



DELIVERABLE 4.1

Unified, crop-specific standards and protocols for the evaluation of the phenotypes and agronomic characteristics of PGR, incorporating the ECPGR, MIAPPE, Crop Ontology, EMPHASIS and final user recommendations and methodologies Call identifier: HORIZON-INFRA-2022-DEV-01-01 PRO-GRACE Grant agreement no: 101094738

Promoting a plant genetic resource community for Europe

Deliverable No. 4.1

Unified, crop-specific standards and protocols for the evaluation of the phenotypes and agronomic characteristics of PGR, incorporating the ECPGR, MIAPPE, Crop Ontology, EMPHASIS and final user recommendations and methodologies.

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1. Introduction
2. Activities
3. Results
3.1 Main sources of information5
3.1.1. The resources developed under FAO auspices5
3.1.2. Resources developed in relation to industry needs6
3.1.3. The ecosystem of resources developed by the plant research community7
3.2 CROP-SPECIFIC DESCRIPTORS10
3.2.1 Fruit trees
3.2.2 Fruit vegetables13
3.2.3 Grain crops16
3.2.3.1 Cereals16
3.2.3.2 Pseudocereals
3.2.3.3 Grain Legumes19
3.2.4 Leafy Vegetables22
4. Gap and redundancy analysis23
Annex 1

1. Introduction

The **phenotype** is the set of structural, physiological, and performance-related traits of a genotype in a given environment. Plant phenotyping is the act of determining the quantitative or qualitative values of these traits. It is a procedure leading to understanding of structural and functional plant traits and the relationships between them. Plant phenotypes are inherently complex because they result from the interaction of genotypes with a multitude of environmental factors. Until a few decades ago, it was mostly based on visual observations and scoring systems or on simple instrumental measures of the whole plants and their parts. It has a pivotal importance in breeding activities for producing varietal innovations with superior traits such as higher yield, disease and pest resistance and adaptation to abiotic stresses.

Technological advancements in several sectors have produced methodologies for high-throughput phenotyping. This has led to a new branch of biology, **phenomics**, which is the natural complement to genome sequencing as a route to rapid advances in biology towards the full characterization of the complete set of phenotypes encoded by a genome. The explosion of novel non-invasive methods, such as high-throughput imaging, drones, robots, or artificial intelligence (AI) offers unprecedented possibilities, but poses a new problem as well: the standardization of protocols and methods. **Standardization can also support semantic interoperability which is necessary for reusing and comparing data that are obtained through different phenotyping platforms**.

In the context of genetic resources, three types of information must be taken into consideration:

- **Passport data** allow to identify the accessions in their collection: identifiers and name of the accession, the species to which it belongs and information about its origin, who is holding it, etc.
- **Primary descriptors** are generally morphological traits with simple heredity that characterize an accession: e.g. color and shape of the mature fruit, hairy or hairless leaves....
- **Secondary descriptors** are traits with complex heredity that necessitate several years of observation and/or experiments: e.g. flowering time, bud break, yield...

Over time, an ecosystem of resources has been produced, contributing on one side to standardize the way descriptors are measured, and on the other side to make the data collected FAIR (*i.e.* they meet the principles of findability, accessibility, interoperability, and reusability).

This ecosystem has been developed by three distinct communities with different dynamics: 1) the genebank community, intergovernmental networks and international bodies under the auspices of the FAO; 2) UPOV/CPVO (International Union for the Protection of New Varieties of Plants / The Community Plant Variety Office); and 3) the Plant Science research community.

The aim of deliverable D4.1 is to **review and map in more details the current initiatives in plant phenotyping and related ontologies** and propose, in deliverable 4.3, a unified crop-specific standardization of protocols methods for the evaluation and valorization of Plant Genetic Resources (PGRs).

2. Activities

During online meetings between the project participants, we decided to carry out our inventory on 4 groups of species. In this deliverable we consider only Plant Genetic Resources for Food and Agriculture (PGRFA). In particular, we identified:

- 1) Fruit trees
- 2) Fruit vegetables
- 3) Leafy vegetables

4) Grains (cereals and legumes).

For each group, we identified referents as follows:

- Group 1, Ignazio Verde (CREA)
- Group 2, Véronique Lefebvre (INRAE), Maria José Díez (UPV) and Jaime Prohens (UPV)
- Group 3, Filippo Guzzon (CGIAR), Jelka Šuštar Vozlič (KIS)
- Group 4, Filippo Guzzon (CGIAR), Patrizia Vaccino (CREA), Elisabetta Mazzucotelli (CREA).

Concerning the traits, we decided to concentrate on those that are important for breeding rather than traits used for taxonomy or varietal classification (e.g. DUS, Distinctness, Uniformity, Stability), and in particular on:

- Yield
- Quality characteristics (before and after processing)
- Resistance to biotic stresses
- Tolerance to abiotic stresses
- Plant and root architecture.

An important aspect is the mapping and organization of the existing initiatives. In agreement with the proposal of WP1 (D1.1), we decided to **establish criteria for generating a harmonized system of standards and descriptors for phenotypic data and their related ontologies**.

3. Results

3.1 Main sources of information

In the context of genetic resources, passport and phenotypic descriptors for evaluation of genetic resources have been largely developed by several international organizations such as FAO, ECPGR, or IPGRI/BIOVERSITY. In addition to these organizations, UPOV/CPVO prepared technical protocols and guidelines for DUS tests of varieties. In a larger context of research on plants, consortia of researchers, ontologists and research infrastructures have developed a large set of resources (*e.g.* databases, ontologies, metadata standards, guidelines, training materials) supporting FAIR data management in the context of plant phenotyping experiments. Hereafter is presented the list of references to these initiatives with some general information.

3.1.1. The resources developed under FAO auspices

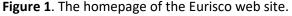
- <u>The List of Multi-Crop Passport Descriptors (MCPD)</u> is a reference tool developed in 2001 jointly by IPGRI and FAO to provide international standards to facilitate germplasm passport information exchange across crops: <u>https://cgspace.cgiar.org/handle/10568/105205</u>. This metadata standard has been updated twice:
 - MCPD V.2: it is the result of a thorough revision in 2012: https://cgspace.cgiar.org/handle/10568/91224
 - MCPD V.2.1: it is an update to MCPD V.2, released in 2015, and expanded in order to accommodate emerging needs, such as the broader use of GPS tools, or the implementation of the International Treaty on Plant Genetic Resources for Food and Agriculture's Multilateral System for access and benefit-sharing (Alercia et al 2015): https://cgspace.cgiar.org/handle/10568/69166.
- The history and usefulness of <u>Bioversity International's descriptor lists</u>: <u>https://cgspace.cgiar.org/handle/10568/73450</u>. Catalogs of descriptors have been developed by Bioversity International for many species or species groups (see **Annex 1**). In these catalogs, the naming of the descriptors is standardized as well as their scoring methods and scales. These catalogs are a precious resource; however, they are often not machine actionable.

 <u>Genebank Standards for Plant Genetic Resources for Food and Agriculture</u>: prepared under the guidance of the FAO Commission on Genetic Resources for Food and Agriculture, it lays down the procedures that need to be followed for conserving, characterizing, evaluating and documenting plant genetic resources (FAO 2014). <u>https://www.fao.org/3/i3704e/i3704e.pdf</u>.

In Europe, <u>the inter-governmental network of conservation of plant genetic resources</u> (the European Cooperative Programme for Plant Genetic Resources, ECPGR) (<u>https://www.ecpgr.cgiar.org/</u>) has launched the <u>European Evaluation Network (EVA</u>) for PGRFA: it is an international project involving public and private sector partners, aimed at increasing the use of crop genetic diversity conserved in European genebanks and the diversity of stakeholders in plant breeding. The project uses standardized protocols and data collection templates to facilitate comparison of phenotypic data collected in multilocation trials across Europe (<u>https://www.ecpgr.cgiar.org/</u>).

ECPGR also supports EURISCO (<u>https://eurisco.ipk-gatersleben.de/apex/eurisco_ws/r/eurisco/about-eurisco</u>), the web-based catalogue that provides information about *ex situ* plant collections maintained in Europe. The EURISCO catalogue contains passport and phenotypic data for more than 2 million samples of crop representing more than 6,700 genera and more than 45,000 species (genus-species combinations including synonyms and spelling variants) from 43 countries (**Figure 1**).

Episonan Congenier Go Paul Resource ECP/GR	Find	Urisco ing seeds for the future			
Home		lome \			
Search	>	Welcome to EURISCO			
Export data	>	About EURISCO	Featured crops		
2 Statistics & documents	>	The European Search Catalogue for Plant Genetic Resources (EURISCO) provides information about more than 2 million	Barley	Bean	Chickpea
About	>	accessions of crop plants and their wild relatives, preserved ex situ by about 400 institutes. It is based on a network of National			
8 News		Inventories of 43 member countries and represents an important effort for the preservation of world's agrobiological diversity by	12 19		
Newsletter subscription		providing information about the large genetic diversity kept by the collaborating institutions.	Mr. K.	No.	
EURISCO intranet		Between 2003 and 2014, EURISCO was hosted and maintained by			
Imprint		Bioversity International, Rome, Italy. Since 2014, EURISCO is being maintained at the Leibniz Institute of Plant Genetics and Crop Plant	Potato	Sunflower	Tomato
Data protection policy		Research (IPK), Gatersleben, Germany. The central goal of EURISCO is to provide a one-stop-shop for information for the scientific community and for plant breeders . EURISCO contains both passport data and phenotypic data .			
		EURISCO is being maintained on behalf of the Secretariat of the European Cooperative Programme for Plant Genetic Resources	NOC AL		



3.1.2. Resources developed in relation to industry needs

<u>UPOV/CPVO has developed Technical Protocols (TP) or Guidelines</u> to support the process of variety registration: they contain a list of descriptors for several crops. The main aim of this list is to provide directions for cultivar identification, mainly for the assessment of DUS tests. Many traits analyzed have little importance for evaluation and valorization in breeding, however, they can be useful for establishing standard protocols and methods for genetic resources evaluation. The TPs for the crops in the CPVO list can be downloaded at https://cpvo.europa.eu/en/applications-and-examinations/technical-examinations/technical-examinations/technical-protocols while the UPOV guidelines can be reached at https://www.upov.int/test_guidelines/en/list.jsp.

