

# A gap and synergy analysis of the European research infrastructure (RI) ecosystem: advancing the novel GRACE-RI dedicated to plant genetic resources

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• **Background** Plant genetic resources (PGRs) are crucial for sustainable agriculture and food security, but the roadmap of the European Strategy Forum on Research Infrastructures (ESFRI) lacks a dedicated research infrastructure (RI) for their systematic cataloguing, safeguarding and improvement. To fill this gap, we propose a new RI concept specifically for PGRs in Europe.

• **Scope** The proposed RI, called ‘Plant Genetic Resources Community for Europe’ (GRACE), is aimed to support current and future research projects on PGRs, enhance collaboration across European countries, unlock the adaptive potential of crop biodiversity preserved in PGR collections, and strengthen the current and future sustainability of the food chain in Europe. As part of the preparatory project ‘Promoting a Plant Genetic Resource Community for Europe’ (PRO-GRACE), we analysed the current landscape of European RIs supporting PGR-related research in complementary fields regarding research aims, research products and features/services.

• **Conclusions** Through a robust quantitative approach, we have identified gaps and potential synergies among six RIs from the Health and Food and Environment domains of the ESFRI roadmap. These findings were discussed in the context of European PGR research priorities and current societal needs, and the implementation of GRACE was proposed as a strategic response to these challenges.

**Key words:** Crop diversity, ESFRI roadmap, research infrastructure, GRACE-RI, plant genetic resources, *ex situ* and *in situ* PGR conservation, genebanks, gap analysis, synergy analysis.

## GENERAL OVERVIEW OF PLANT GENETIC RESOURCES IN EUROPE

Plants are essential for life on Earth. Terrestrial plants fix ~50 % of human-made CO<sub>2</sub> and produce ~50 % of the oxygen we breathe, and, directly or indirectly, most of the organic matter that we use as food. There are ~400 000 terrestrial plant species, and we use ~6000 of them for food (Pilling *et al.*, 2020).

We are living at the beginning of the 6th large mass extinction; terrestrial plant species are going extinct at rates 500 times larger than at pre-industrial levels, with projections bringing this figure as high as 10 000 times in the future (Antonelli *et al.*, 2023). Each time a plant species goes extinct, a gene pool of tens of thousands of potentially useful genes for both our survival and that of the ecosystems goes extinct with it. Therefore, the preservation of plant biodiversity by conserving plant genetic resources (PGRs)

both *in situ* (in their natural environments) and *ex situ* (conserving samples of wild populations and/or crop varieties in specialized structures such as botanical gardens, genebanks or conservation seedbanks) is key to our survival on the planet.

The conservation and sustainable use of PGRs is crucial for ensuring food security in Europe in the next decades (Maxted and Kell, 2021; Swarup *et al.*, 2021). Extensive regions of Europe's agricultural landscape are expected to be significantly impacted by the effects of climate change and human activities, increasing losses in biodiversity and habitat degradation (Thuiller *et al.*, 2005, 2011; Darbyshire *et al.*, 2017; Bajocco *et al.*, 2018; Agovino *et al.*, 2019; Bhadouria *et al.*, 2019). Changes in habitat suitability for crop varieties and wild species can have significant economic and social consequences due to the geographical shift of their cultivation areas (Santos *et al.*, 2020; Jägermeyr *et al.*, 2021). The wide effects of climate change on European agriculture (Hannah *et al.*, 2013, Malhi *et al.*, 2021; Skendžić *et al.*, 2021) call for a paradigm shift towards more sustainable food production systems, including crop varieties more efficient in nutrient uptake, as well as crop diversification to mitigate the effects of extreme climatic events. Furthermore, the future sustainability of the food system is threatened by the continuous growth of the world's population: to meet the global food demand by 2050, agricultural productivity must increase by 60 %, without substantially expanding arable land (Silva, 2018).

PGR collections, both *ex situ* and *in situ* (*ex situ* genebanks, on-farm landraces, *in situ* reserves, etc.), are treasure chests of largely unknown functional diversity for many crop species and key sources of relevant genes, and they can significantly contribute to agriculture resilience by enhancing crop adaptations to global change and long-term sustainability of food production (Weise *et al.*, 2020; Aubry, 2023). They represent a barrier against the progressive loss of both intra- and inter-specific diversity and genetic erosion that has occurred over the last century, mainly due to the selection of a few high-yielding plant varieties to meet the majority of food needs (McCouch *et al.*, 2020; Khourey *et al.*, 2022). Therefore, an urgent need is to broaden the genetic base of elite germplasm of plants, for long-term genetic gain and to strengthen resistance to biotic and abiotic stresses. Despite the large adaptive potential of the genetic and phenotypic diversity stored in collections and the non-negligible costs for their preservation, only a small proportion of over 2 million genebank accessions preserved *ex situ* by about 400 institutes and 6384 *in situ* crop wild relative populations from 11 European pilot countries currently listed in the European Search Catalogue for Plant Genetic Resources (EURISCO) ([www.ecpgr.org/eurisco](http://www.ecpgr.org/eurisco); Kotni *et al.*, 2023) have been used in pre-breeding/breeding activities to improve commercial varieties or create new ones (McCouch *et al.*, 2020; Volk *et al.*, 2021; Sanchez *et al.*, 2023; Cheng *et al.*, 2024). The potential use of genebank materials for the genetic improvement of crop species is hampered by the fact that a large proportion of accessions is poorly characterized, with available data often limited to their geographical origin but lacking genetic, molecular and/or phenotypic information. In addition, the efficiency and overall operational quality of genebanks, the conditions governing the access to these resources and the lack of clearly defined access policies can affect final accession availability (Brink and van Hintum, 2020; Smith *et al.*, 2021).

