Introduction to Germplasm Characterization and Evaluation

Aim of the module

At the end of the module, we should be able to:

- Explain what characterization and evaluation are and why they are crucial to the success of pre-breeding

- Describe the range of methods available for characterizing and evaluating genebank materials

- State the importance of documenting genebank accessions

Introduction

- Genebanks are reservoirs of genes – used in plant breeding

- Effective use of genebanks in breeding relies on a thorough understanding of the existing genetic diversity

  – knowledge of the genes present in individual accessions

- Knowledge gained through the activities of characterization and evaluation

- Without knowledge of the traits held in genebanks, they become museums of plant accessions, or living herbaria

Introduction

- Germplasm characterization is the recording of distinctly identifiable characteristics, which are highly heritable

- Germplasm evaluation refers to the agronomic description of the material in a genebank, for traits that are generally important to breeders and researches in crop improvement.

- Generally, genebank managers, breeders and other specialists work together to develop the set of traits that provide the basic description of a species diversity.

Descriptors

- When used for germplasm characterization and evaluation, these traits and their attributes are known as descriptors.

- Descriptors lists include the basic description of the traits, and the different classes of their expression (characterization) or how to measure the range of their variation (evaluation).

- Most of the descriptors for characterization and evaluation are species-specific.

- An important tool for a standardized characterization system, which provides an international format and a universally understood 'language' for PGRFA data.

Descriptors

- The descriptor list is the collation of descriptors for a species or crop.

- Bioversity International has collaborated with many institutions to develop and standardize these internationally accepted descriptors for almost 100 crops

- They are available at http://www.bioversityinternational.org/e-library/publications/categories/descriptors/

or

- http://cropgenebank.sgrp.cgiar.org/index.php/learning-space-mainmenu-455/manuals-and-handbooks-mainmenu-533/descriptors-mainmenu-547

Descriptors

- Molecular markers are replacing morphological descriptors for some purposes e.g.

  - evolutionary studies,

  - for assessing interrelationships among accessions and among geographic groups of accessions,

  - for estimating genetic diversity, and

  - for identifying duplicates.

- Nonetheless, the visible descriptors will remain important for

  - identifying landrace accessions at the farm level and

  - as an adjunct to use of molecular markers for other studies.

- And until the cost of molecular markers falls further

Descriptors

- Descriptor states may be

    - a numeric value such as a weight, a length, or an output from a sensor;

    - a code within a scale, such as a 1 to 9 rating for disease severity or a rating for shade and intensity of color; or

    - a qualifier, such as absence or presence of a trait.

- The name, state, and scale for any descriptor are agreed upon by researchers involved in germplasm characterization and evaluation..

- The descriptors could be

    - qualitative or

    - quantitative

Descriptors

- Qualitative descriptors

  – typically morphological, physiological and molecular (biochemical and DNA) traits

- Quantitative descriptors

  – subject to environmental factors, e.g. yield and components, host plant resistance and stress tolerance.

- Characterization descriptors should show high repeatability values

  – because they are affected relatively little by the testing environment and by genotype-by-environment interaction.

Descriptors

- Quantitative descriptors (showing continuous variation) are often used in classification

  – even when the environment or GXE significantly affects their phenotypic expression.

- How to lessen the environmental and GXE effects:

  – assessing the germplasm in several environments and using the mean values

  – evaluating the germplasm in several environments and defining similar phenotypic responses in each specific environment

  – comparing only those traits which are not affected by the environment

Descriptors

Type	Scale	Measurement	Typical descriptor
Quantitative	**Interval**	Direct measure of a trait	Height, yield, days to flowering, maturity and harvest, protein content, yield and components
	Ratio	Combining two trait measures into a single descriptor	Harvest index, content percentage, length/width index
Qualitative	**Ordinal**	Relative value assigned within a standard scale	Host plant resistance (from 1: highly tolerant to 9: highly susceptible), shapes, overall quality
	Nominal	Qualitative state assigned into arbitrarily number-scale	Color, seed pattern, growth habit
	Dichotomy	Trait presence or absence	Pubescence, color spots
	Gene symbols	Known gene names assigned	*Italic fonts* given to known alleles

Characterization vs. Evaluation

Item	Characterization	Evaluation
Definition	Assessment of attributes in a given accession that are relatively stable across environments	Measurement of attributes in a given accession, generally of agronomic significance, that are environmentally sensitive
Distinct traits	Often qualitative, mono-genically inherited, environmentally stable, and easy to measure and use for classification	Most often quantitative, multigenically inherited, influenced by testing environments and less easy to measure and use for classification
Typical descriptors	Color, pubescence, and shape of plant parts; biochemical and DNA markers	Height, yield and components, time to flowering, maturity, protein or starch content, tolerance to abiotic stresses

Characterization

The main aims of germplasm characterization are to:

- describe accessions and establish accessions' diagnostic characteristics

- classify accessions into groups using sound means

- assess interrelationships among accessions or among traits and among geographic groups of accessions

- estimate the extent of variation in the genebank collection

- identify duplicates in a collection

Methods for characterization

- Characterization of each sample involves a description of the special characteristics that are
  - inherited,
  - easy to score, and
  - expressed consistently in all environments.