- The Agrochemistry industries sponsored the development of a standardized description of plant phenological stages: <u>the BBCH-scale</u> (Meier 2001; downloadable version: <u>https://www.reterurale.it/downloads/BBCH_engl_2001.pdf.</u>
- •
- <u>The International Organization of Vine and Wine, OIV</u>, has developed a catalog of descriptors for grapevine, which was then transferred into a crop ontology format (see **Annex 1** and below).

3.1.3. The ecosystem of resources developed by the plant research community

The international plant science community has actively developed a set of complementary ontologies. **Ontology** is a way to represent the entities with all their interdependent properties and relationships, according to a system of categories by defining a set of terms and relational expressions that represent the entities in a specific subject area (Jacquette 2002). The objective is to enable machine actionable consistent data reuse and comparison across projects and locations. In ontologies, well-defined terms associated with unique identifiers and a set of relationships, are the core for data reusability. In the context of plant phenotyping, a set of ontologies have been created to describe in a standardized way the entities of a plant, their properties and the traits targeted by a phenotyping experiment (see https://groportal.lirmm.fr/, https://planteome.org/; https://agroportal.lirmm.fr/, https://groportal.lirmm.fr/, https://planteome.org/; https://agroportal.lirmm.fr/, https://agroportal.lirmm.fr/, https://planteome.org/; https://agroportal.lirmm.fr/, https://planteome.org/; https://agroportal.lirmm.fr/, https://planteome.org/; https://agroportal.lirmm.fr/, https://planteome.org/; https://agroportal.lirmm.fr/, https://planteome.org/; https://planteome.org/; https://planteome.org/

- **Plant Ontology** aims to establish a structured vocabulary that links plant anatomy, morphology, growth and development to plant genomics data. It extends the concepts set up by the Gene Ontology Consortium to facilitate the annotation of gene products and gene-associated phenotypes (Avraham *et al.* 2008).
- **Trait Ontology** describes phenotypic traits. Each trait is a distinguishable feature, characteristic, quality or phenotypic feature of a developing or mature plant (Cooper *et al.* 2018).
- Crop Ontology aims at capturing the phenotyping practices following a conceptual model that defines a phenotypic variable as a combination of a trait, a method and a scale (Shrestha *et al.* 2010). The guidelines for creating crop-specific ontologies to annotate phenotypic data can be downloaded at https://cgspace.cgiar.org/handle/10568/110906 (Pietragalla *et al.* 2022). Moreover, the ontologies prepared for several crops by the Crop Ontology Initiative can be downloaded (https://cropontology.org/) (Figure 2).
- These general ontologies have been completed by another ontology aiming at describing in a semantic and standardized way phenotypic experiments: the Plant Phenotyping Experiment Ontology (Papoutsoglou *et al.* 2020); https://fairsharing.org/1234).

The **Planteome Project** developed resources aiming at mapping different complementary ontologies relevant to plant phenotyping and corresponding required metadata: The Plant Trait Ontology, The Plant Ontology (description of plant tissue/organ and developmental stages), the Plant Environment Ontology (EO) to describe the experimental conditions, the Plant Stress Ontology (PSO) to describe the treatments with pathogens, stress conditions, some of the Crop Ontologies. The Planteome database has the objective to link the phenomics to the other omics experiments through comparative analysis experiments on transcriptome, proteomics, phenomics and genome annotation projects (<u>https://browser.planteome.org/amigo/term/TO:0000387#display-lineage-tab</u>). The Planteome project brings an integrated approach of adopting common annotation standards / reference vocabularies (ontologies) that can be queried in real time using common query words and a set of reference ontologies for plants to solve conflicting descriptions. Two other central portals allowing to search for ontologies and ontology terms are listed below:

• The Ontology Lookup Service (OLS) of EMBL-EBI: <u>https://www.ebi.ac.uk/ols/ontologies/to</u>

• The Bioportal (<u>https://bioportal.bioontology.org/ontologies/PTO?p=classes</u>) and its portal dedicated to ontologies relevant to agriculture sciences: <u>https://agroportal.lirmm.fr/</u>.

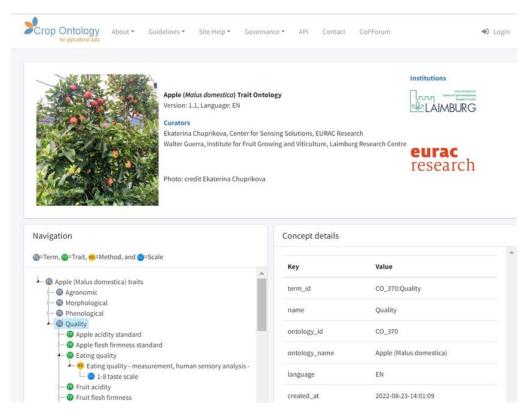


Figure 2. Example of crop ontology for apple. In addition to Crop Ontology, a series of initiatives such as the Minimum Information about a Plant Phenotyping Experiment (MIAPPE), the Planteome database, EMPHASIS, have proposed minimum information, ontologies, and data exchange/database formats to enhance the FAIRness of phenotypic data.

Building on existing resources, the European infrastructures EMPHASIS (<u>https://emphasis.plant-phenotyping.eu/</u>) and ELIXIR (<u>https://elixir-europe.org/</u>), in conjunction with the Wheat Initiative (<u>https://www.wheatinitiative.org/</u>), Bioversity international and the international consortia MIAPPE (<u>www.miappe.org</u>) and the BrAPI (<u>www.brapi.org</u>), have developed a set of coherent resources to support **the FAIR data management of data from plant phenotyping experiments**.

This work was supported by several EU-funded projects (FP7 TranPLANT, H2020 ELIXIR Excelerate, H2020 ELIXIR CONVERGE). The set of tools consists of a set of ontologies (the Plant Phenotyping Experiment Ontology and the Crop Ontologies), aligned with a set of metadata standards (MCPD, MIAPPE) and a standard web service for data exchange (BrAPI). These resources were completed with training resources and dedicated pages in ELIXIR's collaborative gateway supporting FAIR data management (https://rdmkit.elixir-europe.org/plant_sciences).

 MIAPPE is an open, community driven, data standard designed to harmonise data from plant phenotyping experiments and provides specifications including a checklist and a data model of metadata required to adequately describe plant phenotyping experiments (<u>https://www.miappe.org/</u>) (Papoutsoglou *et al.* 2020). MIAPPE has developed a checklist in Excel format that includes all the guidelines for each category of information (https://github.com/MIAPPE/MIAPPE/blob/master/MIAPPE_Checklist-Data-Modelv1.1/MIAPPE_Checklist-Data-Model-v1.1.tsv).

 A collaborative gateway of guidelines and resources supporting FAIR Data management in Life Sciences based on GitHub is managed by ELIXIR: the RDMkit. It contains guidelines, linked to resources (training, databases, tools, data management related recipes, etc.). The Plant Science domain pages (<u>https://rdmkit.elixir-europe.org/plant_sciences</u>) are currently focussing on best practices to ensure FAIR and interoperable phenotyping and genotyping data (Figure 3).

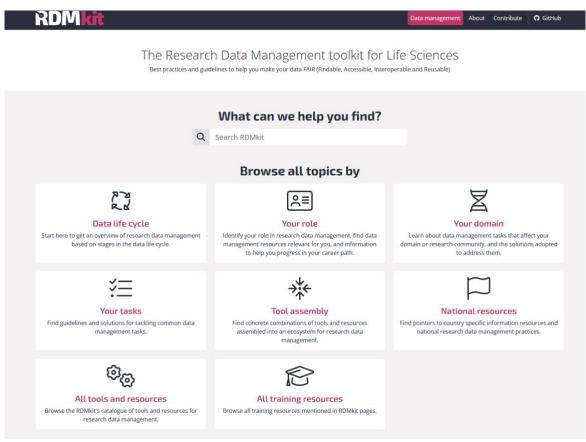


Figure 3. ELIXIR's RDMkit gateway allows to get support on data management from different perspectives and roles.

ELIXIR's RDMkit gateway links with other central catalogues of resources such as FAIRsharing. **FAIRsharing** gives access to a comprehensive view on standards, ontologies, community of practices, policies and databases implementing these policies (*e.g.* in the context of plant ontologies: <u>https://fairsharing.org/search?q=plant%20ontology</u>). FAIRsharing reports for instance 54 initiatives for Plant Ontology, 51 for Trait Ontology and 41 for Crop Ontology (**Figure 4**).

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	NAVATAINED NECOMMENSED	NOT RECOMMENDED			
0		NOT RECOMMENDED	00.350	Oat Trait Ontology	
2 2 2 quistry Q Set	READY SEPARCENTES		co_350	Oat Trait Ontology Reference Plant Ontologies are being developed in the cor the Crop Ontology, which provides harmonized preeders" (Refer Pageaders) Preorders (Arena sater)	

Figure 4. Trait ontology initiatives surveyed in the FAIRsharing website.

The H2020 project **AGENT** is a project that aims to establish a global genebank network to sustainably unlock the genetic diversity of food crops for future generations and make them intuitively accessible for modern breeding programs. It involves 13 genebanks and 5 bioinformatic centres, focusing on wheat and barley (<u>https://www.agent-project.eu/</u>). AGENT contributed to testing and improving the guidelines for FAIR data management in collaboration with the ELIXIR Plant Science community, to ensure interoperability between phenotyping and genotyping data (<u>https://rdmkit.elixir-europe.org/plant sciences</u>). AGENT also completed or improved the set of tools and databases necessary to support FAIR data collection.

The **INNOBREED** project is developing and applying innovative solutions in the organic fruit tree sector, including shared procedures and protocols for the evaluation and valorization of the genetic resources, for developing varieties tailored for the organic fruit industry (<u>https://innobreed.eu/)</u>.

The InnoVar project (<u>https://www.h2020innovar.eu/</u>) is improving the efficacy and accuracy of European crop variety testing and decision-making, using an integrated approach incorporating genomics, phenomics and machine learning. It is focused on wheat initially, then the InnoVar approach will be applied to other major crops. Innovative ways to measure DUS characters will be evaluated. Value for Cultivation or Use (VCU) testing procedures will be revised and shaped to comprehensively address variability in growing conditions, stresses and management approaches.

