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ORIGINAL RESEARCH

Mind the gap: global targets and strategies for *ex situ* conservation of critically endangered plants

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Abstract

An estimated 45% of plants are threatened with extinction, with those classified as "Critically Endangered" (CR) by the International Union for Conservation of Nature at the highest risk and in urgent need of *ex situ* conservation. We performed a gap analysis of CR plants stored in in the Millennium Seed Bank Partnership (MSBP), a global network spanning 101 countries and territories, to assess their current conservation status and guide future seed collection priorities. The MSBP currently holds 2,507 accessions of 474 CR taxa, representing 0.9% of the 52,874 taxa banked and 7.21% of all CR taxa. While most collections have relatively good general information available (information index = 0.81), key aspects such as viability (viability index = 0.31) and genetic diversity (genetic diversity index = 0.31) remain poorly documented. Only 9.49% of conserved CR taxa have sufficient seed numbers (≥1,050 seeds from ≥50 individuals) for restoration research, and just 5.49% have been collected from ≥5 populations and ≥50 individuals across their native distribution. Overall, 6,120 CR plant taxa remain unbanked, of which 11.58 to 17.17% (depending on model) require alternative conservation methods due to desiccation-intolerant seeds. However, the majority (23.32–68.74% taxa) are likely suitable for traditional seed banking techniques (drying to 15% relative humidity and freezing at -20°C). The desiccation sensitivity of 14.02–65.16% taxa remains unknown, requiring urgent research. Ensuring comprehensive *ex situ* conservation of CR taxa will require strategic investment and capacity building to meet global biodiversity conservation needs.

Keywords Seed banking · Orthodox · Exceptional · Storage behaviour · IUCN · Seeds

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Introduction

We depend on the natural world, and particularly plants, for a wide range of services such as food, shelter, medicine, clothing and oxygen. However, biodiversity is facing a dual crisis of extinction and climate change (Pörtner et al. 2021) with an estimated 45% of plants predicted to be threatened with extinction (Bachman et al. 2024). Given limited time and resources, conservation efforts must be prioritised to maximise impact.

One widely used criterion to prioritise species for conservation is extinction risk, as categorised by the International Union for Conservation of Nature (IUCN)'s Red List of Threatened Species (IUCN 2025). The highest-risk category, Critically Endangered (CR), includes taxa with small populations, restricted geographic range, or a low number of existing mature individuals (IUCN 2021). While IUCN assessments exist for about 66,535 plant taxa, this represents only one in five of the described plant taxa (Kindt 2020; Govaerts et al. 2021). Also, three out of four undescribed taxa are likely threatened and at risk of extinction (Brown et al. 2023a).

Ex situ conservation, which involves maintaining living plants or propagules outside their natural habitats, is a crucial strategy for safeguarding taxa experiencing threats and severe declines in the wild. Seed banking, one of the most widely used *ex situ* conservation methods, generally involves drying seeds to ~15% relative humidity and storing them at −20 °C, providing a cost-effective and long-term means of preserving plant diversity (Li and Pritchard 2009; Breman et al. 2021). Seed banks can store seeds from a broad range of taxa and have the potential to store inter- and intra-specific genetic diversity in a compact space for extended periods (decades to centuries). However, for seed banks to be effective, stored seeds must be legally acquired, accurately identified, genetically representative, viable over time, and available in sufficient quantities for research and restoration (Way 2021).

Despite its advantages, seed banking is not universally applicable, as some taxa (so called "exceptional") do not respond to standard seed banking methods (Pence et al. 2022a, b). Exceptional taxa fall into four categories: (1) taxa with no, inadequate or inaccessible seeds, (2) "desiccation sensitive" or "recalcitrant" seeds that cannot survive drying at 15% relative humidity, (3) "intermediate" seeds that are short-lived under conventional seed banking techniques and lose viability more rapidly under controlled storage at low temperature, and (4) deeply dormant seeds with long germination times. Exceptional taxa require alternative conservation approaches such as cryopreservation, propagation and/or living collections (Breman et al. 2021; Pence et al. 2022a). Between 8 and 66% of plant taxa have been predicted exceptional (Wyse and Dickie 2017; Chau et al. 2019; Colville and Pritchard 2019) and understanding seed storage behaviour is a critical step in developing *ex situ* conservation strategies for critically endangered taxa.

