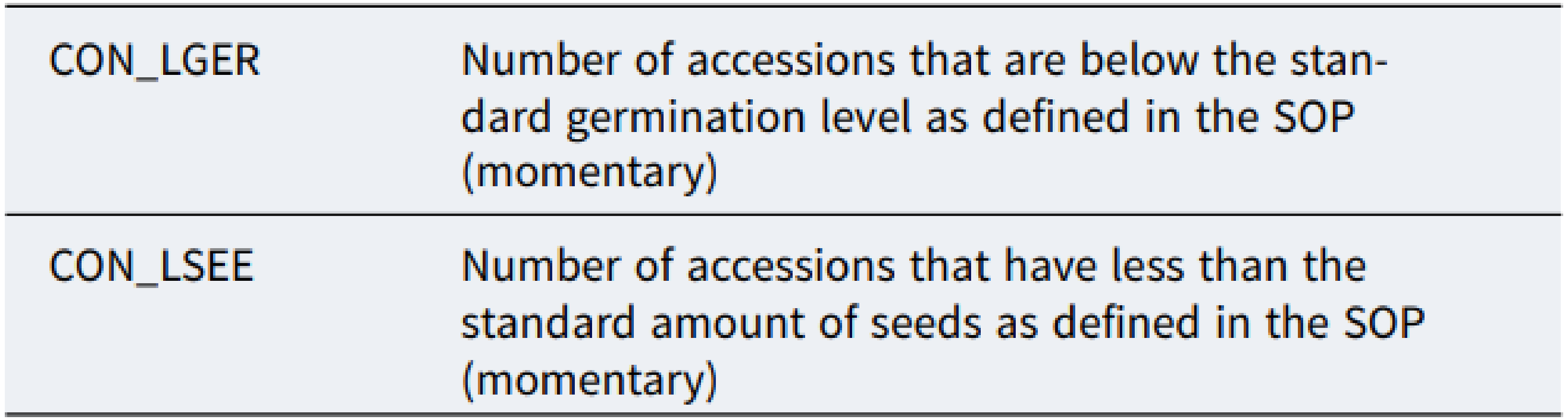
III. Conservation



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 entirely depend on the SOPs of the genebanks. **The comparison with** the other Conservation metrics (**number of viability tests and regenerations done**) gives an **overview of potential backlogs** in the genebank operations.

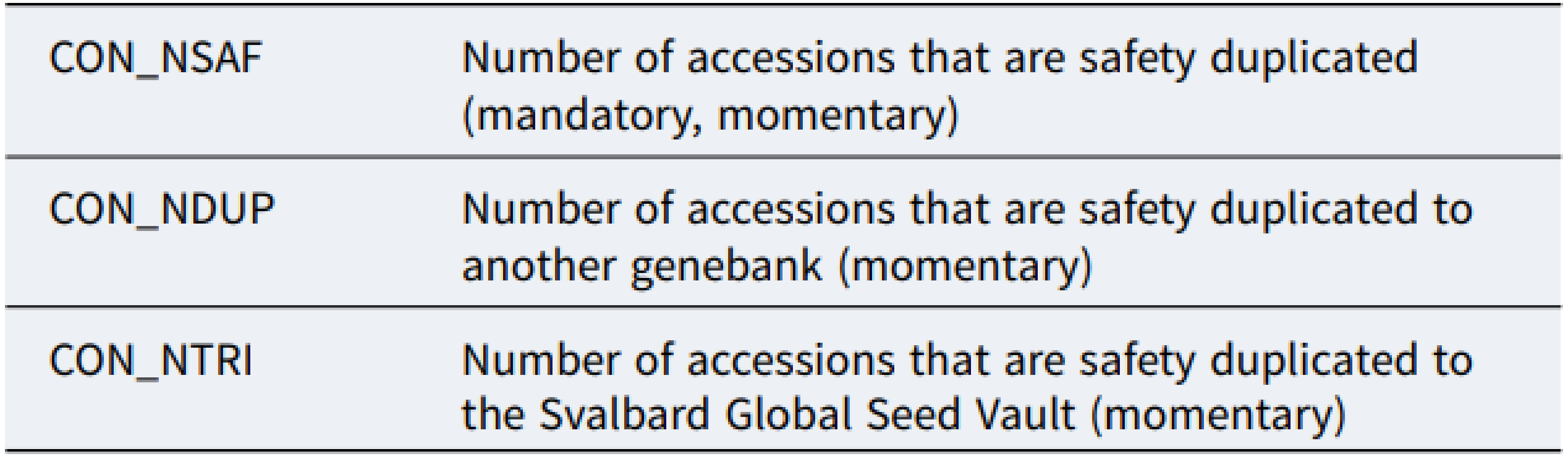
III. Conservation



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)

They provide **an overview of the needs for regeneration**. These entirely depend on the SOPs of the genebanks.