3.2 CROP-SPECIFIC DESCRIPTORS

3.2.1 Fruit trees

Fruit Trees are clonally propagated perennial crops. Several initiatives have been conducted so far. **ECPGR** in connection with CGIAR proposed descriptor lists for several temperate and sub-tropical fruit crops. They produced lists of descriptors for the following fruit tree crops:

• Almond (*Prunus dulcis*) <u>https://cgspace.cgiar.org/handle/10568/104209</u> <u>https://cgspace.cgiar.org/handle/10568/72793</u>

- Anona (Annona cherimola) https://cgspace.cgiar.org/handle/10568/104849
- Apple (Malus x domestica) <u>https://cgspace.cgiar.org/handle/10568/72794;</u> <u>https://cropontology.org/term/CO_370:ROOT</u>
- Apricot (*Prunus armeniaca*) <u>https://cgspace.cgiar.org/handle/10568/73447</u>
- Avocado (*Persea spp*) <u>https://cgspace.cgiar.org/handle/10568/72796</u>
- Banana (*Musa spp.*) <u>https://cgspace.cgiar.org/handle/10568/72799;</u> https://cropontology.org/term/CO_325:ROOT
- Cherry (Prunus avium, P. cerasus) https://cgspace.cgiar.org/handle/10568/72853
- Citrus (Citrus spp) https://cgspace.cgiar.org/handle/10568/72733
- Coconut (Cocos nucifera L.) <u>https://cropontology.org/term/CO_326:ROOT</u>
- Coffee (<u>C. canephora</u> & C. arabica) <u>https://cgspace.cgiar.org/handle/10568/72788</u>
- Durian (*Durio zibethinus*) <u>https://cgspace.cgiar.org/handle/10568/72585</u>
- Fig (*Ficus carica*) <u>https://cgspace.cgiar.org/handle/10568/72691</u>
 Grapes (*Vitis vinifera*) <u>http://www.eu-vitis.de/docs/descriptors/mcpd/Descriptors EUVitisDB 11Jan12.pdf</u>; <u>https://cropontology.org/term/CO 356:ROOT</u>
- Hazelnut (Corylus avellana) https://cgspace.cgiar.org/handle/10568/72598
- Jackfruit (Artocarpus heterophyllus) https://cgspace.cgiar.org/handle/10568/72703
- Litchi (Litchi chinensis) https://cgspace.cgiar.org/handle/10568/72694
- Mangaba (Hancornia speciosa) <u>https://cgspace.cgiar.org/handle/10568/90693</u>
- Mango (Mangifera indica) <u>https://cgspace.cgiar.org/handle/10568/72607</u>
- Papaya (*Carica papaya*) <u>https://cgspace.cgiar.org/handle/10568/72903</u>
- Peach (Prunus persica) https://cgspace.cgiar.org/handle/10568/72905
- Pear (Pyrus communis) https://cgspace.cgiar.org/handle/10568/72906

•	Pistachio	and	relatives	(Pistacia	vera	and	Pistacia	spp)
	https://cgsp	bace.cgiar.o	rg/handle/105	<u>68/72917</u>				;
	https://cgsp	bace.cgiar.o	rg/handle/105	<u>68/72916</u>				
•	Plum	(Prunus	domesti	са, Р.	salic	ina,	Prunus	spp)

- Plum (*Prunus domestica*, *P. salicina*, *Prunus* <u>https://cgspace.cgiar.org/handle/10568/72940</u>
- Rambutan (*Nephelium lappaceum*) <u>https://cgspace.cgiar.org/handle/10568/72693</u>
- Tropical fruit (various) <u>https://cgspace.cgiar.org/handle/10568/73058</u>
- Grape species <u>https://www.upov.int/edocs/tgdocs/en/tg050.pdf</u>
- Walnut (Juglans regia) https://cgspace.cgiar.org/handle/10568/73159

Regarding ontology, the Rosaceae community (Genome Database for Rosaceae, GDR) has made an effort to standardize the names and the abbreviations for all the traits entered in the database. GDR QTLs are associated with these trait terms and QTL labels, assigned by GDR, use the abbreviations for the listed traits. Each of these terms is either an existing term or a child term of the existing term of the plant trait ontology. One term can belong to multiple Root Trait Ontology terms. The trait list can be reached at https://www.rosaceae.org/trait (Figures 5 & 6).

+ yield trait

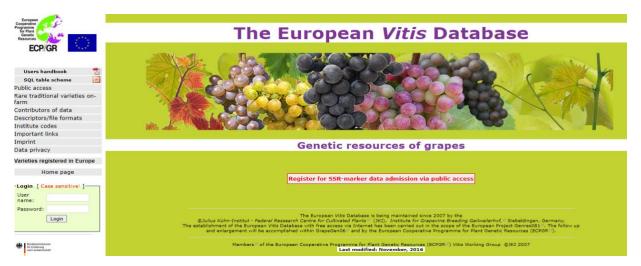
KGDR Species - Data - Search - Tools - General	I - Help - Community - Login Search Q
Rosaceae Trait Ontology	
GDR has made an effort to standardize the trait names and the abbreviations for all the trait dat labels, assigned by GDR, use the below abbreviations for the listed traits. Each of these trait te ontology. One trait term can belong to multiple Root TO term. When possible, we have used ab were developed they have been submitted to the Trait Ontology consortium for inclusion. We we have a new trait or are unsure about the naming please contact us . To see all the traits, click to expand the trait category below. Or narrow the list using the keywork Keyword Search	terms is either an existing term or a child term of the existing term of the plant trait bbreviations that are consistent with established trait or crop ontologies. Where new ones would appreciate if new studies could use these standardized terms where possible. If you
Category	Count
+ biochemical trait	155
+ plant growth and development trait	56
+ plant morphology trait	215
+ quality trait	94
+ stature or vigor trait	14
+ sterility or fertility trait	6
+ stress trait	37

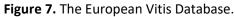
Figure 5. Main Trait Ontology categories on the Genome Database for Rosaceae (GDR).

樥 GDR 🔉 spe	ecies - Data - Search	- Tools - General - He	lp - Community - Login Search	h Q
Rosaceae Trait On	itology			
abels, assigned by GDR, use the ontology. One trait term can belon vere developed they have been s have a new trait or are unsure abo	below abbreviations for the lister ag to multiple Root TO term. Whe submitted to the Trait Ontology co but the naming please contact u	d traits. Each of these trait terms is e in possible, we have used abbreviation posortium for inclusion. We would app	ed in the database. GDR QTL are associated with these ither an existing term or a child term of the existing term ons that are consistent with established trait or crop ontol reciate if new studies could use these standardized term h.	of the plant trait logies. Where new one
Category	Abbreviation	Trait Name	Definition	Coun
+ biochemical trait				155
	t trait			155 56
+ plant growth and development	t trait			07.0
+ plant growth and development + plant morphology trait	t trait ASA	L-Ascorbic acid content	amount of L-ascorbic acid in fruit	56
+ plant growth and development + plant morphology trait		L-Ascorbic acid content anther color	amount of L-ascorbic acid in fruit color of anther	56 215
+ plant growth and development + plant morphology trait	ASA			56 215
+ plant growth and development + plant morphology trait	ASA ATCL	anther color	color of anther	56 215
+ plant growth and development + plant morphology trait	ASA ATCL BTPT	anther color bitter pit	color of anther pitting of the cortical flesh	56 215
+ plant growth and development + plant morphology trait	ASA ATCL BTPT CAPPING	anther color bitter pit ease of calyx removal	color of anther pitting of the cortical flesh Ease of calyx removal	56 215
	ASA ATCL BTPT CAPPING CITA	anther color bitter pit ease of calyx removal citric acid content	color of anther pitting of the cortical flesh Ease of calyx removal amount of citric acid n fruits	56 215 94
+ plant growth and development + plant morphology trait	ASA ATCL BTPT CAPPING CITA DMC	anther color bitter pit ease of calyx removal citric acid content dry matter content	color of anther pitting of the cortical flesh Ease of calyx removal amount of citric acid n fruits dry matter content A combined assessment of flavour, acidity, sv	56 215 94 weetness, ne

Figure 6. Examples of quality traits surveyed in GDR Trait Ontology.

For Vitis spp., **The European Vitis Database** (<u>http://www.eu-vitis.de/index.php</u>) includes cultivated grapes (Vitis vinifera sub. vinifera) as well as wild grapes (Vitis vinifera sub. sylvestris) (**Figure 7**). Ontology considers different descriptors. Descriptors are primary (mainly ampelographic traits), secondary (resistance to disease, traits for wine, table quality) and genetics (SSR markers) as established by Genreso81 and GrapeGen06 projects. The database also reports descriptors for phenotyping (bud swelling, leaf fall and berry enocarpological traits) (**Figure 8**).





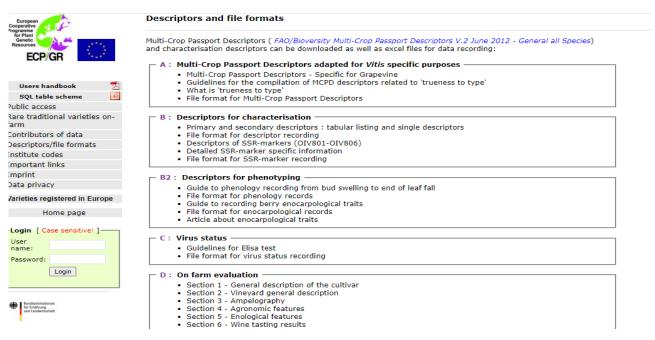


Figure 8. Main Trait Ontology categories on The European Vitis Database

3.2.2 Fruit vegetables

Fruit Vegetables are annual crops mostly of the Cucurbitaceae and Solanaceae families generally propagated by seed, although some such as pepino (*Solanum muricatum*) are vegetatively propagated. In addition, strawberry (*Fragaria x ananassa*), which belongs to the Rosaceae family is commonly considered as a fruit vegetable. Several initiatives have been conducted so far for the development of crop-specific descriptors. In this way, **ECPGR in connection with CGIAR** proposed descriptor lists for the following major crops: melon and other Cucurbitaceae (*Cucumis* spp., *Cucurbita* spp. and *Citrullus* spp.), Capsicum peppers, eggplant and tomato, as well as for a minor Solanaceae crop (pepino), and for strawberry.