Recognising the urgency of biodiversity conservation, the 2022 Kunming-Montreal Global Biodiversity Framework (GBF) outlined 23 targets to be achieved by 2030. Although seed banking and *ex situ* conservation are not explicitly referenced, seed banking can contribute to several key objectives: halting biodiversity loss (Target 1), restoring degraded ecosystems (Target 2), preventing extinctions and protecting genetic diversity (Target 4), and ensuring equitable sharing of genetic resources (Target 13). The Global Strategy for Plant Conservation (GSPC) 2011–2020, a component of the Convention for Biological Diversity, specifically aimed to secure 75% of threatened taxa in *ex situ* collections with at least 20% available for recovery and restoration (Target 8). The recent upgrade of the GSPC targets for 2030 (CBD COP 16 2024) underscores the need to assess gaps in CR taxa conservation to prioritise conservation efforts.

The Millennium Seed Bank (MSB) of the Royal Botanic Gardens, Kew, established in 2000, is the world's largest *ex situ* seed conservation initiative. The Millennium Seed Bank Partnership (MSBP) is a global network of partners from over 100 countries and territories who collaborate to collect and store seeds in their country of origin and/or at the MSB. To date, the MSBP have collectively conserved 223,876 seed collections representing 52,874 taxa from 190 countries including active and past partners, one-off seed collections and donations, and duplicates from other seed banks (Data Warehouse 2025). The MSBP prioritises taxa that are threatened, endemic, or of ecological, economic, social, cultural or scientific value (so called "useful plants"; see review by Liu et al. 2023). A 2018 review highlighted the MSB's significance as a biodiversity resource but found that only 6% of known CR taxa were conserved at the time (156 taxa out of 2640 reported in IUCN; Liu et al. 2018).

The aim of this work is to assess the current *ex situ* conservation status of CR plants across the MSBP, covering Angiosperms, Bryophytes, Ferns, Gymnosperms, Lycophytes, and Marchantiophytes. Specifically, we (i) compile data from multiple sources to identify taxonomic gaps in the collections, (ii) develop three indices to evaluate data availability, germinability and genetic representation within collections. We then (iii) establish two key collection targets: (a) ensuring a sufficient seed supply for small-scale reintroduction and restoration and (b) capturing genetic diversity through sufficient native range collections. Finally, we (iv) assess seed storage behaviour of unbanked CR taxa (orthodox, intermediate and exceptional) and map their distribution, and (v) summarise relevant Access and Benefit Sharing (ABS) measures.

Materials and methods

Data sources and name matching

We compiled data for CR taxa from two sources: (i) plants listed as Critically Endangered (CR) by the IUCN through conservation assessments hereafter named CR_{iucn} (IUCN accessed 19 September 2025), (ii) plants predicted to be CR through modelling hereafter named CR_{pred} (Bachman et al. 2024). The term CR is used throughout to designate the combined CR_{iucn} and CR_{pred} dataset. To assess how many CR were banked by the MSBP, we compiled data on viable collections of plants from the MSBP Data Warehouse (Data Warehouse 2025). Finally, we downloaded a published list of exceptional species (Pence et al. 2022a; Cincinnati Zoo & Botanical Garden; accessed 19 September 2025) to determine which CR might require cryopreservation.