In the last few decades, cutting-edge research has been conducted in the frame of various EU-funded projects on PGRs, such as HARNESSTOM (<https://cordis.europa.eu/project/id/101000716/reporting/it>), BREEDINGVALUE

(<https://breedingvalue.eu/>), AGENT (<https://agent-project.eu/>), G2P-SOL (<http://www.g2p-sol.eu/>), ECOBREED (<https://ecobreed.eu/project/>), TRADITOM (<https://traditom.eu/it/>) and INCREASE (<https://www.pulsesincrease.eu/>). These projects generated a large amount of PGR-related passport data, phenotypic characterization and evaluation (C&E) data as well as multi-omic data stored in different repositories and platforms (König *et al.*, 2020; Barchi *et al.*, 2021, 2023; Gonzalo *et al.*, 2021; Tripodi *et al.*, 2021; Calle García *et al.*, 2022; Mellidou *et al.*, 2023; von Steimker *et al.*, 2024), but which may not have been regularly maintained after the end of the project, so there is a risk that they will be discontinued with data loss. In addition, the above-reported repositories/platforms often offer different accessibility and usability of data/datasets, and different ontologies/semantic standards are often adopted, which can result in data fragmentation and duplication (Gabdank *et al.*, 2018). Such siloed efforts and insufficient data interoperability among platforms ultimately lead into a complex labyrinth that is often difficult to navigate by users, although the application of FAIR principles (Findable, Accessible, Interoperable, Reusable) has gained more prominence in recent years (Wilkinson *et al.*, 2016). Additionally, the connection between the plant biological material used or sampled and the data from multi-omic experiments is too often missing (Jamil *et al.*, 2020). This hampers the genomic-based prediction of performances of crop species and hinders their selection or use in breeding programmes for the improvement of cultivated varieties (Blätke *et al.*, 2021; Aubry, 2023).

Since 1980, the European Cooperative Programme for Plant Genetic Resources (ECPGR, [www.ecpgr.org](http://www.ecpgr.org)) has been active in promoting the effective conservation and sustainable use of PGRs through a network of national PGR programmes, the development of infrastructures, frameworks and tools, and building capacity and knowledge. In the ECPGR Plant Genetic Resources Strategy for Europe (ECPGR 2021), the establishment of a robust PGR research infrastructure (RI) with a secure and sustainable financial basis is presented as crucial to safeguard Europe's plant genetic resources for future generations and to contribute to global efforts towards biodiversity conservation and food security.

The above scenario emphasizes the need for a coherent European policy framework and the development of a long-term European RI dedicated to PGRs, encompassing large-scale facilities, digital platforms and essential services (Goritschnig *et al.*, 2025).

The European Strategy Forum on Research Infrastructures (ESFRI) supports the development and integration of high-quality RIs across Europe promoting a coordinated approach among EU Member States, Associated Countries and the European Commission. Although PGRs are essential in many research and innovation activities that mobilize genetic diversity and therefore require infrastructure-based approaches for their conservation and access, no RI dedicated to PGRs is currently listed in the ESFRI Roadmap 2021 (<https://roadmap2021.esfri.eu/>), the EU's strategic planning document which identified major pan-European RIs of strategic importance. This represents a relevant gap in the European RI landscape, particularly because food security has already been recognized as crucial in the future EU 'one-health' scenario (OHEJP 2023).

## PGRs: TURNING CHALLENGES INTO OPPORTUNITIES

Recent advancements in technology have significantly enhanced our ability to generate and analyse big data. This creates

an unprecedented opportunity to develop new strategies for conserving and exploiting PGRs, and for promoting their use in agriculture. Furthermore, using advanced sequencing and phenotyping technologies to screen PGR collections would improve the maintenance of crop germplasm, reducing its costs by optimizing basic genebank operations, from prioritizing the regeneration of plant material to identifying gaps or redundancies in the collections (van Treuren and van Hintum, 2014). Some examples of the application of -omic technologies on collections held in genebanks are reported below. Sequence-based genotyping methods can help maximize genetic variability within genebanks through the development of core collections (Jia *et al.*, 2017). Genomics can also be used to identify redundancies in collections, as proposed by Singh *et al.* (2019), who assessed genetic diversity in a panel of 1143 accessions of *Aegilops tauschii* Coss., an economically important wheat wild relative, from three genebanks and found an average of about 50 % duplicates, highlighting the importance of optimizing the composition and size of the collection to improve the efficiency of funds spent on conservation. In other cases, such as *Solanum melongena* L. and its relatives, redundancy is much less, ranging between 0.6 and 15 % (Barchi *et al.*, 2023). The extent of detected redundancy depends on the sensitivity of the barcoding method adopted, and the need to rely on both molecular methods and phenotypic data to assess redundancy has been stressed (Barchi *et al.*, 2023).

