PRO-GRACE

PROMOTING A PLANT GENETIC RESOURCE COMMUNITY FOR EUROPE

DELIVERABLE 2.6

A system for the unique identification of PGR based both on DOIs and DNA barcoding

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Promoting a plant genetic resource community for Europe

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2. Executive Summary

Deliverable D2.6 presents the design and proposed implementation of an integrated system for the **unique identification of Plant Genetic Resources (PGR)** developed within the framework of the European project PRO-GRACE. Recognizing the need for robust identification from the outset, the system combines **Digital Object Identifiers (DOIs)** and **DNA-based identification methods**, including traditional DNA barcoding and broader genomic approaches, such as reduced representation sequencing, and whole-genome resequencing. These combined approaches support traceability, validation, and interoperability of PGR data, enabling identification at both taxonomic and accession/population levels.

The report addresses long-standing challenges in the documentation and exchange of PGR across ***in situ*** and ***ex situ*** conservation systems. Traditional identification methods, relying on inconsistent naming, local accession codes, and morphological traits, often lead to confusion, duplication, and loss of valuable data. While DOIs provide a stable digital reference for linking and citing PGR globally, they do not verify accession/population and taxonomy identification. Conversely, DNA-based identification often lacks integration into broader information systems. This deliverable proposes a combined solution to ensure each accession is both **digitally traceable** and **genetically identified**, in line with international recommendations from the **ITPGRFA** and the FAIR data principles.

The key components of the proposed system include:

- Assignment of **DOIs** through the **EURISCO** and **GLIS** platform, supported by structured metadata aligned with **MCPD** and genetic identification other genetic identification applicable PGR data standards.
- Generation of **DNA barcodes** or genotypic data, submitted to internationally recognized sequence repositories: **BOLD**, **GenBank**, and **EMBL-EBI (ENA)**.
- Integration of both identifier types within the **PGR-RI platform**, which functions as a central portal for unified accession records.

A seven-step workflow is proposed, encompassing accession or population acquisition, DOI registration, DNA sequencing/barcoding, data deposition, integration, external system linking, and feedback from users. Use cases illustrate the system's adaptability for **Crop wild relatives**, **farmer-managed landraces**, and **existing genebank holdings**, highlighting its potential to address identification inconsistencies and uncover hidden duplicates.

The deliverable and associated proposed data management process further outlines:

- Interoperability with major PGR and biodiversity data infrastructures (EURISCO, Genesys, GBIF, GGBN).
- Technical requirements for API-based data exchange and synchronization with GLIS, EMBL-EBI, BOLD, and GenBank.
- Policy alignment with ITPGRFA, CBD, and Nagoya Protocol obligations.
- Best practices for metadata curation, quality control, and data governance.
- Infrastructure needs, including central sequencing services, improvements of linkage of DOIs and DNA barcodes, and training for those actively managing PGR holdings.

Key benefits of the system include:

- Improved data quantity, quality and traceability, enabling better tracking of PGR.

- Seamless **interoperability** across national, regional and global platforms, as well as *ex situ* and *in situ* ed resource integration.
- Increased **efficiency and reliability** in PGR documentation and exchange.
- Greater **compliance with international agreements** and enhanced support for research and breeding efforts.
- Enhanced **linkage** between **agrobiodiversity** and broader **biodiversity conservation** efforts.

This deliverable presents a practical, scalable, and policy-aligned system for the unique identification of plant genetic resources across conservation settings. By linking digital and genetic identifiers, it facilitates improved data management, usage tracking, and scientific transparency. The success of this initiative depends on the realization of GRACE-RI or a comparable coordination structure, but interim progress can be achieved through existing collaborations and national initiatives. The system is designed to evolve alongside advances in genomics and policy, ensuring long-term relevance and sustainability.
In conclusion, this deliverable provides a pragmatic and robust roadmap for the integrated digital and genetic identification of PGR, offering significant benefits in terms of data integrity, global interoperability, and long-term utility. The approach positions the EU as a global leader in digitally integrated, genomically validated PGR conservation and use.

3. List of Abbreviations

Abbreviation	Full Form
ABS	Access and Benefit-Sharing
API	Application Programming Interface
BOLD	Barcode of Life Data System
CBD	Convention on Biological Diversity
CWR	Crop Wild Relative
DOI	Digital Object Identifier
DSI	Digital Sequence Information
ECPGR	European Cooperative Programme for Plant Genetic Resources
ESFRI	European Strategy Forum on Research Infrastructures
EURISCO	European Search Catalogue for Plant Genetic Resources
FAIR	Findable, Accessible, Interoperable, Reusable
FAO	Food and Agriculture Organization (of the United Nations)
GBIF	Global Biodiversity Information Facility
GBS	Genotype-By-Sequencing
GGBN	Global Genome Biodiversity Network
GLIS	Global Information System (under the ITPGRFA)
GRACE-RI	Genomic Resources and Characterization Infrastructure for Europe – Research Infrastructure
GRC	Genetic Resource Centre
ID	Identifier
IP	Intellectual Property
ITPGRFA	International Treaty on Plant Genetic Resources for Food and Agriculture
LR	Crop landrace
MCPD	Multi-Crop Passport Descriptors
NCBI	National Center for Biotechnology Information
NGS	Next-Generation Sequencing

PGR	Plant Genetic Resources
PGRFA	Plant Genetic Resources for Food and Agriculture
PMC	PubMed Central
PUID	Persistent Unique Identifier
SMTA	Standard Material Transfer Agreement
URI	Uniform Resource Identifier
WIEWS	World Information and Early Warning System on Plant Genetic Resources