All datasets included plants named at family, genus, species, subspecies, and variety level. Taxa named at genus level only (or above) were removed from all datasets prior to any analysis. Because all datasets had differences in nomenclature and taxonomic concepts, we used the R package *rWCVP* to interface with RBG Kew's World Checklist of Vascular Plants (WCVP v13; accessed 19 September 2025) in Plants of the World Online as the taxonomic backbone that unified all Tracheophyta names (Govaerts et al. 2021; Brown et al. 2023b). We followed the protocol of Nic Lughadha et al. (2020) for name matching. We allowed for both exact and fuzzy matching. For fuzzy matching, we set a strict edit distance ≤ 0.9 to restrict matching to names with no more than ~2 letters different. No restrictions were set for author name matching, because not all taxa had author names. Where multiple matches were returned, we first attempted to match the dataset name to an accepted WCVP taxon name. When WCVP returned multiple matches without an accepted name, we used a synonym identified by WCVP if available. A synonym is an alternative (but valid) scientific name that can be mapped to an accepted scientific name. If multiple synonyms were identified by WCVP, meaning the taxon name could be mapped to multiple accepted names (for example because of taxonomic splits), we used a homotypic synonym identified by WCVP if available. A homotypic synonym is a synonym that is based on the same type specimen as the accepted name and therefore represents a purely nomenclatural change (e.g. see Fig. 3 in Brown et al. 2023). If a taxon name had multiple exact accepted names matched, but no exact author match (when author name was available), we used the WCVP name with the most similar author name. All other names that did not match these criteria then went through another cycle of name matching against the World Flora Online (WFO) using the R package *WorldFlora* (Kindt 2020; WFO 2025 v.2023.12; accessed September 2025). This was particularly important for non-Vascular plants that were listed as CR by the IUCN. Again, we allowed for both exact and fuzzy matching, setting a strict limit of no more than 2 different letters for the matching, first finding exact matches, and where multiple matches were found, then using accepted names and then synonyms. Any names that were not matched against WCVP or WFO were marked as "unmatched". Where name splits or merges occurred, we kept both the original database taxon name and the name-matched taxon name (Appendix S1).

Taxonomic gaps

Once name matching was completed, we developed family level statistics to evaluate the taxonomic gaps in the collections. We mapped all taxon names to their families using rWCVP and WFO during the name-matching step. This allowed us to use family-level matching to map all CR collections to their families in the *V.PhyloMaker2* vascular plant family tree (Jin and Qian 2022). We used the *ggtree* package to plot family-level banking statistics (Xu et al. 2022). While our dataset included 37 non-vascular plants that could not be plotted, these represented only 0.5% of CR taxa. Summary statistics for these taxa are available in Appendices S2 and S3.

Collection quality indexes

We used a scoring approach to evaluate the quality of collections (or accessions, both are used interchangeably in this study) of CR taxa in the MSBP by establishing three indices (information, viability and genetic diversity indices), each with sub-indices estimated from a set of variables. Each variable was measured by adopting a numerical scoring system with a scale between 0 (low) and 1 (high), followed by estimating the scores of each variable and sub-index, either by summing, averaging or combining values (see below for full details). This approach allowed flexibility in scoring, ensuring that each variable was evaluated as fully as possible given the data available. The indices are described below with their variables and the scores assigned are indicated within brackets. An overall quality index was estimated as the mean of the three indices.

Information index

To ensure seed banks maintain useful repositories of seeds for future conservation, reintroduction and restoration programs and research, it is vital to capture critical information such as precise geographic origin of harvested seeds, accurate identification of taxon and the year of seed collection. We measured three sub-indices:

- *Geographic sub-index (original provenance listed with)*: latitude and longitude coordinates (assigned as score of 1), locality description without coordinates (0.75), country/territory information only (0.5) or no information (0);
- *Taxonomic sub-index (certainty level of taxonomic identity):* if the accession has been assigned a taxonomically accepted name (1), if the accession has been given a name that could not be matched to an accepted name, or not assigned a name (0); and.
- *Year (of collection) sub-index:* year recorded (1) or no information (0).