To fully exploit the adaptive potential of the phenotypic diversity preserved in genebanks, it is essential to make available phenotypic information about the collections along with the genetic characterization of the material. Linking genotypic and phenotypic data can help exploit core collections tailored to specific traits or facilitate efficient querying of germplasm catalogues to find lines with desired genetic elements, ultimately strengthening the role of genebanks in maintaining PGR genetic diversity useful to breeding (Halewood *et al.*, 2018; Wambugu *et al.*, 2018; Mascher *et al.*, 2019). For example, genome-wide association studies (GWAS) of a global collection of *Capsicum* spp. comprising 10 000 accessions from 130 countries and five continents were carried out to reconstruct the evolutionary history of the species and allowed the identification of several markers associated with important traits under selection (Tripodi *et al.*, 2021). Challenges posed to agriculture by environmental changes may be addressed by predicting genotype-by-environment ( $G \times E$ ) interactions through the massive sampling of a genepool across a broad spectrum of environmental conditions, which may lead to the development of crop varieties tailored to specific environmental contexts (Halewood *et al.*, 2018; El Hanafi *et al.*, 2023), thereby mitigating harmful impacts of climate change as demonstrated with *Triticum aestivum* L. (Fradgley *et al.*, 2023) or *Zea mays* L. (Welcker *et al.*, 2022). The challenge of characterizing and exploring the large number of accessions held in genebanks requires a concerted effort by a wide range of conservation and research institutions. An effective framework for this type of collaboration is not yet in place. Furthermore, due to limited resources, the efforts of genebanks need to be oriented towards ensuring the long-term conservation and availability of accessions and they sometimes have limited access to facilities and expertise connected to multi-omic technologies (Gupta *et al.*, 2020). In addition, the application of -omic technologies requires the development of standardized protocols to ensure

the quality and reproducibility of results (Weise *et al.*, 2020). In this scenario, better coordination and support for improving characterization, conservation and access to genetic resources is urgently needed. This includes establishing specific standards for PGR management in Europe and, *inter alia*, developing a common, widely accepted system for the certification of genebanks (van Hintum and Wijker, 2024).

Enhancing the use and valorization of PGR collections also requires structured and easily accessible documentation of the preserved germplasm. Weise *et al.* (2020) emphasized the importance of transitioning from the current local management of PGR data to networked/federated remote repositories to ensure broader access to PGR documentation and its safe, long-term storage. Such a transition is essential to prevent the loss of documentation over time due to, for example, changes in future storage technologies and/or the turnover of local personnel managing these collections. To this end, EURISCO represents a successful model of an information system collecting and providing passport data from 43 national collections and ongoing efforts to enhance the coverage of C&E data and information on *in situ* conserved populations. A further step will be the integration of accession documentation systems with databases and data archives such as the EMBL (<https://www.ebi.ac.uk/>), which are intended for -omic data.

## GRACE-RI: A NEW PILLAR FOR THE PGR COMMUNITY

The PRO-GRACE project consortium (funded by Horizon Europe, <https://www.grace-ri.eu/pro-grace>) proposes a pan-European research infrastructure named GRACE (Plant Genetic Resources Community for Europe) to strengthen the implementation of *ex situ*, *in situ* and on-farm conservation of PGRs and to establish a broader, coordinated network of conservation centres. *Ex situ* conservation will be supported by a structured framework, with standardized methodologies and coordinated efforts across Europe – most notably through initiatives such as AEGIS (<https://www.ecpgr.org/aegis>), which standardize the activities of individual genetic resource centres, improving their quality and eventually aiming at a certification system. In contrast to genebanks, *in situ* conservation remains less developed, often relying on fragmented, locally coordinated initiatives, involving a wide variety of stakeholders both at the regulatory and implementation level. Despite these limitations, *in situ* conservation is best suited for preserving the widest genetic diversity of landraces and crop wild relatives, making it an essential component of a comprehensive conservation strategy. GRACE-RI will be dedicated to endowing the European region with an efficiently conserved, well-documented and accessible reservoir of PGRs, maintained in genetic resource centres and in natural habitats, and made available for research and the public good at all times. Moreover, building on existing national conservation programmes and international networks and initiatives, GRACE-RI will develop a range of technological and scientific services to enhance and optimize the long-term conservation of PGRs and promote their accessibility and use in breeding. To this end, the implementation of a Quality Management System (QMS) for the conservation and accessibility of PGRs, in collaboration with AEGIS, aims to address an important gap in the current EU landscape and represent a reference model for European genebanks,