4. Introduction

4.1 Background and Rationale

Plant genetic resources are fundamental to food security and crop improvement. Europe alone conserves approximately two **million accessions** across numerous genebanks, genetic reserves and on-farm conservation sites (FAO, 2025). In recognition of the evolving role of these facilities, the more inclusive term *Genetic Resource Center* (GRC) has been proposed to better reflect their integration of both *ex situ* and *in situ* conservation activities, beyond the traditional focus on stored, collected samples (Maxted *et al*., 2025a). Efficient utilization of this agrobiodiversity hinges on precise documentation, including identification, characterization and evaluation. Traditional PGR accession and population identification methods were based on passport data, genebank or population IDs, and botanical (taxonomic) determination have limitations due to naming inconsistencies or disagreements, duplicated accession numbers across holdings, and human errors in morphological identification. To address these, the International Treaty (ITPGRFA) launched the **Global Information System (GLIS)** in 2017 to unify PGR information and recommended **Persistent Unique Identifiers (PUIDs)**, specifically DOIs, for accessions and *in situ* populations. In parallel, advances in genomics have introduced **DNA barcoding** as a powerful tool for taxonomic identification. Traditionally defined as short, standardized sequences (~400-800 bp) used for taxon-level identification, DNA barcoding has evolved. Modern approaches now include both targeted and non-targeted methods, like genotyping-by-sequencing (GBS), Diversity Arrays, skim sequencing, DNA microarrays, Single Primer Enrichment Technology (Fig 1) allowing identification at both the taxon and individual levels.

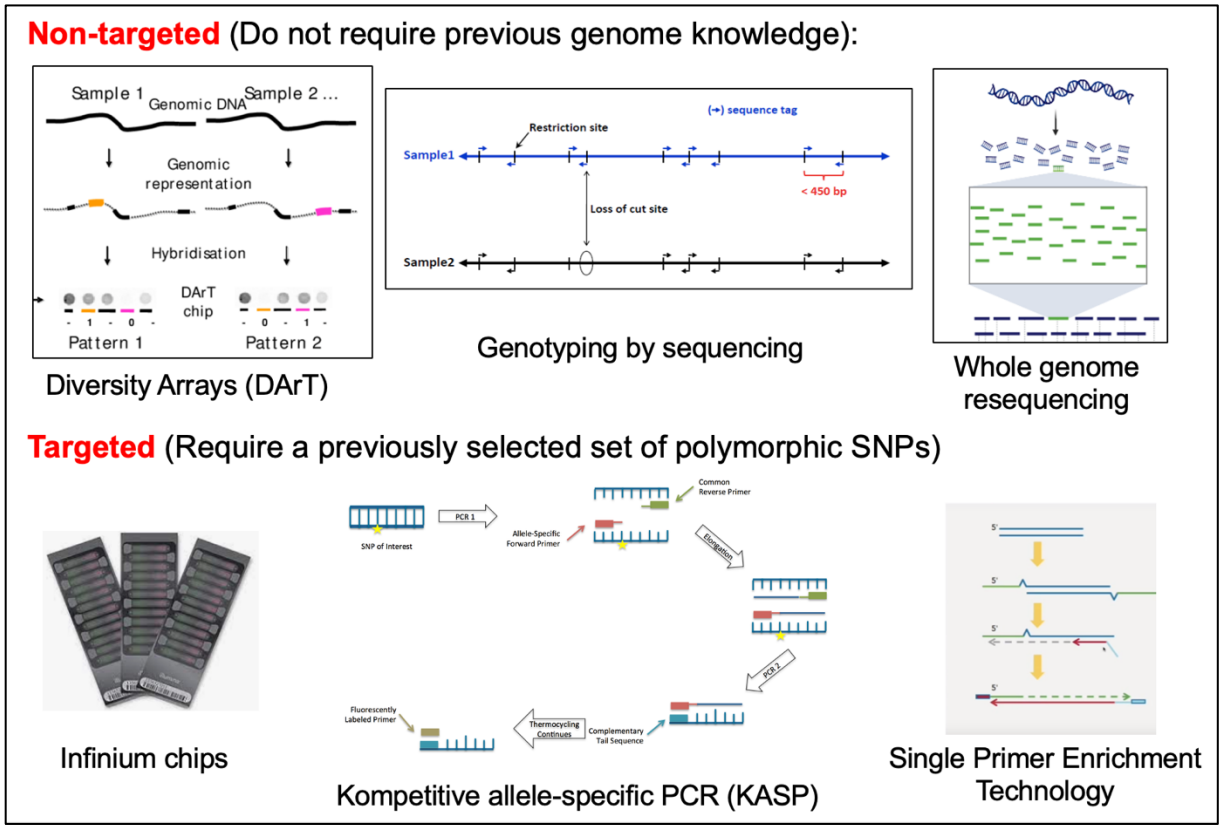

Figure 1: *Examples of non-targeted and targeted DNA barcoding methods*

However, the application of **genetic identification** in PGR collections or populations presents distinct challenges. Such material encompasses a wide **spectrum of biological diversity,** including pure lines,

inbred cultivars, outcrossing populations, heterogeneous landraces, and wild-collected material. This diversity, coupled with different genetic structures (largely influenced by the degree of allogamy of the crop or species), influences sampling strategies and complicates data interpretation and management. While a single barcode may be sufficient for uniform material, it may fail to capture the within-accession or population variability typical of landraces or wild populations. Bulked DNA samples can obscure this variation, whereas individual-plant genotyping is resource-intensive and not always scalable. Furthermore, standard **barcode markers often lack resolution** for distinguishing closely related cultivars, requiring more data-rich methods. These approaches demand **specialized infrastructure, trained personnel, and robust bioinformatics pipelines**. Lastly, aligning genetic data with existing passport information, often incomplete or inconsistently recorded, adds an additional layer of complexity. As such, there is a clear **need for harmonized**, context-aware strategies to effectively apply DOIs and genetic identification of accessions within genebank systems.

4.2 Problem Statement

While **DOIs provide a digital identifier** for linking and citing PGR globally, they do not **unassailably verify** the identity of the material. Conversely, DNA barcoding verifies biological identity, but without a global digital pointer its link to broader information may be lost. A combined system is needed to ensure each accession's identity is both **digitally traceable** and **biologically grounded**. Ensuring both digital traceability and biological verification is increasingly important as PGR are exchanged between conservation settings and various stages of utilization, such as research, breeding, or on-farm application, and as the volume and complexity of related data continue to grow through large-scale PGRFA initiatives. The European **GRACE-RI** (an ESFRI infrastructure in development) aims to harmonize PGR collection, conservation, study and valorization efforts for improving research and sharing equitably the benefits deriving from its use; design of integrated identification systems from the outset is key to reaching these objectives.