III. Conservation



CON_NSAF	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 indicate the **level of safety backup. Internal duplication 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 centre of the same institution), this is considered safety duplication and can be reported in these metrics.

III. Conservation

Discussion points

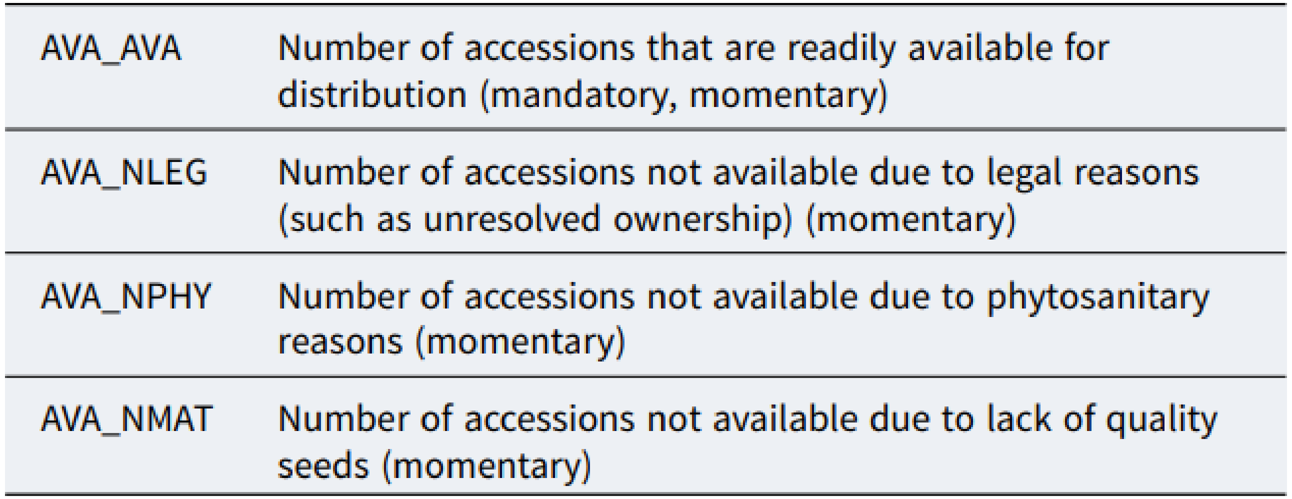
- Are we missing any additional metric?
- Will it be possible to calculate the number of accessions needing viability testing and regeneration in your genebank?
- Is it correct not to limit the number of accession regenerated only to base samples?
- Would it make sense to add a new metric indicating the number of samples that are in need for germination testing since a few years (>3)? To further highlight priority accessions for testing.
- Do you consider the definition of safety duplication clear?

IV. Availability


Kew Gardens

A problematic category, **availability not always depends on the genebank collections**, processes and policies since it might depend also on some characteristics of the requestor; legal or phytosanitary reasons can make it impossible to distribute material to specific countries or users.

IV. Availability



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 indicates that **seeds of the accession are ready for distribution** under SMTA or other MTAs.

The other three explore the **reasons for the unavailability**: I) **Legal unavailability** implies that material cannot be distributed under an SMTA or other MTAs; II) **Phytosanitary** implies that it cannot be moved according to phytosanitary regulations in the country of the genebank; III) **Lack of quality seeds**, implies that the accession does **not have sufficient seeds**. 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.

IV. Availability

Discussion points

- Are we missing any additional metric?
- Are we accounting properly for all the main reasons for accessions' unavailability?

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V. Distribution

Even if the material is available, that does not mean it is actually requested and **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.

It is essential that the 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.