The seven produced books of descriptors for these seven fruit vegetable crops are the following.

• Melon (Cucumis melo): https://cgspace.cgiar.org/handle/10568/72690

- Cucurbitaceae (*Cucumis* spp., *Cucurbita* spp. and *Citrullus* spp.): https://cgspace.cgiar.org/handle/10568/104810
- Capsicum peppers (*Capsicum* spp.): <u>https://cgspace.cgiar.org/handle/10568/72851</u>
- Eggplant (Solanum melongena): <u>https://cgspace.cgiar.org/handle/10568/72874</u>
- Tomato (*Solanum lycopersicum*): <u>https://cgspace.cgiar.org/handle/10568/73041</u>
- Pepino (Solanum muricatum): <u>https://cgspace.cgiar.org/handle/10568/72608</u>
- Strawberry (Fragaria x ananassa): https://cgspace.cgiar.org/handle/10568/72947

Minimum descriptor lists that encompass the former Solanaceae and Cucurbitaceae crops, as well as other fruit vegetable crops from these families have been produced, respectively by the **ECPGR Solanaceae Working Group and ECPGR Cucurbitaceae Working Group**. These lists of minimum descriptors can be used for crops that have no full descriptors; they are the following.

- Cucurbitaceae: Cucurbita spp., cucumber, melon and watermelon: <u>https://www.ecpgr.cgiar.org/fileadmin/templates/ecpgr.org/upload/NW and WG UPLOAD</u> <u>S/Cucurbits DescriptorLists.pdf</u>
- Solanaceae (major fruit crops): Eggplant, *Capsicum* (sweet and hot pepper) and tomato: <u>https://www.ecpgr.cgiar.org/fileadmin/templates/ecpgr.org/upload/NW and WG UPLOAD</u> <u>S/Solanaceae Miscc/Solanaceae descriptors.pdf</u>
- Solanaceae (minor fruit crops): Pepino, groundcherry and tree tomato: <u>https://www.ecpgr.cgiar.org/fileadmin/templates/ecpgr.org/upload/NW and WG UPLOAD</u> <u>S/Solanaceae Miscc/Descriptors minor crops NEW for Web 22022013.pdf</u>

Ontologies of fruit vegetables for Solanaceae have only been developed by the Sol Genomics Network (<u>https://solgenomics.net/</u>). A considerable effort has been made to develop an Ontology Browser (<u>https://solgenomics.net/tools/onto/</u>; **Figure 9**), which allows searching ontologies for phenotypes, as well as for other items such as molecular functions, cellular components, biological processes, plant structure development stages, plant anatomical entities, sequence characteristics, quality and volatile compounds. The various classifications of terms are viewable in a tree display (**Figure 10**). This tree indicates if a trait is a variable of another trait or part of another one.

\leftarrow \rightarrow C $$ https://solgenomics.ne	t/tools/onto/	
Sol Genomics Network Search	Maps Genomes Projects Tools About	
		Ontology browser
	Search and browse ontologies	
	Find exact ID Find Clear highlight Search for text SP (Solanaceae Ontology)	│ reset view ✓ Search
	GO:0003674 molecular_function GO:0003674 molecular_function GO:0005575 cellular_component GO:000912 plant structure development stage PO:0025131 plant anatomical entity SO:000010940 sequence_tature SO:000010940 sequence_attribute SO:0001060 sequence_tating SO:0001060 sequence_cattribute SO:0001060 sequence_cattribute SO:0001268 sequence_cattribute SO:0001268 sequence_cattribute SO:000128 sequence_cattribute SO:000128 sequence_cattribute SO:0001268 sequence_cattribute SO:0001268 sequence_cattribute SO:0001269 sequence_cattribute SO:000128 sequence_cattribute SO:001288 sequence_cattribute SO:000128 s	
	BTI BOYCE THOMPSON INSTITUTE	USDA
	SGN is supported by NSF (#0820612), USDA CSREES and hosted at BTI. Cite SGN using Fernandez-Pozo et al. 2014 Disclaimer	

Figure 9. Main categories in the Solanaceae ontology browser (<u>https://solgenomics.net/tools/onto/</u>).

$\leftrightarrow \rightarrow C$ \oplus https://solgenomics.net/tools/onto/
Sol Genomics Network Search Maps Genomes Projects Tools About
○ Search and browse ontologies Find exact ID Find Find Clear highlight reset view
Search for text SP (Solanaceae Ontology) 👻 Search
 ⇒ SP:0001000 Solanaceae phenotype ontology I-st_a SP:0000129 allocyme variant i=t_a SP:0000151 flower i=t_a SP:0000015 flowering i=t_a SP:0000017 truit color i=t_a SP:0000121 specific gravity i=t_a SP:0000121 specific gravity i=t_a SP:0000121 specific gravity i=t_a SP:0000115 truit metabolites i=t_a SP:0000115 fluit metabolites i=t_a SP:000
PO:0009012 plant structure development stage
PO:0025131 plant anatomical entity SO:0000110 sequence_feature
Gr SO:0000400 sequence_teatine
E-S0:0001060 sequence_variant
a SO:0001260 sequence_collection

Figure 10. Example of tree display for the fruit mass trait in the Solanaceae ontology browser (<u>https://solgenomics.net/tools/onto/</u>).

Ontologies of strawberry have been developed by the Genome Database for Rosaceae (GDR), which has made significant strides in creating a comprehensive ontology for strawberries, similarly as indicated for Rosaceae fruit trees (Section 3.2.1). This effort is evident in the standardized naming and abbreviation of trait data within the database <u>https://cropontology.org/term/CO_372:ROOT</u> (Figure 11). The GDR's trait terms, including those for strawberries, are either existing terms or child terms of existing terms from the plant trait ontology. These terms are associated with GDR's Quantitative Trait Loci (QTL), and the labels for QTL are assigned using these standardized abbreviations. The GDR has submitted new trait terms to the Trait Ontology consortium, aiming to align with established trait or crop ontologies wherever possible. Researchers are encouraged to use these standardized terms in new studies to maintain consistency.

C https://cropontology.org/term/CO_3				
	Site H	elp 👻 Governance 👻 API CoP Tools	▼ Contact	🔊 Login
	Curator Heng Su, Genome Database for Rosaceae credit: GDR			
	Navigation	Concept details		
	Navigation @=Term, @=Trait, @=Method, and @=Scale	Кеу	Value	
	Trait, Trait, Method, and Scale G Strawberry traits G Agronomic		Value CO_372:ROOT	^
	Trait, Starwberry traits O Strawberry traits O Strawberry traits O Biochemical O Biochemical O Biotic stress	Key		
	©=Term, @=Trait, @=Method, and @=Scale	* Key term_id	CO_372:ROOT	^
	Trait, Hethod, and Scale G Strawberry traits G Agronomic G Biotic stress G Morphological	key term_id name	CO_372:ROOT Strawberry traits	•
	©=Term, @=Trait, @=Method, and @=Scale	key term_id name ontology_id	CO_372:ROOT Strawberry traits CO_372	······································
	©=Term, @=Trait, @=Method, and @=Scale	Key term_id name ontology_id ontology_name	CO_372:R00T Strawberry traits CO_372 Strawberry	

Figure 11. Screenshot of the strawberry ontologies at the Genome Database for Rosaceae (GDR), displaying the main ontology categories.

3.2.3 Grain crops

3.2.3.1 Cereals

Cereal grain crops include rice, wheat, rye, oats, barley, millet, sorghum and maize. Cereals belong to the family Poaceae, commonly known as grasses. **ECPGR in connection with CGIAR** proposed descriptor lists for them, some recently updated in Crop Ontology.

Barley:

1994: Descriptors for barley (Hordeum vulgare L.) (cgiar.org)

2009: Key access and utilization descriptors for barley genetic resources (cgiar.org)

2020: CO_323, https://cropontology.org/term/CO_323:ROOT

Wheat:

1978: Descriptors for wheat and Aegilops (cgiar.org)
1985: Descriptors for wheat (Revised) (cgiar.org)
2019: CO_321, <u>https://cropontology.org/term/CO_321:ROOT</u>

<u>Maize</u>

1991: Descriptors for maize/Descriptores para maiz/Descripteurs (cgiar.org)
2009: Key access and utilization descriptors for maize genetic resources (cgiar.org)
2021: CO_322, https://cropontology.org/term/CO_322:ROOT

<u>Rice</u>

2007: Descriptors for wild and cultivated rice (*Oryza* spp.) (cgiar.org)
2009: Key access and utilization descriptors for rice genetic resources (cgiar.org)
2016: CO_320, <u>https://cropontology.org/term/CO_320:ROOT</u>

Sorghum

2010: Key access and utilization descriptors for sorghum genetic resources (cgiar.org) 2018: CO_324, <u>https://cropontology.org/term/CO_324:ROOT</u>

Rye and Triticale

1985: Descriptors for rye and triticale (cgiar.org)

<u>Oat</u>

1985: Oat descriptors (cgiar.org)

2019: CO_350, https://cropontology.org/term/CO_350:ROOT

Finger millet

1985. Descriptors for finger millet (cgiar.org)

2010: Key access and utilization descriptors for finger millet genetic resources (cgiar.org)

Pearl millet

1993: Descriptors for pearl millet (Pennisetum glaucum (L.) R. Br.) (cgiar.org)

2010. Key access and utilization descriptors for pearl millet genetic resources (cgiar.org)

2016: CO_327, https://cropontology.org/term/CO_327:ROOT

A specific focus on wheat is here presented as a case study. A Trait and Phenotype Ontology has been specifically developed for wheat, called WHEATPHENOTYPE, since 2010 (Nédellec et al., 2020) and it is accessible through Wheat Trait and Phenotype Ontology | AgroPortal (lirmm.fr). The objective was to answer breeders and scientists' needs for wheat trait and phenotype information management and retrieval at varying abstraction scales. Its supports two objectives: (1) building a formal shared representation of wheat trait whose knowledge organization closely reflects the expert knowledge model, and (2) making phenotypic information extraction from text easier. It has been evaluated in respect to FAIR scores, according to O'FAIRe (an open-source FAIRness assessment methodology and tool for ontologies, vocabularies and semantic resources developed within D2KAB and FooSIN projects). WHEATPHENOTYPE covers a wide range of bread wheat traits (e.g. observable physical plant properties), phenotypes (e.g. trait values) and their related environmental conditions (e.g. disease, extreme temperature) organized in three trees. It has a deep and balanced structure, moreover the classes of the 'Trait' subtree are linked to the corresponding phenotypes by the "Trait_has_value" relationship. For instance, 'ear emergence time' trait class is linked to the 'late heading' phenotype class. This structure can help managing data at different levels of aggregation, and mining data for different objectives with high-level queries. The responses of the plant to biotic stresses are expressed in two ways: either by the disease name or by the causative agent names (their standard names and the other names, because names corresponding to different life stages can be found). A given disease name may have synonyms and a disease may be caused by more than an agent.