Objective: This deliverable proposes a **system architecture and workflow** that integrates DOI assignment with DNA barcoding methods for PGRs. It addresses:

- The **components** (DOI, DNA barcode/genetic identification, metadata scheme) and how they interrelate.
- A stepwise workflow guiding the process from accession/population acquisition at a GRC to DOI assignment, genetic identification, data management, and availability.
- The expected **benefits** (accuracy, interoperability) and potential **challenges** (logistical, technical, policy-related).
- Implementation within a PGR-RI, including needed infrastructure, leveraging of existing databases, and ensuring compatibility with European frameworks (e.g., EURISCO DOI service).
- **Best practices** for data standardization (use of MCPD, Darwin Core, GGBN standards), API-based data exchange, and quality control (sequence validation, metadata curation).
- Policy and governance considerations ensuring alignment with international agreements (ITPGRFA, CBD, Nagoya Protocol) and respecting intellectual property rights of data and materials.

5. Activities

To design and detail the combined DOI–DNA barcode system, the following activities were undertaken.

5.1 Literature & Policy Review

We reviewed technical documentation (e.g., FAO's GLIS DOI guidelines; Alercia *et al*., 2018; FAO 2017; FAO 2025; Nakazato *et al*., 2022; and D2.3 Phillips *et al*. 2025), scientific studies on DNA barcoding (D3.2 Barchi *et al*., in prep; Gostel *et al*., 2022; Kress 2017; Letsiou *et al*. 2024; Zhang *et al*., 2019), and policy analyses (Nagoya Protocol, GLIS reports). This provided insight into current standards, ongoing initiatives (e.g., EURISCO's DOI integration; Kotni *et al*., 2023, and lessons from global databases (GBIF, BOLD, EMBL-EBI, GenBank).

5.2 System Component Definition

We defined key components:

- **Foundation Resource**: **PGR** are defined as the taxonomic and genetic diversity of plants that is of value as a resource for the present and future generations of people (IPGRI, 1993). PGR form a continuum of natural resources from the most advanced cultivars to wild species and include modern cultivars, obsolete cultivars, breeding lines, clones, populations and genetic stocks, crop landraces, weedy races, related wild species, non-food socio-economic species to other wild species (Maxted et al., 2020). These resources are found spontaneously in nature or cultivated on-farm.

- **DOI (Digital Object Identifier):** A persistent, globally unique identifier string (e.g., doi:10.xxxx/PGRFA.12345) assigned to a PGR accession or population. Through GLIS or similar, each DOI is associated with a **metadata record** containing essential descriptors (e.g., **Holder**, **Local ID**, **Taxon name**, **Acquisition (or designation) Date** and **Method**). Comprehensive and up-to-date metadata aligned with **MCPD (Multi-Crop Passport Descriptors)** is not necessarily included in the DOI registration itself to avoid frequent updates; rather, such detailed and current information is made available through the DOI landing pages hosted in the GLIS portal and synchronized with systems like EURISCO and Genesys.

- **DNA Barcode:** Using a broad genomic definition, this includes traditional DNA barcoding, and other genotyping or genome sequencing approaches, facilitating identification of individual genotypes within heterogeneous accessions.

- **Metadata & Data Repositories:** Passport data and DOI information are stored in global and regional systems such as GLIS (Global Information System) and EURISCO (European Search Catalogue), both of which support DOI integration. DNA sequence data is deposited in repositories such as BOLD, GenBank, and EMBL-EBI, which offer cross-referencing capabilities. For instance, GenBank and EMBL-EBI records may reference BOLD IDs, and sequence submissions to GenBank and EMBL-EBI utilize **BioSamples**, each uniquely identified by a **BioSample ID**, which provides a structured means of linking genetic data directly to PGR DOIs and related metadata. The **PGR-RI platform** would serve as a central hub, linking each accession's DOI with its genetic sequence and associated metadata to provide a unified, interoperable record.

5.3 Workflow Design

We created a **workflow diagram** (Figure 1) and a detailed description of the process:

- **Step 1: Accession Acquisition, Population Designation & Data Capture:** When an accession is added to a collection or an in situ or on-farm population is designated for active conservation, the responsible organization or individual records key passport data, including taxonomic identification, origin, and donor information, and assigns a locally unique identifier. If the accession or population comes from a source already associated with a DOI (i.e. a backup sample held in a GRC for a genetic reserve or on-farm conserved population), the donor's DOI

is recorded explicitly to ensure continuity, traceability, and accurate documentation of its conservation history.

- **Step 2: DOI assignment:** The genebank or *in situ* PGR population maintainer registers the accession or population in EURISCO and then it will be uploaded to GLIS). Mandatory descriptors (e.g., holder institute code, local ID, scientific name, acquisition or designation date, method) must be provided. A DOI is assigned and returned, linking to a **GLIS record** accessible via DOI resolvers. The GLIS record may include links to external data (e.g., a Genesys accession page).

- **Step 3: DNA Barcoding:** In parallel or subsequently, it is proposed that leaf or seed tissue from the accession is sent to a DNA barcoding lab (in-house or external). DNA is extracted and sequenced using an appropriate method. To ensure consistency and comparability across laboratories, the PGR-RI should establish species-specific panels of **Single Nucleotide Polymorphisms (SNPs)** known to effectively capture genetic diversity. Additionally, the number of sampled plants per accession and the possibility of sample pooling ("bulking") are critical protocol considerations, and the PGR-RI will provide standardized guidelines according to species-specific reproductive biology and accession type.