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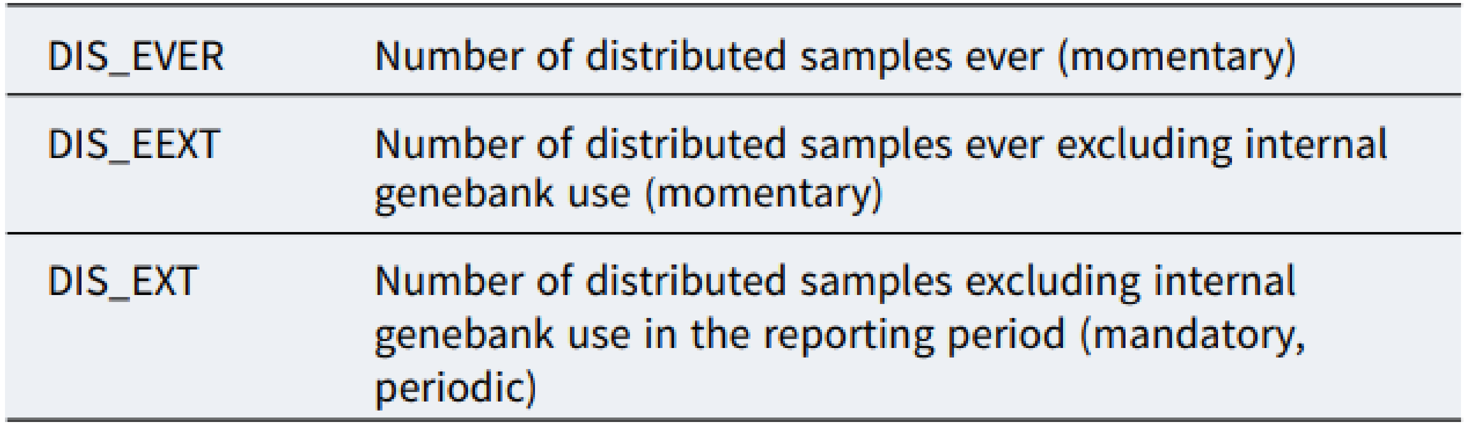
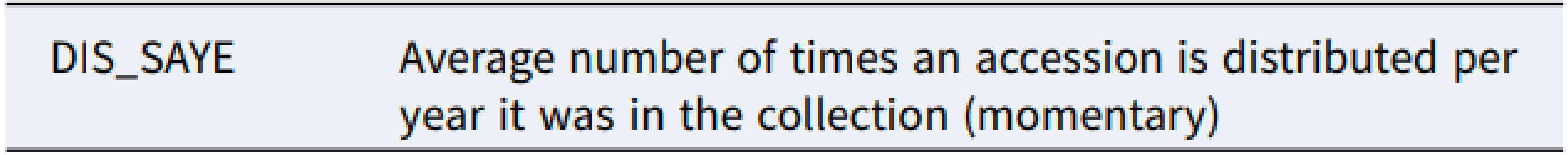
V. Distribution



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 indicate the total use of material in the genebank.
Only the first metric in this category **includes internal use:** 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 early distribution accounts might not be available, **a later starting date** from the beginning of the genebank operations **can be proposed**.

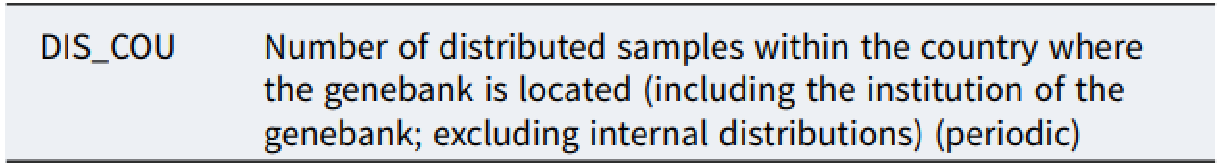
V. Distribution



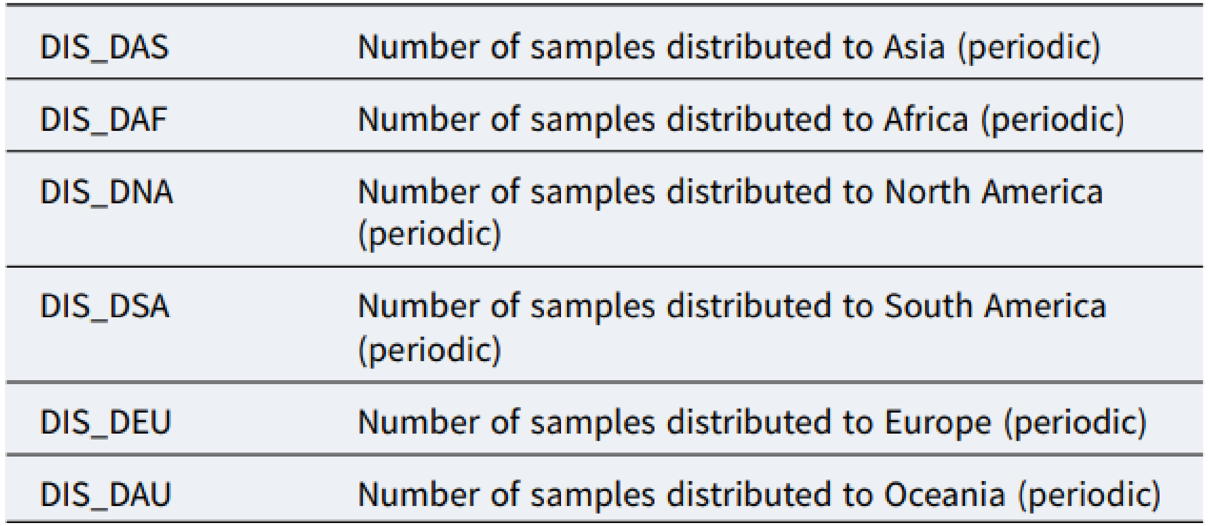
DIS_SAYE	Average number of times an accession is distributed per year it was in the collection (momentary)