- Most germplasm characterization is carried out in precision fields
  - by spaced planting
  - under adequate agronomic conditions and plant protection.

- Proper statistical analysis yield further information

Value of characterization in pre-breeding

- Adequate characterization of genebank accessions is needed to facilitate the utilization of germplasm by end users

- Genetic diversity assessment of the variation among genebank accessions is the main aim of germplasm characterization

- Systematic description of each accession should

  - lead to classification in small and well-organized groups

  - will facilitate their enhanced utilization in pre-breeding

Evaluation

- Main aim of evaluation is to reveal potentially useful variability for further use in genetic enhancement of crops

- Evaluation may be expensive and time consuming but is of great value for a precise phenotyping of genebank accession(s) of interest

Evaluation

- Evaluation goes deeper than characterization. It usually includes

  - agronomic performance,

  - yield and

  - reaction to biotic and abiotic stresses, such as drought or pests

- These traits are important to plant breeders and researchers in crop improvement

- It may require special biochemical techniques or DNA-based methods to analyse a plant's genetic diversity

Evaluation

The information obtained is used for

- Collection management: verifying that an accession belongs to the original description

- Query answering: supplying users with the most suitable accession or with information that will allow them to select their own accessions

- Genetic resources research: defining diversity patterns and relating them to the origin and history of the crop

Evaluation

- The initial evaluation may be:

  - undertaken in small nursery plots,

  - followed by a more detailed field trial to assess useful traits that show quantitative variation.

- Screening techniques are required to assist in identifying sources of host plant resistance to main pathogens and pests

- Control or check line(s) – often the most used locally adapted cultivar(s), should be included as a reference standard(s) for comparisons with the accessions being evaluated.

Evaluation

The value of evaluation information for pre-breeding

- The key to successful utilization of accessions available in genebanks is to have a clear concept of what variability the users want to tap.

- Knowing this, the pre-breeder can search for the trait and incorporate such genetic diversity into a more usable form for further use in plant breeding.

Documentation

- There may be distinct documentation systems but all of them should agree on the descriptors.

- The descriptor lists as well as the descriptor states must be well defined and available in a code dictionary.

- Information should be published in a catalogue that should be easy to retrieve and read.

- Web or printed versions should only have useful information on accessions available for any external user.

Databases

- Sources of information at the accession/sample/species level

  - Individual genebank

  - Country

  - Regional and/or sub-regional

  - Global

- Sources of information at the metadata level, e.g. FAO's WIEWS --- http://apps3.fao.org/wiews/wiews.jsp

- Scientific literature

- Other sources

Databases -- Genesys

Genesys as portal for access to germplasm

- https://www.genesys-pgr.org/welcome

- bring together accession-level data from three major networks:

  - The European Plant Genetic Resources Search Catalogue (EURISCO)

  - CGIAR's System-wide Information Network for Genetic Resources (SINGER)

  - The United States Department of Agriculture's Genetic Resources Information Network (GRIN)

Database – Use in Pre-breeding

- Search for potentially promising accessions may be facilitated through free exchange of ideas and information among researchers.

- Outstanding sources of host plant resistance or tolerance to abiotic stresses can be found where the pathogens, pests or stresses are endemic.

  - An intensive screening of accessions originating from such endemic stressful areas may lead to identifying high levels or host plant resistance or stress tolerance.

Characterization and evaluation data in pre-breeding

Core collections.

- Serves as an entry point to the whole collection

    – and improves the access of the plant breeder, research geneticists and other users to the germplasm collection .

- As a representative sample of the alleles from the entire collection,

    – characterization and evaluation of this subset assesses accurately the variation across the entire collection.

- Efficient way to estimate likelihood of finding useful genes, and at what frequency.

- However rare alleles may be missed.

Genebank Learning Resources

Crop Genebank Knowledge Base

http://cropgenebank.sgrp.cgiar.org/

Genebank Standards
for Plant Genetic Resources
for Food and Agriculture

COMMISSION ON
GENETIC RESOURCES
FOR FOOD AND
AGRICULTURE

http://www.fao.org/agriculture/crops/themat
ic-sitemap/theme/seeds-pgr/gbs/en/

Summary: Utilization of genebank accessions through pre-breeding

Search for alleles, genes, traits for use in genetic improvement requires:

- characterization and evaluation (genotypic and phenotypic)

- more thorough advanced evaluation (perhaps through a core subset) for desirable trait or allele diversity

- finding the trait(s) or allele(s) of interest (in core set or whole germplasm)

- incorporating such desired trait or allelic diversity into the breeding materials