- **Step 4: Sequence Data Handling:** The resulting DNA sequences are compared against reference databases (preferably: genus level super-pangenomes) to verify species or accession identity and to flag any discrepancies. Challenges may arise, especially for minor crops and crop wild relatives due to insufficient reference data, high diversity, and/or low differentiation among accessions, warranting caution in interpreting initial results and highlighting the need for ongoing reference database enrichment and method development. Verified sequences, along with associated metadata, are submitted to international repositories such as BOLD, GenBank, and EMBL-EBI, which mirror each other as part of the International Nucleotide Sequence Database Collaboration. BOLD requires core metadata which largely overlaps with the metadata captured through DOI registration. GenBank and EMBL-EBI submissions can include similar metadata and may also incorporate cross-references to BioSample IDs. For optimal traceability, we explicitly recommend including the PGR DOI in the GenBank/EMBL-EBI “specimen voucher” field in a standardized format.

- **Step 5: Integration in a PGR-RI Platform:** A new PGR-RI information system serves as a **hub** aggregating all accession information. When a DOI is assigned (Step 2), the DOI and metadata are fed into the PGR-RI platform (via GLIS’s API or data dump). When a DNA barcode is obtained (Step 4), its record (sequence and metadata) is also linked into the platform. Thus, the PGR-RI platform maintains a **unified accession profile**: DOI, passport data, sequence data, and any additional phenotype or genotypic data. The platform can periodically **harvest updates** from GLIS (new DOIs or metadata changes), from sequence databases (new sequences or annotations) and from GRCs data repositories such as EURISCO or Genesys (new phenotypic data sets).

- **Step 6: Linking to External Systems:** The platform will be interoperable with European and global PGR conservation and relevant databases:

    - It pushes or shares DOI-tagged data with **EURISCO** (Europe’s PGR catalog), which already stores DOI references for accessions and populations, and with **Genesys** (a global PGR portal) to ensure the resource is discoverable globally.

- It interfaces with biodiversity databases like **GBIF** (Global Biodiversity Information Facility) for occurrence records and **GGBN** (Global Genome Biodiversity Network) for genomic samples, using DOI and genetic data as bridges.
- It leverages APIs whenever available (e.g., GLIS's DOI API, BOLD's API, GenBank's Entrez API and EMBL-EBI's ENA API) to maintain live links, synchronize data across platforms, and ensure up-to-date information is accessible through the system.

- **Step 7: Utilization and Feedback:** Researchers or breeders using the system can retrieve an accession by DOI to get its full profile, and when they generate new data (e.g., a publication on that accession), they cite the DOI. The system could include services to **harvest literature** that cites DOIs, adding those references to the accession's profile. Additionally, if users find discrepancies (e.g., DNA barcode suggests a different species than recorded), they can flag this for curators, feeding back to improve data quality. GRCs can use the resource for identifying or verifying potential duplication within and between their collections, flag potential mix-ups, and conduct gap analyses, comparing the genetic diversity held in their collections vs. the whole genetic variation of the taxon/species

5.4 Concept Development

Conceptual modelling and workflow visualization (Figure 1) were created to demonstrate system viability, clearly depicting the integration points between DOI and DNA barcode data within the PGR-RI platform.

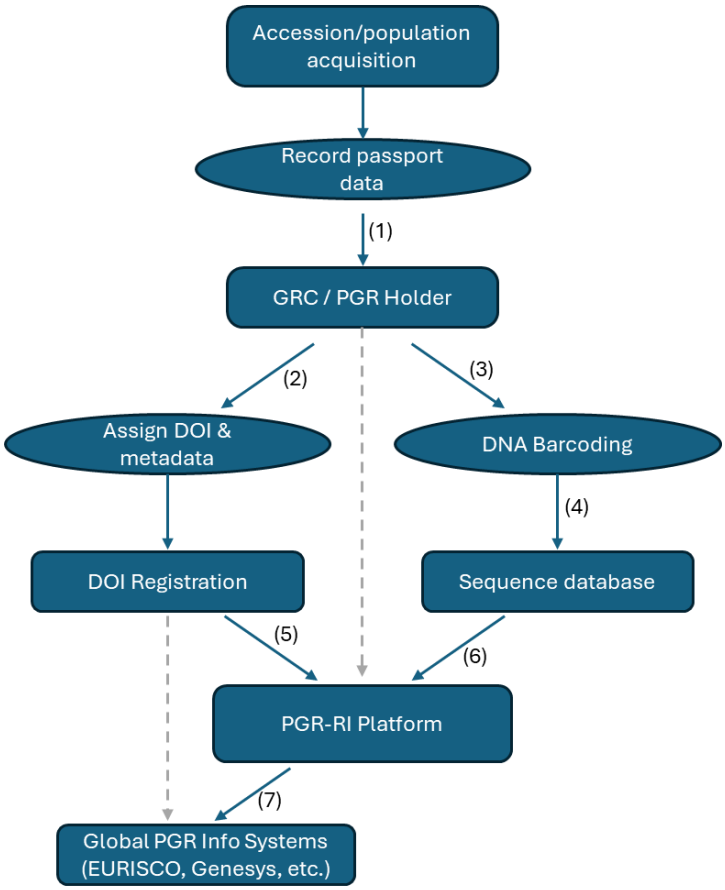

Figure 2: *Proposed workflow integrating DOI registration and DNA barcoding for PGR identification. Steps: (1) Addition of a new accession/population and the recording of passport data by a Genetic Resource Center (GRC) or plant genetic resource (PGR) holder; (2) Assign a DOI and associated metadata; (3) Perform DNA Barcoding; (4) Deposit sequence in BOLD/EMBL-EBI/GenBank repositories; (5)-(7) The resulting DOI registration and sequence data are both integrated into the PGR-RI platform,*

which serves as a central hub. From there, accession data are shared with global plant genetic resource information systems such as EURISCO and Genesys, ensuring broad visibility, traceability, and interoperability.

5.5 Consultation & Use Cases

We considered use cases including: a **crop wild relative** maintained *in situ*, a **farmer's landrace** shared in a community seedbank, and a **GRC accession** with historical data. For each, we examined how the system would handle the designation of unique identifiers:

- Crop Wild Relative (CWR) *in situ:* The population managers (e.g., national GRC and individual site managers) assigns a ID, sequences a DNA barcode to verify taxonomic identification (especially helpful if morphology is unclear), then the national GRC, in collaboration with the site managers, registers a DOI, linking the *ex situ* back-up sample representing the *in situ* population (metadata can include coordinates or an *in situ* reference), both the *in situ* population and back-up samples would be assigned DOI. The DOI and DNA data together ensure that even if the sample is used or duplicated in a further GRC or propagated, its wild origin identity is preserved.