providing end users – such as researchers, breeders, farmers and seed companies – with high-quality germplasm materials along with the related data, documentation and knowledge. Safety duplication of unique accessions conserved *ex situ* and *in situ*, as well as reconstruction and maintenance of pedigree information and kinship relationships of the plant materials conserved in genebanks, are additional objectives of GRACE-RI that are largely incomplete or currently lacking in the existing RIs. Moreover, the identification of duplicated accessions and potential gaps in diversity within and between genebanks and *in situ* collections will be coordinated by GRACE-RI at the European level. To this end, standard workflows, procedures and practices for the maintenance and characterization of the experimental material are required, and this is currently a gap in the PGR scenario and in the European RI landscape. Further, the novel infrastructure will promote cooperation with several existing RIs for improving current taxonomic validation services with specific and intraspecific information on crop taxa. Finally, GRACE-RI will provide the PGR community with tools to enhancing access to PGRs, i.e.: (1) advanced protocols for phytosanitary assessment and sanitation; (2) legal services for navigating the international treaties governing PGR exchange, such as the International Treaty on Plant Genetic Resources for Food and Agriculture (<https://www.fao.org/plant-treaty/en/>) and the Nagoya Protocol on Access and Benefit Sharing (<https://www.cbd.int/abs/>); and (3) supporting training and capacity building in the above sectors.

Data storage and management, ensuring fast data access, data integrity and compliance with policies and regulations will also be major tasks of the proposed GRACE-RI. This infrastructure will develop solutions to connect passport, phenotypic, molecular and other types of (meta)data, both within and between studies as well as from past and future research, supporting the transformation of current germplasm collections (e.g. genebanks) into bio-digital resource centres (Mascher *et al.*, 2019; Aubry, 2023). The semantic interoperability of GRACE with existing RIs will be promoted by the adoption of common ontologies, shared vocabularies that are well-established and widely used in PGR research for both data and metadata (Rocca-Serra *et al.*, 2010; Selby *et al.*, 2019; Papoutsoglou *et al.*, 2020) as well as relevant already existing resources supporting FAIR data management (D'Anna *et al.*, 2024). Moreover, enforcing permanent unique identifiers (PUIs) to each accession (as recommended by the FAO; Alercia *et al.*, 2015) and dataset (as recommended by the good practices of Open Science; Wilkinson *et al.*, 2016), such as DOIs, will facilitate the tracking of resources across different repositories.

Multi-omic approaches have led to the creation of a new generation of tools designed to characterize and leverage the biodiversity of PGRs stored in collections. The implementation of these methods in GRACE-RI will disclose essential information about the accessions and make it accessible to external users. Furthermore, GRACE-RI will provide additional services to end-users: e.g. genome-wide prediction models to assess the field performance of accessions (Keilwagen *et al.*, 2014; Yu *et al.*, 2016; Jiang *et al.*, 2021; Wang *et al.*, 2024); or spatial modelling of crop performances/habitat suitability across Europe under different future climate scenarios (Wang *et al.*, 2010; Booth, 2018; van Leeuwen *et al.*, 2024).

## LANDSCAPE ANALYSIS OF PGR-RELATED RI IN EUROPE: GAPS AND SYNERGIES

The Landscape Analysis described in the ESFRI roadmap 2021 offers an overview of the RIs and their service portfolios accessible to European scientists and technology developers. It also highlights the scientific needs and the existing gaps in the ecosystem of the RIs, providing recommendations for future strategic investments that reduce duplication of effort and will help sustain Europe's global leadership. The ESFRI 2021 Landscape Analysis includes RIs in Health & Food (H&F) and Environment (ENV) domains that provide support and resources to prevent biodiversity loss and promote sustainable agriculture, but there is no RI that addresses the challenges of the PGR research community. Consequently, comprehensive landscape analyses specifically focused on PGR research have not been conducted, though some reports and position papers have highlighted shortcomings in existing RIs operating in related fields of research (Morisse *et al.*, 2019; Stelzl *et al.*, 2023). As an example, biodiversity-oriented services have been analysed in the preparative phase of various RIs, such as the DiSSCo preparatory phase (Goodson *et al.*, 2020; Smith *et al.*, 2022) and ELIXIR preparatory projects, which surveyed biological databases throughout Europe (Southan and Cameron, 2009). The BiodivERsA network mapped gaps in biodiversity and ecosystem services of RIs (Manrique *et al.*, 2021). Additionally, the EU-funded RISCAPe project provided an extensive overview of the major European RIs within the international research infrastructure landscape (Asmi *et al.*, 2019).

As part of the PRO-GRACE project consortium and in collaboration with representatives of other European RIs, we have developed the gap and synergy analysis below. Our contributions reflect the collective perspective and strategic objectives of the proposed GRACE RI to be included in the ESFRI panorama.