Analogously, the Wheat Trait Ontology (CO-WHEAT, https://bioportal.bioontology.org/ontologies/CO-WHEAT) defines traits of several information systems such as the International Wheat Information System (IWIS database from CIMMYT, https://orderseed.cimmyt.org/iwin-results.php) and the Wheat Information System (WheatIS, http://www.wheatis.org/) endorsed by the Wheat Initiative. The WheatIS released guidelines on the best practices, tools, recommendations, and examples to create, manage and share data related to wheat, including phenotypes (https://ist.blogs.inrae.fr/wdi/). About phenotype data formats, it refers to MIAPPE recommendations; for observation variables, which include trait and environment variables, WheatIS refers to the Crop Ontology, especially the Wheat Trait Ontology for phenotypes (http://agroportal.lirmm.fr/ontologies/CO 321), and the FAO-IPGRI Multi-CropPassport Ontology (http://agroportal.lirmm.fr/ontologies/CO 020) for germplasm.http://genome.jouy.inra.fr/bibliome/WheatPhenotypeOntology/WheatPhenotypeOntolo gy-v2.0

3.2.3.2 Pseudocereals

Pseudocereal are crop species grown to produce starchy grain suitable for human food, excluding the cereals, legumes, oilseeds and nuts (Fletcher 2016). The major pseudocereals are grain amaranth (*Amaranthus*), quinoa (*Chenopodium quinoa*, both belonging to the Amaranthaceae family), and buckwheat (*Fagopyrum*, belonging to the Polygonaceae family).

Descriptors have been developed by IPGRI / Bioversity International for:

 Quinoa: descriptors first developed in 1981, and updated in 2013, HYPERLINK "https://cgspace.cgiar.org/handle/10568/69165" including also descriptors for crop wild relatives (CWR): <u>https://cgspace.cgiar.org/handle/10568/69165</u>, Buckwheat, developed by IPGRI in 1994: <u>https://cgspace.cgiar.org/items/f708e2a7-f40d-</u>
 4e43-82df-547265e10696.

A list of descriptors for **amaranth** is provided by the **US National Plant Germplasm System**: <u>https://npgsweb.ars-grin.gov/gringlobal/cropdetail?type=descriptor&id=159</u>.</u>

Ontology for quinoa was prepared by the **Crop Ontology Initiative:** <u>https://cropontology.org/term/CO 367:0000048</u>.

3.2.3.3 Grain Legumes

Grain legumes are plants of the family Fabaceae whose dry seeds are consumed by humans for food (Michaels 2016). They include several crops, *e.g.* common bean, runner bean, lima bean, tepary bean, pea, chickpea, faba bean, lentil, pigeon pea, peanut, *Lathyrus* species, *Vigna* species, grass pea, horse gram, soybean and lupin. **ECPGR** in connection with CGIAR proposed descriptor lists for most of them.

Characterization and evaluations descriptors were developed by the International Board for Plant Genetic Resources (**IBPGR**), followed by the International Plant Genetic Resources Institute (**IPGRI**).

These include descriptors for several species of the genus *Phaseolus*, as following:

- **Common bean** (*Phaseolus vulgaris*; IBPGR, 1982): https://cgspace.cgiar.org/handle/10568/72698
- Runner bean (Phaseolus coccineus; IBPGR, 1983): https://cgspace.cgiar.org/handle/10568/72914
- Tepary bean (*Phaseolus acutifolius*; IBPGR, 1985): <u>https://cgspace.cgiar.org/handle/10568/73381</u>
- Lima bean (*Phaseolus lunatus*; IBPGR, 1982): https://cgspace.cgiar.org/handle/10568/91220

Moreover, IBPGR and IPGRI developed descriptors for several other grain legumes, including:

-	Chickpea	(Cicer	(arietinum;	IE	BPGR,	1993):
	https://cgs	pace.cgiar.org/han	dle/10568/72	<u>2855</u>			
-	Cowpea	(Vigna	u	nguiculata;	I	BPGR,	1993):
	https://cgs	pace.cgiar.org/han	dle/10568/72	<u>2871</u>			
-	Faba	bean	(Vicia	faba	;	IBPGR,	1985):
	https://cgs	pace.cgiar.org/han	dle/10568/72	<u>2876</u>			
-	Peanut (Arc	achis hypogaea; IB	PGR and ICRI	SAT, 1992):			
	https://cgs	pace.cgiar.org/han	dle/10568/72	<u>2881</u>			
-	Pigeon pea	(Cajanus cajan, IB	PGR and ICRI	SAT, 1981 upo	dated in 199	0):	
https:/	/oar.icrisat.o	org/8138/1/RP%20	<u>1147.pdf</u> ,	https://a	<u>lliancebiove</u>	rsityciat.org/pub	lications-
<u>data/d</u>	escriptors-pi	geonpea-cajanus-c	ajan-l-millsp				
-	Lathyrus		spp.		(IPGRI,		2000):
	https://cgs	pace.cgiar.org/han	dle/10568/72	<u>2702</u>			
-	Lentil	(Lens cu	linaris;	IBPGR	and	ICARDA,	1985):
	https://cgs	pace.cgiar.org/han	dle/10568/72	<u>2887</u>			

-	Lupin	(Lupinus	spp.	;	IBPGR,	1981):
	https://cgspace	.cgiar.org/handl	<u>e/10568/73417</u>			
-	Mung	Bean	(Vigna	radiata;	IBPGR,	1980):
	https://cgspace	.cgiar.org/handl	<u>e/10568/73435</u>			
-	Soybean	(Glycine	та	x;	IBPGR,	1984):

https://cgspace.cgiar.org/handle/10568/72944

A series of **key access and utilization descriptors** were subsequently developed for several legumes species by **Bioversity International** in collaboration with several other institutions, comparing and harmonizing existing descriptors lists. These key descriptors aim at establishing minimal descriptors sets i.e. priority sets of descriptors to describe, access and utilize genetic resources. Key access and utilization descriptors were developed for:

- Bean (Bioversity International and CIAT, 2009): https://cgspace.cgiar.org/handle/10568/73356. This list is based on the aforementioned IBPGR descriptors (1982), the descriptors list was subsequently compared and harmonized with a number of sources such as:
 - 'Descriptors for Phaseolus' (USDA, ARS, GRIN, <u>https://npgsweb.ars-grin.gov/gringlobal/cropdetail?type=descriptor&id=83</u>),
 - UPOV technical guidelines (2005, <u>https://www.upov.int/en/publications/tg-rom/tg012/tg 12 9.pdf</u>),
 - 'Handbook on evaluation of Phaseolus Germplasm' (PHASELIEU, 2001; <u>https://digital.csic.es/bitstream/10261/103897/1/Cuadra Handbook evaluation.pdf</u>),
 - 'Standard System for the Evaluation of Bean Germplasm' (CIAT, 1987, <u>https://cgspace.cgiar.org/handle/10568/69557</u>).
- Chickpea (Bioversity International, ICARDA, ICRISAT and IARI 2010): <u>https://cgspace.cgiar.org/handle/10568/73371</u>. This list is based on the aforementioned IBPGR descriptors (1993), the descriptors list was

subsequently **c**ompared and harmonized with a number of sources such as: o UPOV technical guidelines for Chickpea (2005, https://www.upov.int/en/publications/tg-

- 0 UPOV technical guidelines for Chickpea (2005, <u>https://www.upov.int/en/publications/tg-rom/tg143/tg_143_4.pdf</u>),
- o 'Descriptors for CHICKPEA' (USDA, ARS, GRIN, <u>https://npgsweb.ars-grin.gov/gringlobal/cropdetail?type=descriptor&id=54</u>),
- o 'Core Collection of Chickpea as a Means to Enhance Utilization of Genetic Resources in Crop Improvement' (ICRISAT, <u>https://oar.icrisat.org/4178/1/Web Art 2000 Core Collection of Chickpea.pdf</u>),
- o 'Global Strategy for the *Ex situ* Conservation of Chickpea (*Cicer* L.)' (Global Crop Diversity Trust, 2008.
- Cowpea (Bioversity International, ICARDA, ICRISAT and IARI 2010): <u>https://cgspace.cgiar.org/handle/10568/73346</u>. This list is based on the aforementioned IBPGR descriptors (1983), the descriptors list was subsequently compared and harmonized with a number of sources such as:
 - o 'Descriptors for VIGNA' (USDA, ARS, GRIN, <u>https://npgsweb.ars-grin.gov/gringlobal/cropdetail?type=descriptor&id=188</u>)
 - o 'Cowpea (*Vigna unguiculata* (L.) Walp.) core collection defined by geographical, agronomical and botanical descriptors' (Mahalakshmi *et al.* 2007)
 - o 'Descriptors for Characterization and Evaluation of Cowpea' (National Institute of Agrobiological Sciences, Genebank of Japan, see: <u>https://www.gene.affrc.go.jp/manuals-</u> plant characterization en.php).