- *Farmer's Landrace On-Farm:* A farmer's variety whether actively maintained on-farm, stored in a community seedbank, or held as a sample in a formal GRC will be assigned a DOI by the designated national GRC in collaboration with the landrace manager (e.g., farmer, market gardener, gardener). Relevant on-farm/*in situ* metadata would be documented. A sample will undergo DNA barcoding, with the resulting genetic profile linked to the corresponding sample, whether maintained on-farm, in a community seedbank, or conserved ex situ in a GRC. This linkage may also extend to other related samples or populations derived from the same original source or species. Such connections help determine whether the landrace is identical to another accession or is unique. The DOI facilitates traceability, particularly when the landrace is shared under a SMTA or other agreements.

- *Existing Genebank Accession:* Many genebanks already have thousands of accessions with passport data. Retrofitting involves batch registration of DOIs (EURISCO has facilitated this for many European collections; Kotni *et al*., 2023) and targeted barcoding. Over time, the genebank sequences more samples, building a barcode library that can detect labelling errors or duplicates. If two accessions in different genebanks have the same genetic profile and similar metadata, it could indicate an unrecognized duplicate – DOI records could then be cross-referenced to mark them as the same genetic entity, an advantage noted in GLIS guidelines.

5.6 Identification of Infrastructure Needs

We identified what existing infrastructure can be leveraged and what new developments are needed:

- GLIS (by ITPGRFA) exists for DOI registration, but **integration modules** for DNA data are not yet implemented. The system might need a feature to attach sequence data or at least a link to sequence databases in the DOI metadata.

- BOLD, GenBank and EMBL-EBI exist for sequence deposition. The key need is to ensure they can reference the PGR's DOI. BOLD could use the "catalog number" (which could include the DOI or a URI to the DOI record), GenBank could use the BioSample to link to a DOI and EMBL-EBI supports metadata fields in which DOIs can be referenced.

- EURISCO's DOI service exists and can be extended to also store a pointer to a barcoding status or sequence ID. **Genesys** already display DOIs for accessions and could similarly incorporate barcode links. Integration here, likely means modifying database schemas to store sequence

identifiers and adding API calls to retrieve sequences from BOLD/GenBank/EMBL-EBI when users query an accession.

- The PGR-RI will require an **interoperability layer**: APIs to query accession by DOI, retrieve combined data, and possibly a unified portal UI. This likely means developing middleware that regularly syncs with GLIS (for DOI records) and with sequence repositories. Ensuring **common identifiers** (DOI as the primary key) is critical to joining data.

5.7 Best Practices & Standards

We compiled best-practice guidelines:

- **Data Standards:** Use MCPD v2.1 for ex situ passport data (which now includes a field for DOIs), for *in situ* passport data (Alercia *et al.*, 2022; van Hintum and Iriondo, 2022), the minimum quality standards for *in situ* management of PGR (Maxted *et al.* 2025b), Darwin Core for biodiversity records (Wieczorek *et al*., 2013) (if integrating with GBIF), GGBN Data Standard for genomic samples (Droege *et al*., 2016) (if storing extracted DNA/tissue info). Ensure the DNA barcode sequence is linked to a voucher specimen identifier, normally the accession or population's DOI, to enable crosswalk between genetic data and accession data.

- **Interoperability:** Prefer exchanging data via APIs or standardized formats (JSON, XML). GLIS offers batch upload and APIs for DOI registration; BOLD has a REST API for data retrieval; GenBank data can be accessed via NCBI API and EMBL-EBI provides a suite of APIs (including RESTful and FTP-based services) for programmatic access to sequence submissions, metadata, and cross-references. The system should be designed to automatically fetch updates (e.g., if a sequence is added later) and update linked records. Use of **persistent URIs** for data (e.g., DOI resolves to a landing page with accession info) ensures any stakeholder can use the DOI to find data.

- **Quality Control:** Include checkpoints: e.g., **metadata validation** before DOI assignment (GLIS enforces mandatory fields to avoid missing identifiers). **Sequence validation**: using reference libraries to confirm if the DNA barcode is plausible for the reported taxon. BOLD's requirements (trace files, etc.) encourage high-quality data. Periodic audits could be done to reconcile DOI records and sequence records (flagging any mismatches in species names or geographic origin).

- **Capacity Building:** Recommend training for genebank staff on DNA barcoding protocols and data curation, as well as providing tools to fill skills gaps and raise professionalism of PGR data management.

5.8 Policy & Governance Analysis

Recognizing that implementing such a system intersects with PGR and PGR-related policy.

- Under the ITPGRFA, DOIs are voluntary but strongly encouraged; many countries have commenced implementation, but many PGR holdings still lag behind (Gullotta *et al*., 2023). We consider incentives or mandates, e.g., making DOI registration part of routine genebank reporting, as ECPGR (ECPGR 2017) and EURISCO (Kotni *et al*., 2023) proposed.

- DNA sequence data ("Digital Sequence Information", DSI) is currently being debated in the ABS (benefit-sharing) obligations context. While the current policy (as of 2025) doesn't enforce ABS on sequence data, there is discussion about how open genetic data should be. We recommend following the **open data norms** (as per CBD and genomes community agreements) but staying alert to future policy changes. Any sensitive data (e.g., precise location of an endangered wild population) can be handled with controlled access if needed, but generally, the DOI & barcode system deals with non-confidential identifiers and sequences meant for public research.

- Intellectual Property (IP): Normally, DOIs and barcodes are not patentable themselves; they are documentation tools. However, if a certain DNA barcode reveals a trait or if the PGR is under Plant Variety Protection, care must be taken that publishing its sequence doesn't infringe agreements. We suggest obtaining appropriate permissions when barcoding material is received under restrictive terms, though material in GRC via SMTA is generally for public domain use with benefit-sharing conditions, which our system facilitates by tracking usage via DOIs.