The analysis involved six European RIs that cover scientific areas complementary to the conservation, management and use of PGRs, namely: ELIXIR (domain H&F – focused on biological data for life sciences), EMPHASIS (H&F – plant phenotyping), DiSSCo (ENV – digitization of natural science collections), LIFEWATCH (ENV – biodiversity and ecosystem research), METROFOOD (H&F – metrological applications for the enhancement of food quality and safety) and MIRRI (H&F – preservation, investigation and valorization of microbial resources). For comparison, recent EU-funded projects dedicated to PGRs (PRO-GRACE, HARNESSTOM, BREEDINGVALUE, AGENT, G2P-SOL, ECOBREED, INCREASE and TRADITOM – Supplementary Data Table S1) were used as a 'proxy' for the role and function that a future GRACE-RI could take and have. The above-mentioned RIs were compared with the future GRACE based on three different aspects: (1) research aims, as inferred from the EU-Cordis Field of Science (FS) (the CORDIS dataset – Fig. S1); (2) research products, as inferred from the Web of Science™ (WoS) categories of the papers acknowledging each RI (the WoS dataset – Figs S2 and S3); and (3) PGR-related features/services, based on a list of Key Performance Indicators (KPIs) screened and scored across the selected RIs (the KPI dataset – Table S2). A detailed description of the procedures and methods applied in the data collection can be found in Appendix S1. The three datasets obtained (CORDIS, WoS and KPIs) were subjected to minimum-spanning network



## A Research aims

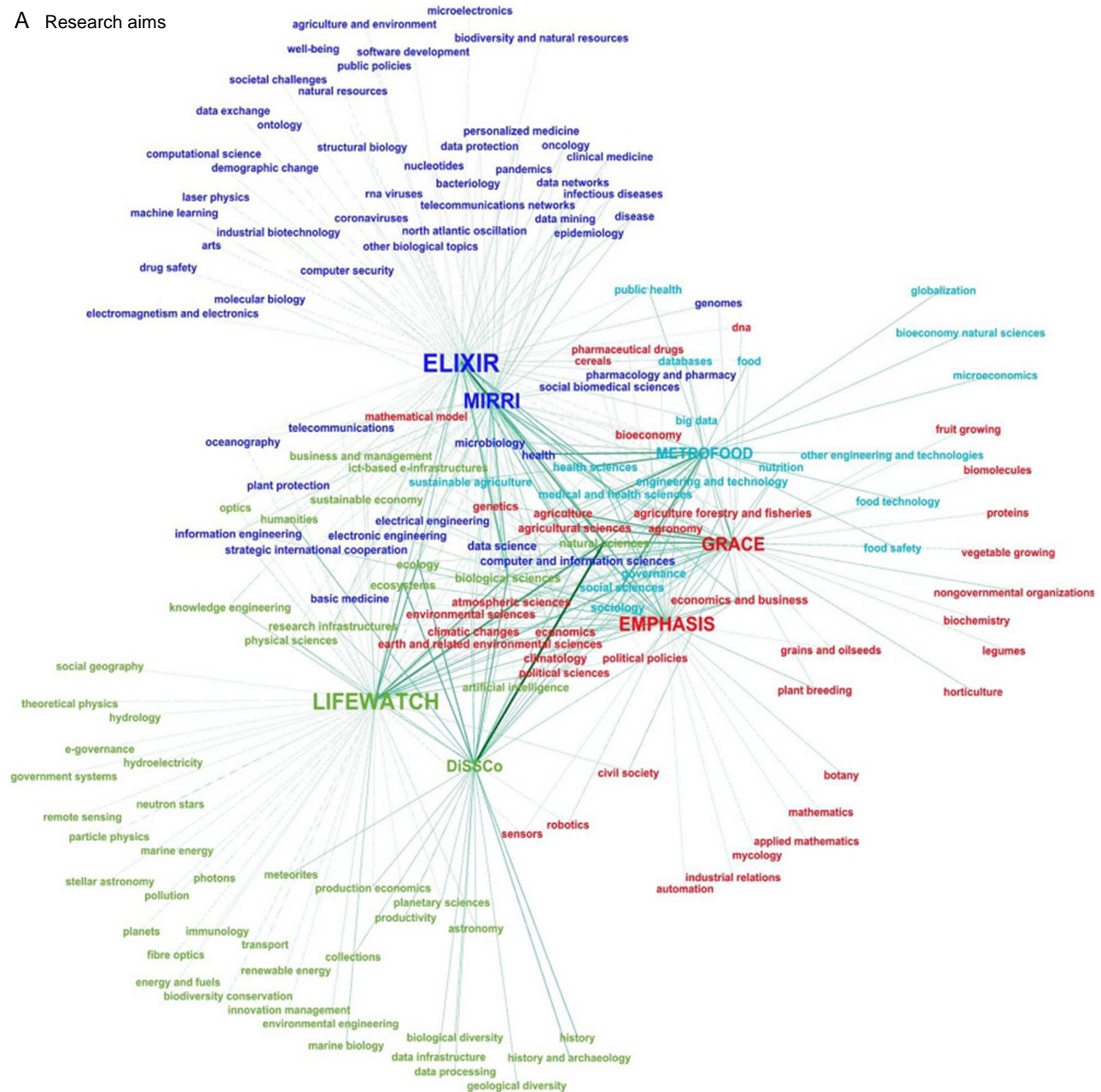


FIG. 1. Minimum-spanning network (Force Atlas Algorithm) of the seven selected RIs based on: (A) research aims (frequency of CORDIS-EU FS of 70 projects); (B) research products (WoS categories of 314 papers); (C) service/facilities (scores of 80 KPIs). The thickness of the connecting lines is proportional to the frequency. Highly connected nodes are central in each diagram, while nodes with lower connections or specific for each RI are peripheral. The size of the RI labels is proportional to the number of interconnections with nodes. Different colours highlight different node communities after multiscalar modularity analysis. RI, research infrastructure; WoS, Web of Science™; KPI, key performance indicator. The analysis was conducted using the software Gephi version 0.10 (Bastian *et al.*, 2009).