Viability index

For taxon reintroduction or restoration projects, an ample quantity of viable seeds is essential to establish plant populations that thrive and reproduce in the wild. Therefore, seed banks need an adequate supply of seeds to conduct viability assessments, to research and develop germination and propagation protocols for restoration, without depleting the original collection. We measured three sub-indices:

- *Count sub-index (current seed quantity):* reflects the quantity of seeds in that collection (or accession) at the time of study, whether it was estimated (1) or not (0);
- *Adjusted count sub-index (adjusted current seed quantity):* reflects the quantity of potentially viable or usable seeds at the time of study, whether it was estimated (1) or not (0). “Adjusted seed count” represents the quantity of potentially viable seed and is calculated from the proportion of full seeds visible in an x-ray of 20–50 seeds from a collection, and is standard practice at the MSB, but less common at other seed banks. This number allows us to adjust the baseline number of seeds that are unlikely to germinate during testing because of the presence of empty or infested seeds.
- *Germination sub-index (viability assessment):* whether the collection has been germination tested in the last 15 years (1), if its germination test was older than 15 years (0.5) or if it has not been tested (0). Germination testing allows us to develop protocols for breaking seed dormancy, and to assess the potential number of viable seeds in the collections (although if the germination protocol is not yet optimal, not all viable seeds will germinate, and germination needs to be assessed under different environmental conditions).

Genetic diversity index

Genetically representative collections are essential for ensuring that future generations can access the full genetic toolkit necessary to address challenges like disease, climate change, or agricultural demands as it allows the resilience, adaptability, and usefulness of the seeds for future breeding, restoration, and research. In the absence of true genetic analysis, we used a surrogate method to evaluate the potential genetic diversity within and among CR taxa. The 'Genetic diversity' index was calculated differently depending on whether the collection originated from cultivated or wild materials. The cultivation index was used as the genetic diversity index if the collection came from a cultivated source, and the wild-origin index was used as the genetic diversity index if the collection was of wild origin.

- *If cultivated, we used a Cultivation sub-index:* whether the relation to wild parent and isolation technique (the method used to ensure that plants bred without unintended cross pollination, maintaining purity of specific traits) are known (1), only one of the previous variables is known (0.5), and no information (0).
- *If wild, we used Wild Origin sub-index:* three additional variables were considered to evaluate whether seeds were harvested from 50 mature individuals (important consideration for clonal taxa) and if not, to ensure seeds were harvested from all mature individuals in the sampled population. These variables were the number of plants sampled (plant sampled), number of mature plants found in the sampled area (plant total), and the percentage of population giving seeds (plant seed). Scores were assigned to combinations of variables if these data were recorded for a given collection: all three (1), plant sampled and plant total or plant seed (0.8), plant sampled (0.6), plant total and plant seed (0.4), plant total or plant seed (0.2) or no information (0).

Seed banking targets

We also define two seed banking targets: A "recovery target" (target 1) and a "geographic target" (target 2). Both seed banking targets are defined to allow us to measure our progress towards another set of targets, the GBF targets, of restoring degraded ecosystems (GBF target 2), and protecting protect genetic diversity (GBF target 4). Indeed, the recovery target is achieved when the minimum number of seed is available to carry out restoration. The geographic target is achieved when seed are collected from enough populations across the native range of a taxon.

Recovery targets (Target 1)

Target 1 is a "recovery target" which aims to capture the restoration potential of the collection. According to MSB standard operating procedures, when a collection has over 1,050 seeds it can be used in restoration, given the seeds have been collected from enough parent individuals to avoid inbreeding, usually over 50 individuals (Way 2003, 2021; Menges et al. 2004; FAO 2014; CPC 2020; MSBP 2022).

The 1,050 number is estimated from the adjusted seed count (see Adjusted count sub-index for description). This number is derived from using 500 seeds as a base collection as the absolute minimum number of seeds that can be used to re-establish a population if lost in the wild (Way 2003; FAO 2014; MSBP 2022). Additionally, 100 seeds are needed for developing a germination protocol for the taxon, with an additional 50 seeds used for an initial germination test to establish the viability of the collection (MSBP 2022). This leaves 400 remaining seeds as a buffer, for monitoring or for research. This might involve further germination tests, developing cryopreservation protocols, boosting seed supply by growing and cross-pollinating plants of known maternal lineages, trialling nursery or field experiments to determine optimal growing conditions and field planting protocols etc… In such cases, 50 seeds are typically used per experiment, although this can vary depending on requirements.