- It should however be considered that barcoding of an accession whose use is protected under the ITPGRFA and/or Nagoya protocol, is likely to prevent its unauthorized commercial use, and therefore improve the equitable sharing of benefits derived from its use. Therefore, the legal benefits of DNA barcoding greatly outweigh the potential misuse of the public sequence information for commercial purposes. Actually, it is the publicity of this information that constitutes the best guarantee against misuse of the biological material attached to it.

Each of these activities built the foundation for the **Results** section, where we articulate the final system design and findings from this process.

6. Results & Discussion

Through the above activities, we formulated a **system for unique identification of PGR** that combines the strengths of DOIs and DNA genetic identification. The main results and features are:

- **Unified Unique Identification System Design:** The proposed system is composed of three integrated layers: **Identification (DOI)**, **Validation (DNA Barcode)**, and **Information (Metadata)**. Each accession is assigned a DOI which acts as its **permanent unique digital identifier** globally, and one or more DNA barcodes which act as its **genetic identifier**. Metadata connects these, describing the accession and linking the DOI to the sequence record. This design means any user can reference the accession or population by DOI in publications or databases, and if needed, verify the taxonomic identity via the DNA barcode sequence in a reference library (for instance, confirming that two accessions with the same DOI or claimed to be the same are indeed genetically identical). The system's novelty lies in **binding a digital system with a genetic system** for PGR identification.

- **Detailed Workflow (from accession to open data):** As depicted in Figure 1, the workflow ensures that when an accession is actively conserved by either collection, transfer and deposition or designation and management:

    - It immediately gets documented (metadata recorded and DOI assigned).

    - It gets genetically characterized (DNA barcode sequenced).

    - Both aspects are fed into a shared platform.

    - This results in a **complete accession or population record** accessible via a single query (e.g., inputting the DOI returns passport info, taxonomic identification, location origin, and a link to or display of its DNA records and any matches to known species).

    - **Integration points** were successfully identified: e.g., use of GLIS DOI service to obtain identifiers; use of BOLD/EMBL-EBI/GenBank for storing sequences; use of EURISCO/Genesys for aggregating regional/global info with DOIs. We effectively bridge these such that updating one part (like adding a new sequence) can propagate to others.

- **System Architecture within the PGR-RI:** We drafted an architecture where the **PGR-RI portal** is central. It acts as a mediator: on one side interfacing with providers (GRC, farmers, breeders, conservationists) who input data and on the other with stakeholders (researchers, farmers, breeders, policymakers) who retrieve data. The portal maintains an internal database linking DOIs to their metadata and to any sequence IDs. For example, an internal table might have columns: DOI, GenebankID, Taxon, Holder, etc., and a field for **sequence identifier** (like EMBL-EBI/GenBank accession number or BOLD process ID). The platform can either store sequences or more likely just reference them to avoid duplicating large quantities of data. We envision a **dashboard** where a curator can see, for each new DOI registered, if a DNA barcode has been added; if not, it could flag "Pending barcode" to prompt sequencing. Conversely, if a sequence comes in for which no DOI exists (which is unlikely as sequencing usually follows accessioning, but is possible if legacy sequences exist), it flags to register a DOI. This bidirectional check ensures completeness of identification.
    - Additionally, the architecture includes a **public API** for the PGR-RI portal to allow other systems to query data (e.g., a breeding platform could call the API with a DOI to get genetic ID and trait data).
    - We also considered an approach to integrate **machine-readable** links: for instance, using a **DOI landing page** that includes a reference to the sequence, so even general web searches could associate the DOI with available sequence data.
- **Benefits Analysis:** The integrated system yields numerous benefits:
    - **Improved Traceability:** Any sample distributed with a DOI can be unambiguously traced in literature or in databases. If a researcher later generates -omics data or a publication, the DOI ensures that knowledge is linked back to the exact associated accession. DNA barcoding ensures that if the sample was mislabeled or confused, such errors are highlighted, thus the DOI remains linked to the correct biological entity. This is especially useful for "tracking **families of related PGRFA**" like breeding lines or duplicates.
    - **Interoperability & Data Linkage:** The DOI provides a **single standard identifier** across communities and databases. This means GRC, genetic reserves, on-farm systems, herbaria, databases like GBIF or journals like Genetic Resources can all use the same identifier to refer to material, simplifying integration. Because DOIs are web-resolvable, it means data about an accession can be automatically aggregated by computers (e.g., a script can find all mentions of a DOI in EMBL-EBI/GenBank or literature). DNA barcodes, meanwhile, provide an independent way to relate entries: for example, if two DOIs from different genebanks have the same barcode sequence, the system can highlight a probable link between the material. This could solve the long-standing issue of **duplications in genebanks** by providing evidence of genetic identity.
    - **Enhanced Data Quality:** DOIs enforce a discipline of providing at least a minimum set of metadata, curbing undocumented samples. DNA barcoding adds quality by validating taxon identification (if a barcode sequence does not match the claimed genus, the curators can re-examine the accession's ID), identifying potential duplicates within and between GRCs, and providing traceability, against potential mix-ups or biopiracy. The system also encourages periodic updates – e.g., if new information arises, updating the DOI metadata in GLIS (which is possible through update services)

means all connected systems can get the refined data. As a result, data in PGR systems stays more up-to-date and accurate.

- **User Compliance and Collaboration:** From a policy viewpoint, citing DOIs in publications helps fulfil Treaty obligations (SMTA Article 6.9) by making research results on the material publicly linked. It simplifies how **recipients** of material report back, simply by referencing DOIs rather than sending separate reports. Also, collaboration between laboratories becomes easier: a breeding program and a genebank can ensure they are talking about the same plant if they share the DOI (even if internally they use different IDs). Our system supports that by decoupling internal tracking from the shared identifier.
- ***In situ* / on-farm / *ex situ* conservation integration:** Historically *in situ*, on-farm and *ex situ* conservation have too often been seen as distinct activities implemented by distinct scientific communities working in isolation, and they have further distinction from the bulk of the biodiversity conservation community. The application of DOIs/barcodes will highlight the links between conserved resources and help promote the maximum, sustainable exploitation of the conserved resources with the mutual goal of improving food security.