analysis (Blondel *et al.*, 2008), principal component analysis (PCA) and Pearson correlation analysis to find PGR-related gaps in the current European RI landscapes and potential synergies with the existing RIs.

Minimum-spanning network analysis of research aims and products revealed a highly interconnected and correlated landscape in the EU research infrastructure ecosystem (Fig. 1A, B), with ELIXIR, MIRRI and LIFEWATCH being the most interconnected RIs in terms of research aims, and EMPHASIS, ELIXIR and METROFOOD RIs in terms of

research products. In both cases, GRACE-RI (as represented by recent EU-funded research projects on PGRs) was half-ranking for the number of connections, with minimal overlaps with other RIs. However, it is worth underlining that the different maturity levels of the selected RIs may affect their interconnectivity, e.g. a higher number of publications could have been indexed on the WoS platform for the ‘older’ RIs (Supplementary Data Appendix S1). Nonetheless, the above analyses revealed a distinct grouping of the GRACE ‘proxy’ compared with the selected RIs, showing close relationships

## B Research products



Fig. 1. Continued

only with EMPHASIS regarding research aims (Fig. 1A). The results of PCA in terms of research aims confirmed the relationship between EMPHASIS and GRACE-RI and showed a correlation between DiSSCo and LIFEWATCH on the one hand and ELIXIR, MIRRI and METROFOOD on the other (Fig. 2A). The analysis based on research products identified two distinct groups: (1) DiSSCo and LIFEWATCH, and (2) ELIXIR, EMPHASIS and METROFOOD. MIRRI was classified as an outlier probably due to the low number of related papers found. In this context, the positioning of the future GRACE seemed to be mid-way among the other RIs (Fig. 2B). The analysis of PGR-related features and services based on the KPI dataset highlighted the distinctiveness of GRACE among the selected RIs (Figs 1C and 2C) and its potential to develop services that are currently missing in the landscape of EU research infrastructures. GRACE-RI was identified as having unique KPIs related to PGRs, including ‘quality management system for PGR/genebanks’, ‘safety duplications of PGR materials’, ‘multiplication/cultivation/

conservation protocols’, and ‘phytosanitary aspects and regulation’ (Table S2). Furthermore, the results of both network analysis and PCA suggested a set of initiatives that GRACE will undertake (see below) to integrate, enhance and support cutting-edge PGR research in Europe.

The Pearson correlation coefficients calculated between the seven RIs using the three datasets showed many significant correlations (Fig. 3). For research aims, EMPHASIS had the largest number of significant correlations with other RIs, including with GRACE (Fig. 3A). Conversely, no significant correlations were observed between GRACE and other RIs surveyed for both research products and facilities/services (Fig. 3B, C). Overall, the results of the above analysis proved that GRACE has the potential to bridge gaps in the existing RIs by implementing current PGR research in Europe and interconnecting DiSSCo and LIFEWATCH on one side with ELIXIR, EMPHASIS and METROFOOD on the other.



C Facilities/services

The diagram illustrates a complex network of facilities and services, centered around several key entities: **GRACE-RI** (red), **ELIXIR** (blue), **EMPHASIS** (orange), **METRO FOOD** (yellow), **LIFEWATCH** (green), and **MIRRI** (black). These entities are interconnected by a dense web of lines, representing the flow of data, collaboration, and service provision. The nodes are color-coded to match their respective entities. The diagram illustrates a highly integrated and collaborative network of facilities and services, with a central hub-and-spoke structure radiating from the main entities. The connections are dense and complex, indicating a high level of interaction and data exchange between the various components of the network. The overall structure suggests a well-coordinated and interconnected system of facilities and services, designed to support the plant genetic resources domain. The diagram is a visual representation of the complex relationships and interactions between these various entities, highlighting the central role of the main entities and the extensive network of connections that link them to a wide range of other facilities and services. The use of color and size helps to distinguish between the different entities and their relative importance within the network. The overall layout is a dense, interconnected web of nodes and edges, with the main entities acting as central hubs and the surrounding nodes representing a wide range of other facilities and services. The diagram effectively communicates the complexity and interconnectedness of the plant genetic resources domain, showing how various entities are linked together through a network of data, collaboration, and service provision. The use of a network diagram is a powerful way to visualize these complex relationships, allowing for a clear and concise representation of the entire system. The diagram is a valuable tool for understanding the structure and function of the plant genetic resources domain, and for identifying key areas for further research and development. The overall impression is one of a highly organized and interconnected network, with a clear focus on the central entities and their relationships to the rest of the domain. The diagram is a testament to the complexity and interconnectedness of the plant genetic resources domain, and to the importance of collaboration and data exchange in this field.