- Faba bean (Bioversity International, NBPGR and IITA 2010): https://cgspace.cgiar.org/handle/10568/73351.
 This list is based on the aforementioned IBPGR descriptors (1985), the descriptors list was subsequently compared with a number of sources such as:
 - o 'Descriptors for Faba bean' (USDA-ARS, <u>https://npgsweb.ars-grin.gov/gringlobal/cropdetail?type=descriptor&id=103</u>),
 - o UPOV Technical guidelines (2003, https://www.upov.int/edocs/tgdocs/en/tg206.pdf),
 - o Minimal descriptors of Faba bean (IBPGR),
 - o 'Global Strategy for the *Ex Situ* Conservation of Faba Bean' (GCDT, 2009, <u>https://www.genebanks.org/resources/publications/faba-strategy-2009/</u>).
- Lathyrus spp. (Bioversity International and ICARDA 2009): https://cgspace.cgiar.org/handle/10568/73328
- Lentil (Bioversity International, ICARDA and NBPGR 2010): <u>https://cgspace.cgiar.org/handle/10568/73368</u>
 This list is based on the aforementioned IBPGR descriptors (1985), the descriptors list was subsequently compared with a number of sources such as:
 - o 'UPOV technical guidelines for Lentil' (2003,see here the 2015 version: <u>https://www.upov.int/edocs/tgdocs/en/tg210.pdf</u>),
 - o 'Descriptors for LENTIL' (USDA, ARS, GRIN, <u>https://npgsweb.ars-grin.gov/gringlobal/cropdetail?type=descriptor&id=107</u>),
 - o 'Methodology to establish a composite collection: case study in lentil' (Furman et al. 2007),
 - o 'Global Strategy for the Ex Situ Conservation of Lentil' (GCDT, 2008, <u>https://www.genebanks.org/resources/publications/lens-strategy-2008/</u>).
- Pigeon pea (Bioversity International, ICRISAT and ICAR 2010): <u>https://cgspace.cgiar.org/bitstream/handle/10568/73367/brief.pdf?sequence=3&isAllowed=</u> <u>γ</u>
 This list is based on the

aforementioned IBPGR descriptors (1990), the descriptors list was subsequently compared with a number of sources such as:

- o 'Descriptors for PIGEON-PEA' (USDA, ARS, GRIN, <u>https://npgsweb.ars-grin.gov/gringlobal/cropdetail?type=descriptor&id=134</u>),
- O 'Development of a Strategy for the Global Conservation of Pigeonpea Genetic Resources' (GCDT, 2006).

Moreover, ontologies were prepared for several grain legumes by the **Crop Ontology Initiative**, including:

- Common bean: https://cropontology.org/term/CO_335:ROOT
- **Soybean**: <u>https://cropontology.org/term/CO_336:ROOT</u>, Soybean onthology can also be found as part of **SoyBase**: <u>https://soybase.org/ontology.php</u>.
- Mung bean: <u>https://cropontology.org/term/CO_346:ROOT</u>.
- Lentil: <u>https://cropontology.org/term/CO_339:ROOT</u>
- **Peanut**: <u>https://cropontology.org/term/CO_337:ROOT</u>
- Chickpea: https://cropontology.org/term/CO 338:ROOT
- Cowpea: <u>https://cropontology.org/term/CO_340:ROOT</u>
- **Pigeon pea**: <u>https://cropontology.org/term/CO_341:ROOT</u>
- **Bambara groundnut**: (*Vigna subterranea*): <u>https://cropontology.org/term/CO_366:ROOT</u>.

3.2.4 Leafy Vegetables

Leafy vegetables are a wide group of plant species that includes: "vegetables cultivated for the edible part constituted of foliar and flower structures, comprising lamina, petiole, midrib and veins" (Alvino and Barbieri 2016). This crop group includes several species belonging to different plant families (*e.g.* Apiaceae, Asparagaceae, Asteraceae, Boraginaceae, Brassicaceae, Chenopodiaceae, Lamiaceae, Polygonaceae, Portulaceae, Valerianiaceae). Lettuce, spinach and chicory are generally considered the main leafy vegetables because of the worldwide human consumption and economical importance (van Treuren et al. 2012), while the minor leafy vegetables include, amongst others, rocket salad, lamb's lettuce, asparagus, artichoke and rhubarb (Lebeda and Boukema, 2001).

The International Board for Plant Genetic Resources (**IBPGR**), followed by the International Plant Genetic Resources Institute (**IPGRI**), developed descriptors for leafy vegetables of the family Brassicaceae, including:

- Descriptors for *Brassica* and *Raphanus* (IBPGR, 1990). This document includes descriptors for several **leafy brassicas**: <u>https://cropgenebank.sgrp.cgiar.org/images/file/learning space/descriptors brassica rapha</u> <u>nus.pdf</u>
- Descriptors for rocket (Eruca spp; IPGRI 1999): <u>https://cgspace.cgiar.org/handle/10568/72775</u>

The **ECPGR Leafy Vegetables Working Group** has developed several descriptors for different leafy vegetables, including:

- Minimum descriptors for cultivated lettuce (Lactuca sativa), wild lettuce species (L. serriola, L. saligna, L. virosa), spinach (Spinacia spp.), leaf and root chicory (Cichorium intybus), witloof (Cichorium intybus var. foliosum) and endive (Cichorium endivia). These descriptors were published in 2009 and can be found here:
 https://www.ecpgr.cgiar.org/fileadmin/templates/ecpgr.org/upload/NW and WG UPLOAD S/LeafyVeg misc/LeafyVeg MinDescr.pdf
- Minimum descriptors for asparagus (Asparagus spp.; 2014): <u>https://www.ecpgr.cgiar.org/fileadmin/templates/ecpgr.org/upload/WG_UPLOADS_PHASE_I_X/LEAFY_VEGETABLES/Minimum_descriptors_for_asparagus_.pdf</u>
- Minimum descriptors for rocket (*Eruca* spp.) developed with the EU GENRES project: <u>https://www.ecpgr.cgiar.org/fileadmin/templates/ecpgr.org/upload/NW and WG UPLOAD</u> <u>S/LeafyVeg misc/Eruca descriptor list.pdf</u>
- Minimum descriptors for **corn salad** (*Valerianella* spp.) developed with the EU GENRES project:

https://www.ecpgr.cgiar.org/fileadmin/templates/ecpgr.org/upload/NW and WG UPLOAD S/LeafyVeg misc/Valerianella descriptor list.pdf.

It is important to highlight that internationally agreed descriptors for many leafy vegetables are, to the best of our knowledge, still not available (e.g. celery (*Apium graveolens*) and fennel (*Foeniculum vulgare*)).

A recent initiative (**LettuceGDP**, Guo *et al.* 2023) was launched to provide an omics data hub for lettuce. Moreover, as part of the aforementioned ECPGR European Evaluation Network (**EVA**) for Plant Genetic Resources for Food and Agriculture (PGRFA, <u>https://www.ecpgr.cgiar.org/eva</u>), a Lettuce Evaluation Network was established, this included the development of a standard ontology to collect metadata and evaluation data.

4. Gap and redundancy analysis

Within the PRO-GRACE WP4, devoted to evaluation and valorisation of Plant Genetic Resources (PGRs), the deliverable D4.1 gathers a set of available documents, websites and initiatives aiming at listing catalogues of descriptors of PGR phenotypic and agronomic characteristics. This deliverable helps us to **highlight several gaps in** proposing unified, crop-specific standards and protocols for the evaluation of the phenotypes and agronomic characteristics of PGRs.

We focused our first analysis for D4.1 on Plant Genetic Resources for Food and Agriculture (PGRFA) dedicated to agronomy. We first organised the gathered information into four groups of crop species: Fruit trees, Fruit vegetables, Leafy vegetables, Grains (cereals and legumes). In future, **other groups of crop species should be considered as well**, such as tuber and root crops, woody plants, fibre plants, forage crops, medicinal plants, and so on. It is also important to highlight that internationally agreed descriptors for many species are, to the best of our knowledge, still not available.

We aimed at listing descriptors used for PGRs. A standard descriptor is a combination of a specific trait name, a method used for assessing the trait value, and the scale of the measurement, as well as the protocol used. Trait names, methods, scales and protocols need to be harmonized between catalogues of descriptors. D4.1 emphasizes the heterogeneity of phenotypic descriptors between the 4 groups of crop species and even between the crop species belonging to the same group of crop species, as well as the redundancy of descriptor catalogues for some crop species. PRO-GRACE project partners and ECPGR, MIAPPE, Crop Ontology, EMPHASIS organisations use different phenotypic traits, methods and scales and denominations for each one. However, most of the descriptor catalogues are not necessarily interoperable. They can lack common vocabulary and scales, even for the same species. In addition, the catalogues are not machine-actionable and difficult to access, due to availability in pdf format for example. These drawbacks hinder the comparison between phenotypic data. Furthermore, the fact that these catalogues are not machine-actionable limits the possibility of easily constructing a unified catalogue of standardized descriptors for each specific crop.

We observed that some descriptor catalogues date back to the last century or the beginning of the current one, such as the IPGRI and UPOV descriptors for Apple. More generally, most descriptor catalogues are **not easily upgradeable**, as they are fixed at a specific date. However, in today's era of rapid development of new technology tools used in phenomics, such as image analysis, NIRS (near infrared spectroscopy), etc., it is **crucial to be able to add novel descriptors derived from new technologies**.

Several descriptor catalogues **do not include the collection of metadata** of where and in which conditions the phenotypic trial was carried out. According to the increasing interest in environmental effects on phenotypes (that we summarize as the Genotype by Environment (GxE) effect), it is crucial to systematically collect the environment information for each phenotyping trial (e.g. controlled vs. natural conditions, crop location, climatic curves during the plant development, agronomic itinerary, soil type, biotic and abiotic stresses, etc.). The MIAPPE protocols aim at generalizing this information for each phenotypic trial.

So far, guidelines for harmonizing phenotyping trait names, methods, and scales as well as the minimum metadata information describing each specific phenotypic trial, are lacking from all

catalogues of descriptors for PGRs. These guidelines would help genebanks and international organizations, such as ECPGR, EMPHASIS, Crop Ontology, and others, to develop novel catalogues of descriptors for orphan crops and to improve existing ones. It could facilitate comparative analysis between crop species. Comparisons will also need to consider the environmental parameters, that would help researchers to evaluate the GxE effects on phenotype expression. For example, old descriptor lists, such as apple, pear and *Prunus*, lack information on management, site and weather conditions that are crucial for analysing GxE interactions.