Collecting from 50 individuals is derived from work on crop species suggesting that 30 or 59 individuals should be sampled to maintain genetic integrity, if the population consists of out-breeders or in-breeders respectively (Marshall and Brown 1975). Note however that <50 individuals are sampled when the population size is smaller than 50, or when fewer than 50 individuals are producing seed at the time of collection – as is often the case for CR taxa. In such cases, the recommendation is to harvest no more than 20% of available seeds so that the population remains viable (CPC 2020; MSBP 2022). Although 50 individuals are too small a sample size to produce enough seed to support large-scale restoration or research programmes (Hoban and Schlarbaum 2014; Hoban and Strand 2015), the importance of these CR collections for such uses cannot be overstated. Small samples are still vital to small-scale species reintroduction and restoration research, given that sufficient genetic integrity of wild population is captured by harvesting at least 50 individual plants.

The recovery target was therefore met if 1050 seeds from 50 individuals were collected and was first considered at the collection level, then at a taxon and country level (by pooling collections by taxon, or by taxon per country). Note that for five accessions the number of individuals was given non-numerically, such as, “>100” or “20–500”. For such cases, we manually converted them to the minimum number of know individuals, such as “>100” to “100”, “200–500” to “200”, however, we kept the values above the 50 individual threshold, for instance, converting “25–50” or “11–100” to “50”. This way, our estimates meet the target but are not overestimating the number of parent plants collected from. These were converted from non-numeric to numeric at the collection level, and then collections were pooled by taxon, or pooled by taxon per country.

Geographic target (Target 2)

Target 2 is a “geographic target” and aims to capture whether ≥5 collections have been made across the native range of the taxon and from enough (≥50) individuals. Different populations of the same taxon may have unique adaptations to their local environments, so collecting seeds from multiple locations is essential for capturing this genetic diversity and maintaining adaptability under changing environmental conditions.

There are two ways we capture whether the collections of a CR taxon have enough genetic diversity from across their native range. Firstly, we use the constraint that at least five collections are made, as collections often represent separate populations, and because these are estimated to be sufficient to capture approximately 75% of alleles (Griffith et al. 2015; CPC 2020) and align with spatial sampling recommendations of Hoban and Schlarbaum (2014). In some cases, however, CR taxa can only occur in one population in one location, whereby only 20% of seeds should be collected to avoid overharvesting and to sustain viability of the wild population (MSBP 2022). In such cases, 5 repeated collections over different years are still recommended to capture the genetic variation of that one population (Hoban and Schlarbaum 2014; CPC 2020).

Other CR are more widespread, occurring over many countries or continents. We therefore include a second constraint, that collections be made in all countries of their native range to capture their spatial genetic variation. Occurrence data are commonly withheld for CR taxa due to the threat of poaching, and where available are often too sparse to accurately map distributions. To estimate each taxon's native distribution, we therefore used the *rWCVP* package (Govaerts et al. 2021; Brown et al. 2023b) as the most complete expert-curated list of native "botanical countries" that CR taxa are known to occur in. "Botanical countries" are defined as Level 3 of the World Geographical Scheme for Recording Plant Distributions (Brummitt et al. 2001; Brown et al. 2023b).

We first assigned seed collections to native botanical countries using GPS coordinates. Where no coordinates were available, we used the country where the collection was made to map it to a botanical country using a country mapping (Appendix S4). Name conflicts were manually reassigned. Indeed, not all botanical countries match true political countries. For example, the botanical country "France" includes true countries "France" and "Monaco". However, "Corse" is its own botanical country, although "Corsica" is a territorial collectivity of "France". In such cases, collections made in native botanical country "Corse" would be marked as "occurring in their native area" and would also be assigned political country "France". However, if the same taxon was collected in botanical country "France" (e.g. where it might be popular in horticulture) but was outside the native range of the taxon, then it would be recorded and labelled as "outside of native range" in political country "France". While this does mean that more records are assigned to their metropole as a limitation of data availability, the metropole is also often responsible for coordinating and funding seed collections, and highlighting gaps in collections across their overseas countries, territories or states can help highlight funding gaps.