The potential link between GRACE, ELIXIR and METROFOOD will further implement the use of dedicated EU facilities and resources to achieve the transcriptomic, metabolomic and proteomic characterization of biological tissues from plants having (or not) food and nutritional interest, thus complementing genomic information on these resources. On the other hand, the possible link between GRACE and EMPHASIS will further boost the use of facilities, resources and services for plant phenotyping across Europe. The inclusion of GRACE-RI into the ESFRI landscape will broaden the network of stakeholders for both platforms, ultimately maximizing the results of the investments made.

To streamline and strengthen PGR conservation and use in wider, coherent policies and programmes and to raise awareness of the

The gap analysis showed that the proposed GRACE-RI could address the current gaps in the PGR-related landscape of EU RIs by fostering collaborations and synergies between existing RIs in complementary fields. On the other hand, failure to implement GRACE-RI would deepen the current inefficiency in the European PGR collections, especially considering the new challenges related to climate, environment and food security. It would also fail to create those synergistic effects unfolding from the interaction with the complementary RIs, thus reducing their potential impact on European well-being.



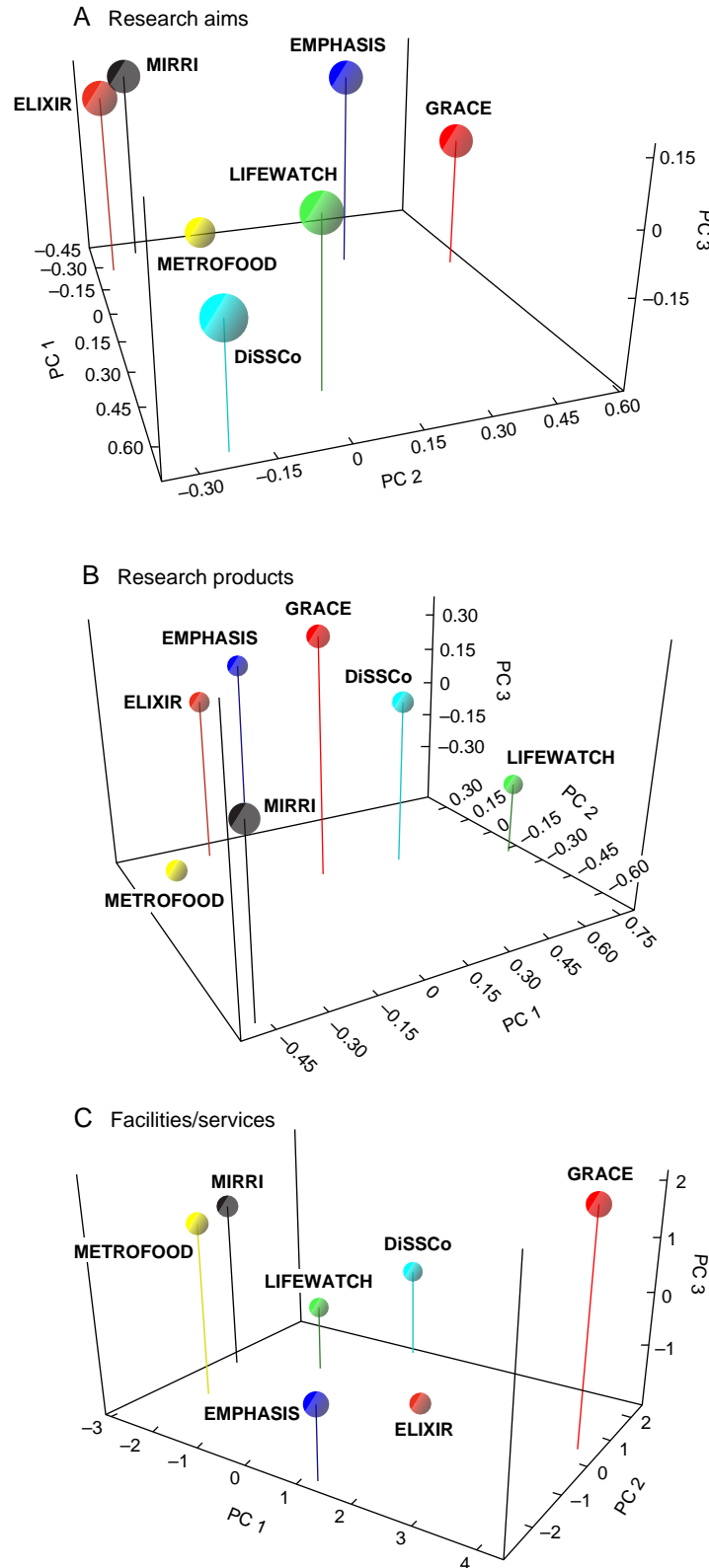


FIG. 2. Principal component analysis (PCA) of the seven selected RIs based on: (A) research aims (frequency of CORDIS-EU FS of 70 projects); (B) research products (WoS categories of 314 papers); (C) service/facilities (scores of 80 KPIs). The first three PC axes accounted for (A) 76.23 %, (B) 80.09 % and (C) 71.27 % of the total variance. RI, research infrastructure; WoS, Web of Science™; KPI, key performance indicator. The analysis was conducted using the software Past 4.02 (Hammer *et al.*, 2001).