- **Challenges & Mitigation:** The results also identify challenges:
  - *DOI Assignment and Accession Dynamics*: Assigning DOIs to PGR accessions presents specific challenges related to the quality and stability of the underlying material. One issue arises when accessions lack sufficient or complete metadata required for DOI registration (e.g., missing or incorrect taxonomic classification, use of different taxonomic systems, origin, or acquisition information), complicating traceability and reducing interoperability value. Additionally, biological processes such as Single Seed Descent (SSD), which are often used to fix genetic lines, can create new derived material from an original accession. These derived lines, although genetically related, will require their own DOI if treated as independent and distinct genetic entities. Furthermore, regeneration cycles, essential for maintaining viability in genebank holdings, can gradually shift the genetic composition of heterogeneous accessions (e.g., populations, landraces, wild-collected material), especially in outcrossing species. This genetic drift or selection pressure over time challenges the assumption of a static identity linked to the original DOI. To mitigate these risks, the system recommends strict documentation of derivation events and considering derivatives as new accessions with their own DOI. Furthermore, as good genebank practice, careful management of regeneration processes (e.g., maintaining bulked population profiles when appropriate), and assigning a new DOI while retaining reference to the parent material through metadata linkage. This ensures transparent lineage tracking while preserving the integrity and meaning of each DOI.
  - *Technical Challenge – DNA barcoding*: Using DNA barcoding in its broader definition, which includes traditional barcode loci as well as advanced genotyping and sequencing methods such as genotype-by-sequencing (GBS), targeted sequencing, and whole-genome sequencing, offers robust potential for the genetic identification of PGRs. However, several challenges persist. Diverse sequencing approaches generate different types and resolutions of data, which can complicate standardization and comparison across collections and institutions. In accessions with high within-sample heterogeneity (e.g., landraces or wild populations), bulk sequencing may obscure

individual genotypes, while individual-plant genotyping may be too resource-intensive for large collections. Moreover, interpreting genotypic data to distinguish unique accessions requires comprehensive reference datasets and bioinformatics capacity, which may be lacking in most Genetic Resource Centre. The integration of this genetic information into existing documentation systems also presents logistical and interoperability hurdles. While broad-spectrum DNA barcoding enhances the resolution and utility of PGR identification, it requires coordinated protocols, infrastructure investment, and thoughtful integration with passport and phenotypic data to reach its full potential.

- *Technical Challenge – Data Integration:* Combining data from different sources (DOI metadata vs sequence databases) can be complex. We found that because DOIs are included in MCPD and many databases now store them, matching on DOI is viable. However, sequence databases do not yet have a dedicated field for a DOI of the specimen. To mitigate, we propose including the DOI in the "Specimen voucher" field when submitting. For BOLD, it is possible to include the DOI as part of the sample ID or in the metadata. We also suggest working with GLIS to adopt a feature where GLIS could store known sequence accession IDs in its records.

- *Technical Challenge – Developing a Flexible System for Genetic Identification*: A critical technical challenge is creating a robust and adaptable genetic identification system capable of accommodating the diverse range of methods currently used across the PGR community. Institutions utilize various genotyping strategies tailored to specific crops, objectives, and available resources. While this methodological diversity meets practical and scientific needs, it complicates data integration and comparability. Rather than enforcing uniformity, the goal is to establish a flexible framework that effectively integrates existing approaches, such as various SNP panels, barcode loci, and genomic sequencing methods, and can seamlessly incorporate emerging technologies as they develop. This adaptive system would ensure sustained interoperability and continuous improvement in genetic identification capabilities.

- *Operational Challenge – Sequencing Resources:* Not all collections have easy access to DNA barcoding facilities. We identified this as a gap: while DOI assignment is relatively low-cost (it's a digital step, and services like EURISCO even do it on behalf of GRC), DNA barcoding requires specialized lab facilities and trained personnel for DNA extraction, sequencing, and data analysis. Implementation within the PGR-RI should therefore consider establishing a **centralized barcoding service**, potentially outsourced to specialized companies. Outsourcing to commercial sequencing providers is likely to be more cost-effective, efficient, and faster than establishing or relying on networks of public labs. However, it will still be essential to invest in training GRC personnel in sample preparation, quality control, and data interpretation, as outsourcing does not eliminate the need for basic in-house competencies.

- *Data Volume Challenge:* With millions of accessions to be genotyped, at a current cost of about 10 € each, genotyping all can involve a considerable cost. The objective is to reach the barcoding of a considerable (60% of active accessions) fraction of GRC holdings. In the case where resources prove to be limiting, we propose a phased approach: prioritize unique and important accessions (e.g., type specimens, unique landraces, crop wild relatives, and any accessions or populations lacking clear identification). In addition, prioritization could be guided by species-level criteria, such as their relevance to food security, conservation status (e.g., endangered or

underrepresented in collections), known importance in breeding programs, or their role in climate resilience. For others, the system can allow an accession to have a DOI even if the barcode is not done yet; as funds permit, they can be sequenced. The DOI helps track which ones are pending barcodes.

- *Interoperability Challenge:* Ensuring cooperation and alignment among all stakeholders e.g., GRC, databases, and biodiversity repositories, is a critical challenge. The proposed system is designed to **be inclusive**: it can accommodate data from institutions not yet using DOIs by temporarily linking records through local or provisional identifiers. However, DOI adoption remains the recommended best practice, as it provides globally unique and persistent identifiers that enhance traceability and data integration. Major platforms such as Genesys, EURISCO, and WIEWS now support and display DOIs where available, which helps to streamline interoperability as uptake increases. For genetic (DNA) data, a key challenge lies in reliably linking sequence records to the corresponding physical samples (e.g., genebank accessions). To address this, the system aligns with established practices in BOLD, EMBL-EBI, and GenBank, all of which require or support the inclusion of voucher information, such as accession numbers, collection codes, and institutional identifiers, that can incorporate or be linked to DOIs. This ensures consistency with the barcoding community's standards and facilitates accurate cross-referencing between genetic and passport data.