In addition, an official list of reference scientists responsible for up-to-date unified crop-specific guidelines for phenotyping PGRs (preferably in pairs to anticipate sudden or expected absence) is lacking. These scientists would have recognised skills either in each crop, in each category of traits, or in each category of phenotypic methods (visual, image analysis, plant product processing...) including the recommended scales, as well as in experimental design. That would guarantee confidence in the evaluation of the phenotypic performance of PGRs. This list of reference scientists would help scientists and genebank curators in charge of describing genetic resources, to design new descriptor catalogues or adapt old ones, to include new traits to be considered or new phenotyping methods. These reference scientists would act as guardians of the up-to-date unified crop-specific guidelines for phenotyping PGRs, following general rules established by the GRACE-RI in collaboration with other relevant European Research Infrastructures, such as EMPHASIS and ELIXIR.

Finally, we suggest that the unified guidelines per crop species should also **address the issues of data management, including their FAIR character** (guaranteeing that they will be findable, accessible, interoperable and reusable). This has not been considered until now.

To conclude, to propose unified, crop-specific standards and protocols for the evaluation of the phenotypes and agronomic characteristics of PGRs, further catalogues of descriptors need to include first the recommended checklist of metadata required to adequately describe the plant phenotyping experiment as recommended by the MIAPPE (Minimum Information About Plant Phenotyping Experiments) requirement. Second, descriptors need to be harmonized according to trait ontology and crop ontology, requiring a panel of reference scientists responsible for up-to-date unified crop-specific guidelines for phenotyping PGRs. Third, scientists and curators involved in phenotypic assessment must ensure the correct storage of phenotypic data to ensure that the data are FAIR and follow a certified data management plan. These preliminary requirements will help to build the standards and protocols adopted by the future GRACE-RI.

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Deviations

D4.1 aiming at producing a unified, crop-specific standards and protocols for the evaluation of the phenotypes and agronomic characteristics of PGR, incorporating the ECPGR, MIAPPE, Crop Ontology, EMPHASIS and final user recommendations and methodologies is a preliminary version. This first version is thus incomplete and does not include all crops. D4.3 dealing with the same goal will be an improved version.

Annex 1

FRUIT VEGETABLES

			date of	
Crop common name	scientific name	urls	publication	main descriptor classes
Capsicum peppers	Capsicum spp.	https://cgspace.cgiar.org/handle/10568/72851	1995	(plant, inflorescence and fruit, seed), Evaluation (plant, abiotic
Cucurbitaceae	Cucumis spp., Cucurbita spp. and Citrullus spp.	https://cgspace.cgiar.org/handle/10568/104810_	1983	Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed), stress susceptibility, disease and pest susceptibility
Cucurbitaceae	Cucumis spp., Cucurbita spp. and Citrullus spp.	https://www.ecpgr.cgiar.org/fileadmin/templates/ecpg r.org/upload/NW_and_WG_UPLOADS/Cucurbits_Descr iptorLists.pdf_	2008	Minimum characterization descriptors
Eggplant	Solanum melongena	https://cgspace.cgiar.org/handle/10568/72874		Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed), stress susceptibility, disease and pest susceptibility
Melon	Cucumis melo	https://cgspace.cgiar.org/handle/10568/72690	2003	Passport, Management, Environment and Site, Characterization (plant, inflorescence and fruit, seed), Evaluation (plant, abiotic stress susceptibility, biotic stress susceptibility)
Pepino	Solanum muricatum	https://cgspace.cgiar.org/handle/10568/72608_	2004	Passport, Management, Environment and Site, Characterization (plant, inflorescence and fruit, seed), Evaluation (plant, abiotic stress susceptibility, biotic stress susceptibility)
Solanaceae (major fruit crops)	Solanum melongena, Capsicum spp., Solanum lycopersicum	https://www.ecpgr.cgiar.org/fileadmin/templates/ecpg r.org/upload/NW and WG UPLOADS/Solanaceae Mis cc/Solanaceae descriptors.pdf	2008	Minimum characterization descriptors
Solanaceae (minor fruit crops)	Solanum muricatum, Physalis peruviana, Solanum betaceum	https://www.ecpgr.cgiar.org/fileadmin/templates/ecpg r.org/upload/NW and WG UPLOADS/Solanaceae Mis cc/Descriptors minor crops NEW for Web 2202201 3.pdf	2013	Minimum characterization descriptors
Tomato	Solanum lycopersicum	https://cgspace.cgiar.org/handle/10568/73041_	1996	Passport, Management, Environment and Site, Characterization (plant, inflorescence and fruit, seed), Evaluation (plant, abiotic stress susceptibility, biotic stress susceptibility)
Strawberry	Fragaria x ananassa	https://cgspace.cgiar.org/handle/10568/72947	1986	Passport, Vegetative, Fenological, Yield, Quality, Susceptibility to stress, pest and disease Crop Onotology

FRUIT TREES						
date of						
Crop common name	scientific name	urls	pubblication	main descriptor classes		
l		https://cgspace.cgiar.org/handle/10568/104209	1981	4		
Almond	Prunus dulcis	https://cgspace.cgiar.org/handle/10568/72793	revision 1985	Passport, Vegetative, Fenological, Yield, Quality, Susceptibility to stress, pest and disease		
Anona				Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,		
	Annona cherimola	https://cgspace.cgiar.org/handle/10568/104849	2008	Susceptibility to stress, pest and disease		
Apple	Malus x domestica	https://cgspace.cgiar.org/handle/10568/72794; https://cropontology.org/term/CO_370:ROOT	1982	Passport, Vegetative, Fenological, Yield, Quality, Susceptibility to stress, pest and disease		
Apricot	Prunus armeniaca	https://cgspace.cgiar.org/handle/10568/73447	1991	Passport, Vegetative, Fenological, Yield, Quality, Susceptibility to stress, pest and disease		
Averade				Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,		
Avocado	Persea spp.	https://cgspace.cgiar.org/handle/10568/72796	1995	Susceptibility to stress, pest and disease		
			1996	Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,		
Banana	Musa spp.	https://cgspace.cgiar.org/handle/10568/72799	1550	Susceptibility to stress, pest and disease		
		https://cropontology.org/term/CO_325:ROOT	-	Crop ontology		
Cherry	Prunus avium, P. cerasus	https://cgspace.cgiar.org/handle/10568/72853	1985	Passport, Vegetative, Fenological, Yield, Quality, Susceptibility to stress, pest and disease		
Coffee				Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,		
	C. canephora & C. arabica	https://cgspace.cgiar.org/handle/10568/72788	1996	Susceptibility to stress, pest and disease		
Citrus	Citaria		1000	Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,		
	Citrus spp	https://cgspace.cgiar.org/handle/10568/72733	1999	Susceptibility to stress, pest and disease Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,		
Durian	Durio zibethinus	https://cgspace.cgiar.org/handle/10568/72585	2007	Susceptibility to stress, pest and disease		
			2007	Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,		
Fig	Ficus carica	https://cgspace.cgiar.org/handle/10568/72691	2003	Susceptibility to stress, pest and disease		
				Transposition in the Crop Ontology format of the OIV descriptors: Morphological,		
Grapevine	Vitis spp.	https://cropontology.org/term/CO_356:ROOT	2017	physiological, Abiotic stress, biotic stress, quality, Agronomic		
				morphological, physiological, Abiotic stress, biotic stress, quality, Agronomic		
Hazalaut	Corylus avellana			Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,		
Hazelnut		https://cgspace.cgiar.org/handle/10568/72598	2008	Susceptibility to stress, pest and disease		
Jackfruit				Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,		
Jackiruit	Artocarpus heterophyllus	https://cgspace.cgiar.org/handle/10568/72703	2000	Susceptibility to stress, pest and disease		
Litchi				Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,		
	Litchi chinensis	https://cgspace.cgiar.org/handle/10568/72694	2002	Susceptibility to stress, pest and disease		
Mangaba				Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,		
	Hancornia speciosa	https://cgspace.cgiar.org/handle/10568/90693	2018	Susceptibility to stress, pest and disease		
Mango				Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,		
	Mangifera indica	https://cgspace.cgiar.org/handle/10568/72607	2008	Susceptibility to stress, pest and disease		
Рарауа	Carica papava	https://cgspace.cgiar.org/handle/10568/72903	1000	Passport, Site (soil, wheather), Vegetative, Fenological, Yield, Quality, Susceptibility to stress, pest and disease		
	Carica papaya	https://cgspace.cgiar.org/nanule/10568/72903	1988	lhest and disease		

Peach	Prunus persica	https://cgspace.cgiar.org/handle/10568/72905	1984	Passport, Vegetative, Fenological, Yield, Quality, Susceptibility to stress, pest and disease
Pear	Pyrus communis	https://cgspace.cgiar.org/handle/10568/72906	1983	Passport, Vegetative, Fenological, Yield, Quality, Susceptibility to stress, pest and disease
	· ·	https://cgspace.cgiar.org/handle/10568/72917	1903	
Pistachio and relatives	Pistacia vera and Pistacia spp			Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,
		https://cgspace.cgiar.org/handle/10568/72916	1998	Susceptibility to stress, pest and disease
Blum	Prunus domestica, P. salicina,	https://cgspace.cgiar.org/handle/10568/72940	109/	Passport, Vegetative, Fenological, Yield, Quality, Susceptibility to stress, pest and disease
Plum	Prunus spp	Inteps://egspace.egial.org/nanule/10508/72940	1964	Passport, vegetative, renological, field, Quality, susceptibility to stress, pest and disease
Rambutan				Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,
Kallibulali	Nephelium lappaceum	https://cgspace.cgiar.org/handle/10568/72693	2003	Susceptibility to stress, pest and disease
Walnut				Passport, Management, Site (soil, wheather), Vegetative, Fenological, Yield, Quality,
	Juglans regia	https://cgspace.cgiar.org/handle/10568/73159	1994	Susceptibility to stress, pest and disease
Tropical fruit (various)				Passport, Site (soil, wheather), Vegetative, Fenological, Yield, Quality, Susceptibility to stress,
Tropical fruit (various)		https://cgspace.cgiar.org/handle/10568/73058	1980	pest and disease.