This metric, (excluding internal genebank use) indicates the **‘popularity’ of accessions**. 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**. For genebanks that do not have a complete historical record of all their distribution, a later starting date can be proposed.

V. Distribution



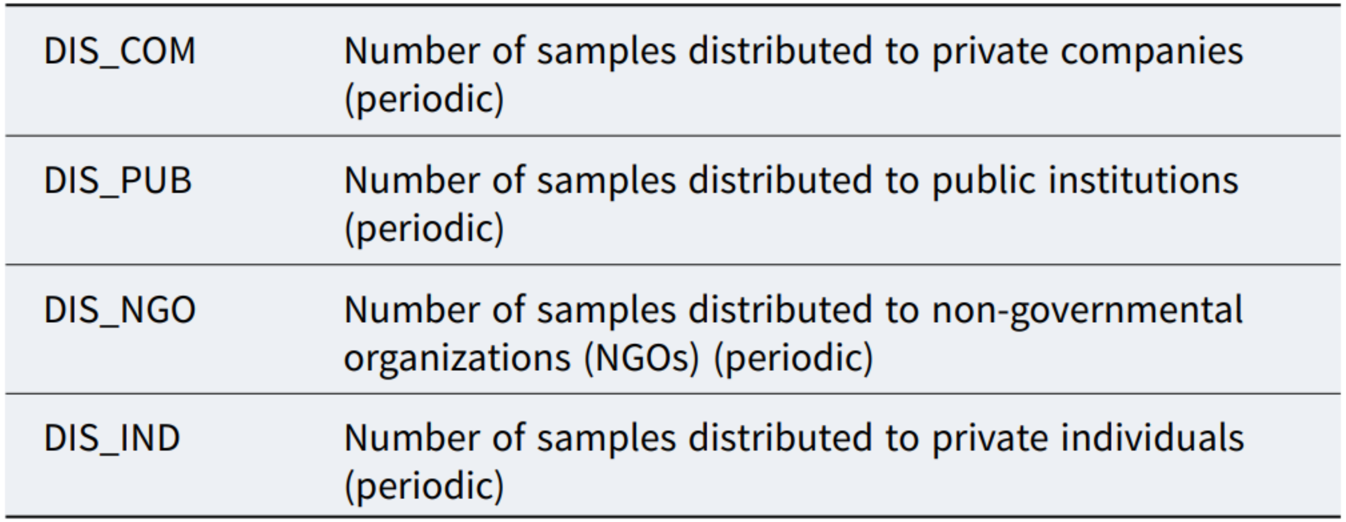
DIS_COU	Number of distributed samples within the country where the genebank is located (including the institution of the genebank; excluding internal distributions) (periodic)



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)

A further specification of DIS_EXT, to indicate the **(inter-)national orientation of the genebank distributions**. These metrics excludes internal genebank use.

V. Distribution



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)

No formal categorization of users exists, **we are proposing these subdivisions.** Public institutions include universities, public research centres and public genebanks.

V. Distribution

Discussion points

- Are we missing additional metrics?
- What do you think of these users' subdivisions?
- Is it possible to account for the use of the distributed material (e.g. research, breeding, conservation, repatriation, direct cultivation etc.)?

Summary of mandatory metrics

Code	Description
NACC	Number of accessions
DOC_PDCI	Average passport data completeness index (PDCI) of the accessions
DOC_PHEN	Average number of phenotypic datapoints per accession
CON_NGER	Number of results of germination/viability tests on base samples generated and stored
CON_NREG	Number of accessions for which newly regenerated seeds were stored
CON_GER	Number of accessions that need a germination test
CON_REG	Number of accessions that need to be regenerated
CON_NSAF	Number of accessions that are safety duplicated
AVA_AVA	Number of accessions that are readily available for distribution
DIS_EXT	Number of distributed samples excluding internal genebank use

CePaCT

Expanding the metrics towards other PGR conservation methodologies

***In vitro**:* (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.

On farm conservation: (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.

What about cryopreservation and field conservation?

Learning from the experience of **Crop Trust key performance indicators**.

UniPV

THANK YOU