- **Leverage of Established Databases:** The system actively uses existing infrastructures:
  - **EURISCO:** Europe's catalog will play a key role by continuing to assign DOIs for nationally conserved PGR and including those DOIs in its dataset. Our system suggests that EURISCO could extend to store a flag or reference for "DNA barcode available (yes/no)" and possibly the GenBank accession if available. EURISCO's recent update highlights that DOIs are gradually becoming the standard (Kotni *et al*., 2023). This aligns perfectly with our approach, reinforcing that we are building on a trend.
  - **Genesys & GLIS:** Genesys (global portal) already ingests data from many genebanks, *in situ* populations and on-farm systems and includes DOIs when available. GLIS is the underlying service for DOI assignment. Our system is effectively an application layer on top of GLIS + barcoding. The PGR-RI would coordinate with Genesys to ensure any sequence info can be displayed for accessions (Genesys could embed links to sequence databases if provided).
  - **GBIF & GGBN:** For *in situ* and wild materials, GBIF includes significant occurrence data and may have images; GGBN focuses on genomic samples, which could include our DNA extracts (if biobanking DNA). Using DOIs in those contexts fosters integration – e.g., a GGBN record for a DNA sample could list the source accession's DOI, making it discoverable. The result is a more connected data ecosystem.
  - **BOLD, EMBL-EBI & GenBank:** We identify these as key repositories for storing and accessing DNA barcode data. BOLD provides curated barcode records with structured metadata and taxonomic validation, while GenBank offers broader sequence accessibility and integration with other bioinformatics tools. EMBL-EBI, as a core partner in the International Nucleotide Sequence Database Collaboration (INSDC), mirrors GenBank entries through ENA, ensuring synchronized global availability of sequence data. Using all three platforms together can significantly enhance the

visibility, accessibility, and scientific utility of DNA barcoding data across the plant genetic resources community.

- **Policy & Governance Outcomes:** Our analysis yields guidance to align the system with policy:
    - The system adheres to **voluntary but strongly encouraged DOI usage** under ITPGRFA Resolution 5/2017. We conclude that the PGR-RI should officially endorse DOIs and possibly require any accession entering its purview to get one (unless sensitive).
    - We maintain **open accessibility** of data: DOIs resolve openly, and DNA barcodes go to public databases. This aligns with FAIR principles and with current expectations that sequence data remain public.
    - We note that some national laws might restrict sharing of genetic data for endemic resources pending ABS agreements. The system can handle that by marking such data as restricted and not depositing sequences until issues are cleared (or depositing in controlled-access databases). But such cases are likely exceptions.
    - IP concerns are minimal given we are mostly dealing with identifiers and short DNA sequences which are not proprietary; still, a result is to create **guidelines for data sharing agreements** so that contributors (genebanks, etc.) are comfortable that assigning a DOI or publishing a DNA sequence does not compromise their interests.
    - **Sensitive data** like traditional knowledge, farmers' info or localities of highly threatened taxa linked to an accession or population should not be in the DOI metadata (which is public). We reaffirm GLIS's approach to non-confidential info only. If needed, the PGR-RI can maintain a separate secure database for any sensitive fields but not tie it to the DOI record.

7. Conclusions

This deliverable outlines a feasible and impactful system for the integrated identification of Plant Genetic Resources (PGR) using Digital Object Identifiers (DOIs) and DNA-based genetic methods. By combining persistent digital identifiers with biological validation, the proposed system significantly improves the traceability, accuracy, and interoperability of PGR data.

The approach builds on existing infrastructures such as GLIS, EURISCO, BOLD, GenBank, and EMBL-EBI, reducing redundancy and aligning with current international frameworks. It supports conservation, research, and breeding efforts by enabling consistent, high-quality documentation across *ex situ*, *in situ*, and on-farm contexts.

However, the successful operationalization of this proposal largely depends on the realization of GRACE-RI as a coordinating and facilitating entity. Should GRACE-RI not materialize or be delayed, it is critical that the core elements of the proposed system remain actionable through alternative mechanisms. To this end, establishing interim collaborative frameworks among existing European Genetic Resource Centres, research institutions, and ECPGR could serve as a transitional structure. Such a coalition could lead efforts in promoting DOI registration and standardized genetic identification protocols, maintaining momentum and facilitating a smooth integration into GRACE-RI or a similar infrastructure when it becomes operational.

To remain effective over time, the system must be adaptable to emerging genomic technologies and evolving policy landscapes. A flexible, modular design and continuous feedback will ensure its resilience.

In summary, this system offers a practical and forward-looking solution for uniquely identifying and managing PGR. Whether through GRACE-RI or other coordinated efforts, its implementation will greatly enhance the utility and management of Europe's plant genetic resources.

8. Deviations

No major deviations occurred in executing this task, but some points are noteworthy:

- **Scope Adjustment:** We aimed to cover both *ex situ* and *in situ* identification equally. During development, we focused more on *ex situ* (genebank) workflows, as DOIs have a clearer implementation path there. *In situ* PGR identification (like living plant populations with DOIs) is still primarily conceptual globally current, but on the cusp of implementation so in situ clarification is very timely. This is a slight deviation to ensure we produce practical outputs. However, we did include considerations for *in situ* and on-farm contexts in the workflow (Step 1 and use cases). Future work in the PGR-RI can expand on community-managed DOI assignment for *in situ* resources.
- **Interdisciplinary Integration:** This activity successfully integrated expertise across policy, bioinformatics, and GRC management. A minor deviation occurred in the depth of policy analysis—complex topics such as the Nagoya Protocol's position on Digital Sequence Information (DSI) were addressed at a high level rather than through detailed legal examination, due to space constraints and the topic's complexity. Nonetheless, key policy implications are clearly summarized to support informed decision-making.

Overall, the work was carried out largely as planned. This deliverable meets its objectives, providing a clear system design and guidance for implementation in GRACE-RI or any future European PGR-based RI. Any aspects not fully executed are recommended as the next steps in subsequent project phases or follow-up projects.

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