LEAFY VEGETABLES

			date of	
Crop common name	scientific name	urls	publication	main descriptor classes
				Passport, Site, Characterization and preliminary evaluation (plant,
		https://cropgenebank.sgrp.cgiar.org/images/file/learning_space/descr		inflorescence and fruit, seed), stress susceptibility, disease and pest
Leafy brassicas	Brassica spp.	iptors brassica raphanus.pdf	1990	susceptibility
				Passport, Site, Characterization and preliminary evaluation (plant,
				inflorescence and fruit, seed), stress susceptibility, disease and pest
Rocket	Eruca spp.	https://cgspace.cgiar.org/handle/10568/72775	1999	susceptibility
	Lactuca sativa, L. serriola, L.			
Cultivates lettuce,	saligna, L. virosa, Spinacia spp.,			Minimum characterization descriptors
wild lettuce, spinach,	Cichorium intybus, Cichorium	https://www.ecpgr.cgiar.org/fileadmin/templates/ecpgr.org/upload/N		
chicory, endive	endivia	W_and_WG_UPLOADS/LeafyVeg_misc/LeafyVeg_MinDescr.pdf	2009	
		https://www.ecpgr.cgiar.org/fileadmin/templates/ecpgr.org/upload/		
		WG_UPLOADS_PHASE_IX/LEAFY_VEGETABLES/Minimum_descriptors		Minimum characterization descriptors
Asparagus	Asparagus spp.	_for_asparaguspdf	2014	
		https://www.ecpgr.cgiar.org/fileadmin/templates/ecpgr.org/upload/N		Minimum characterization descriptors
Rocket	Eruca spp.	W_and_WG_UPLOADS/LeafyVeg_misc/Eruca_descriptor_list.pdf	NA	
		https://www.ecpgr.cgiar.org/fileadmin/templates/ecpgr.org/upload/N		
		W_and_WG_UPLOADS/LeafyVeg_misc/Valerianella_descriptor_list.pd		Minimum characterization descriptors
Corn salad	Valerianella spp.	<u>f</u>	NA	

			GRAINS		
Grain type	Crop common name	scientific name	urls (most recent guideline)	date of publication	main descriptor classes
Graintype		Triticum sp. (durum,			
		aestivum, dicoccum,			phenological, physiological, morphological, agronomic, quality, abiotic stress, biotic
Cereal	Wheat	spelta)	Crop Ontology Curation tool	2018	stress
		, ,			phenological, physiological, morphological, agronomic, quality, abiotic stress, biotic
Cereal	Barley	Hordeum vulgare	Crop Ontology Curation tool	2020	stress
		-			phenological, physiological, morphological, agronomic, quality, abiotic stress, biotic
Cereal	Rice	Oriza sativa	Crop Ontology Curation tool	2016	stress, biochemical, fertility
					phenological, physiological, morphological, agronomic, quality, abiotic stress, biotic
Cereal	Maize	Zea mays	Crop Ontology Curation tool	2016 (2023 updated)	stress, postharvest
			Key access and utilization descriptors for finger millet		
Cereal	Finger Millet	Eleusine coracana	genetic resources (cgiar.org)	2010	phenological, morphological, agronomic, biotic stress
					phenological, physiological, morphological, agronomic, quality, abiotic stress
Cereal	Oat	Avena sativa	Crop Ontology Curation tool	2019	tolerance, biotic stress resistance, biochemical
Cereal	Sorghum	Sorghum bicolor	Crop Ontology Curation tool	2019	phenological, morphological, agronomic, biotic stress, quality
Cereal	Rye	Secale cereale	Descriptors for rye and triticale (cgiar.org)	1985	phenological, morphological, agronomic, quality, abiotic stress, biotic stress
Cereal	Pearl millet	Pennisetum glaucum	Crop Ontology Curation tool	2016	phenological, morphological, agronomic, biotic stress, fertility
Legume	Common bean	Phaseolus vulgaris	https://cgspace.cgiar.org/handle/10568/72698	1982	Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
Leguine		i nuscolus valgans	<u>https://cgspace.egiai.org/nanaic/10500/72050</u>	1502	
Logumo	Runner bean	Phaseolus coccineus	https://cgspace.cgiar.org/handle/10568/72914	1983	Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
Legume		Phuseolus coccineus		1965	
Legume	Tepary bean	Phaseolus acutifolius	https://cgspace.cgiar.org/handle/10568/73381	1985	Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
		, , ,			
Legume	Lima bean	Phaseolus lunatus	https://cgspace.cgiar.org/handle/10568/91220	1982	Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
					Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and
Legume	Chickpea	Cicer arietinum	https://cgspace.cgiar.org/handle/10568/72855	1993	fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
_					Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
Legume	Cowpea	Vigna unguiculata	https://cgspace.cgiar.org/handle/10568/72871	1993	
Legume	Faba bean	Vicia faba	https://cgspace.cgiar.org/handle/10568/72876	1985	Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
Legume	Peanut	Arachis hypogaea	https://cgspace.cgiar.org/handle/10568/72881	1992	Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
Leguine	i cunut	, acting hypogueu	10000/12001	1992	1

Pigeon pea	Cajanus cajan	https://oar.icrisat.org/8138/1/RP%201147.pdf		Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
Pigeon pea	Caianus caian	https://alliancebioversityciat.org/publications- data/descriptors-pigeonpea-cajanus-cajan-I-millsp		Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
i Been bea	cajanas cajan		1000	
Lathyrus spp.	Lathyrus	https://cgspace.cgiar.org/handle/10568/72702	2000	Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
Lentil	Lens culinaris	https://cgspace.cgiar.org/handle/10568/72887	1985	Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
Lupin	Lupinus	https://cgspace.cgiar.org/handle/10568/73417	1981	Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
Mung Bean	Vigna radiata	https://cgspace.cgiar.org/handle/10568/73435	1980	Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
Sovhean	Glycine may	https://cgspace.cgiar.org/bandle/10568/72944		Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
,	,			Minimum characterization descriptors
	5			
				Minimum characterization descriptors
				Minimum characterization descriptors
Faba bean	Vicia faba		2010	Minimum characterization descriptors
Lathyrus spp.	Lathyrus	https://cgspace.cgiar.org/handle/10568/73328	2009	Minimum characterization descriptors
Pigeon pea	Cajanus cajan	https://cgspace.cgiar.org/bitstream/handle/10568/7 3367/brief.pdf?sequence=3&isAllowed=y	2010	Minimum characterization descriptors
Quinoa	Chenopodium quinoa	https://cgspace.cgiar.org/handle/10568/69165	2013	Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
				Passport, Site, Characterization and preliminary evaluation (plant, inflorescence and fruit, seed, grain quality), stress susceptibility, disease and pest susceptibility
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Amaranth	Amaranthus	grin.gov/gringlobal/cropdetail?type=descriptor&id=1	na	Characterization
	Pigeon pea Lathyrus spp. Lentil Lupin Mung Bean Mung Bean Common bean Chickpea Cowpea Faba bean Lathyrus spp. Pigeon pea Quinoa Buckwheat	Pigeon pea Cajanus cajan Lathyrus spp. Lathyrus Lentil Lens culinaris Lupin Lupinus Mung Bean Vigna radiata Soybean Glycine max Common bean Phaseolus vulgaris Chickpea Cicer arietinum Cowpea Vigna unguiculata Faba bean Vicia faba Lathyrus spp. Lathyrus Pigeon pea Cajanus cajan Quinoa Chenopodium quinoa Buckwheat Fagopyrum	Pigeon pea Cajanus cajan https://alliancebioversityciat.org/publications: data/descriptors-pigeonpea-cajanus-cajan-I-millsp Lathyrus spp. Lathyrus https://cgspace.cgiar.org/handle/10568/72702 Lentil Lens culinaris https://cgspace.cgiar.org/handle/10568/72887 Lupin Lupinus https://cgspace.cgiar.org/handle/10568/73417 Mung Bean Vigna radiata https://cgspace.cgiar.org/handle/10568/73435 Soybean Glycine max https://cgspace.cgiar.org/handle/10568/73435 Chickpea Cicer arietinum https://cgspace.cgiar.org/handle/10568/73356 Chickpea Vigna unguiculata https://cgspace.cgiar.org/handle/10568/73351 Lathyrus spp. Lathyrus https://cgspace.cgiar.org/handle/10568/73351 Lathyrus spp. Lathyrus https://cgspace.cgiar.org/handle/10568/73351 Common bean Phaseolus vulgaris https://cgspace.cgiar.org/handle/10568/73351 Chickpea Cicer arietinum https://cgspace.cgiar.org/handle/10568/73351 Lathyrus spp. Lathyrus https://cgspace.cgiar.org/handle/10568/73351 Lathyrus spp. Lathyrus https://cgspace.cgiar.org/handle/10568/73428 Pigeon pea Cajanus cajan 3367/brief.pdf?sequence=3&isAllowed=y	Pigeon pea Cajanus cajan https://car.icrisat.org/8138/1/RP%201147.pdf 1981 Pigeon pea Cajanus cajan https://car.icrisat.org/publications- data/descriptors-pigeonpea-cajanus-cajani-millsp 1990 Lathyrus spp. Lathyrus https://cgspace.cgiar.org/handle/10568/72702 2000 Lentil Lens culinaris https://cgspace.cgiar.org/handle/10568/72887 1985 Lupin Lupinus https://cgspace.cgiar.org/handle/10568/73417 1981 Mung Bean Vigna radiata https://cgspace.cgiar.org/handle/10568/73417 1984 Soybean Glycine max https://cgspace.cgiar.org/handle/10568/73355 2009 Chickpea Cicer arietinum https://cgspace.cgiar.org/handle/10568/73356 2009 Chickpea Cicer arietinum https://cgspace.cgiar.org/handle/10568/73356 2010 Faba bean Wicia faba https://cgspace.cgiar.org/handle/10568/73351 2010 Pigeon pea Cajanus cajan https://cgspace.cgiar.org/handle/10568/73351 2010 Cowpea Vigna unguiculata https://cgspace.cgiar.org/handle/10568/73351 2010 Lathyrus spp. Lathyrus https://cgspace.cgiar.org/handle/10568/73346 2010 <td< td=""></td<>