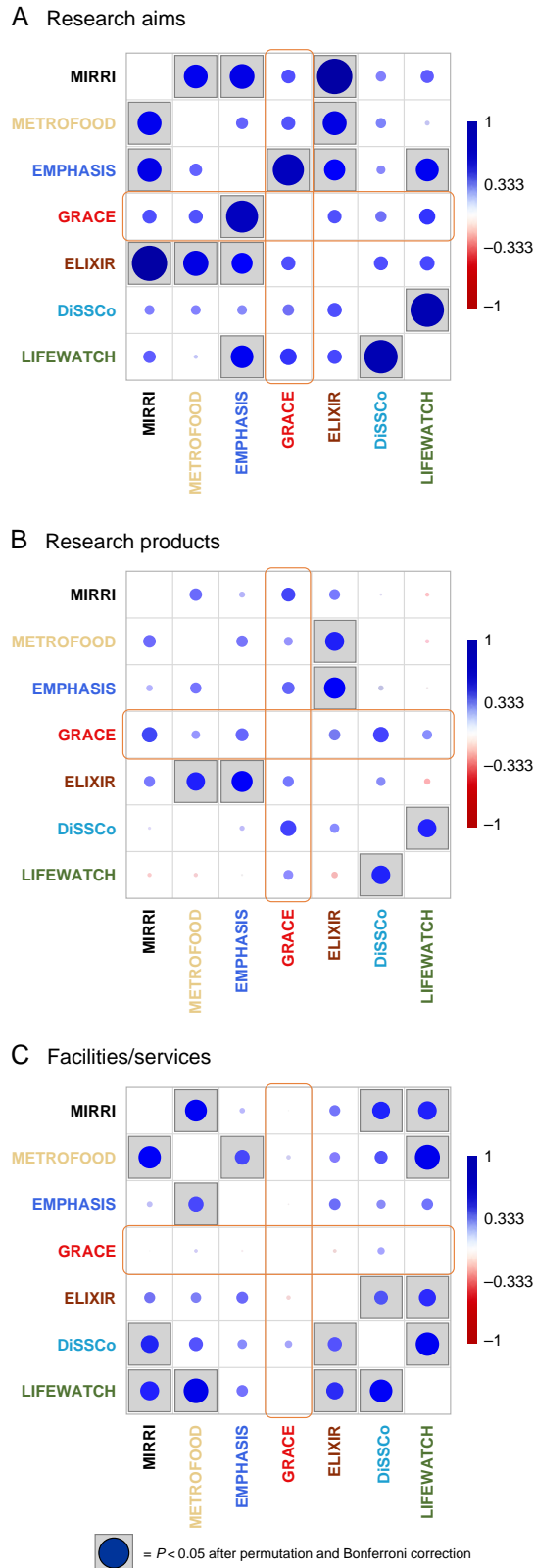


FIG. 3. Pairwise Pearson's correlations between the seven RIs analysed based on: (A) research aims (frequency of CORDIS-EU FS of 70 projects); (B) research products (WoS categories of 314 papers); and (C) features/services (scores of 80 KPIs). Boxed circles indicate significant pairwise correlations ( $P < 0.05$ ) after permutation and Bonferroni's correction. RI, research infrastructure; WoS, Web of Science™; KPI, key performance indicator. The analysis was conducted using the software Past 4.02 (Hammer *et al.*, 2001).

As highlighted by the landscape analysis included in the ESFRI Roadmap 2021, the research infrastructures of the H&F domain represent a pivotal cross-sectorial interaction platform interconnecting the environmental domains, sustainability of food production in the context of climate change and human health. In our perspective, the novel GRACE-RI dedicated to PGRs represents the missing link along the chain connecting health, food and environment, and will further expand interactions within and across existing RIs through an interdisciplinary approach to cross-cutting PGR research.

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## SUPPLEMENTARY DATA

Supplementary data are available at *Annals of Botany* online and consist of the following. Table S1: The complete list of the 70 preparatory/collaborative projects analysed in this study and their parent RIs. Table S2: List of the 80 key performance indicators (KPIs) selected to evaluate the activities of the selected RIs supporting PGR research in Europe. Figure S1: Partition of the preparatory/collaborative RI projects by disciplines derived from the CORDIS-EC Fields of Science (FS). Figure S2: Partition of PGR-related papers retrieved from the Clarivate Web of Science™ platform using the name/acronym (outer circle) of the preparatory/collaborative projects considered in this analysis, and their parent RI (inner circle). Figure S3: Partition of papers ( $N = 314$ ) by disciplines derived from the Web of Science categories.

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