Conversely, countries like Australia and Brazil consist of multiple botanical countries. In these cases, a record was marked as occurring in its native range if it was collected in its native botanical country. However, if it was collected in a non-native botanical country, it was marked as collected "outside of native range", even though it might have been collected in the correct political country. Finally, if it was impossible to determine whether a collection was made in its native botanical country of not, then it was marked as "unknown".

Thus, if a taxon was collected in all countries of its native range (i.e. proportion equal to 1) and from ≥ 50 individuals and with ≥ 5 accessions, then the geographic target was met. The geographic target was also estimated at taxon and country level by pooling collections per taxon, and then per taxon per country.

Seed storage behaviour

Conventional seed banking methodologies are proposed for desiccation and freezing tolerant taxa (hereafter termed "orthodox") not exhibiting biological traits identified as problematic for seed banking (Wyse and Dickie 2017). In contrast, cryopreservation and/or living collection strategies are proposed when taxa are exceptional (Pence et al. 2022b) meaning they are desiccation intolerant ("recalcitrant") and/or have biological traits impeding their storage using traditional seed banking methods.

To determine the suitability of CR_{iucn} and CR_{pred} taxa for conventional seed banking, we first extracted the seed storage behaviour from the Seed Information Database (SID; Society for Ecological Restoration 2024) which describes storage behaviour according to Hong et al. (1998). For taxa that were not listed in SID, we then used the list of exceptional taxa in Pence et al. (2022a). For taxa not listed in either SID or Pence et al. (2022a), we used expert information and a literature review (Appendix S3; Ammons 1940; Allsopp 1952; Lloyd and Klekowski 1970; Endress 1974; Tryon and Tryon 1982; Sharp et al. 1988; Øllgaard 1990; Pence 2000; Pedrotti 2001; Smith 2004; Lai et al. 2008; de León et al. 2008; Chung et al. 2010; Sundue et al. 2011; Olsson et al. 2012; Ballesteros et al. 2012, 2019, 2020; He et al. 2012; Li et al. 2013; Wei and Zhang 2014; nzflora 2017; Ramos Giacosa et al. 2017; Pritchard et al. 2017; Yañez et al. 2017; Bakalin 2018; Chau et al. 2019). In addition, to infer the storage behaviour of ferns and bryophytes based on the chlorophyllous nature of their spores we used expert guidance (Ballesteros et al. 2020). Chlorophyllous spores are known to be short lived in storage (< 10 years when stored at −20 C) and therefore considered "intermediate", while non-chlorophyllous spores are more likely to have a longer life span (> 10 years when stored at −20 C) in storage and are considered "orthodox" (Ballesteros et al. 2019, 2020). We use these general trends for the purpose of our study; however, it is important to note that there are many exceptions to these patterns, and more research is needed in this area (Ballesteros et al. 2019, 2020).

We also used the storage predictor tool from Wyse and Dickie (2017) to predict the probability of the taxon being recalcitrant (*pR*). We assumed that if $pR \leq 0.3$ the taxon's seeds are orthodox, if $pR \geq 0.7$ the taxon's seeds are recalcitrant, and therefore also exceptional, and that if $0.3 < pR < 0.7$ the storage behaviour of the taxon is unknown. Furthermore, the seed predictor tool estimates *pR* at different taxonomic levels based on available data making some taxon predictions more reliable than others (e.g. *pR* estimated at species or genus level is more reliable than *pR* estimated at family level).

Each taxon could therefore have multiple storage prediction estimates from different sources, all including some degree of uncertainty, whether through *pR* with the storage predictor tool, or through prediction categories such as "probably orthodox" in the databases. We therefore developed two prediction categories: those whose storage behaviour is more certain (hereafter named "conservative" estimate), and those whose behaviour is less certain (hereafter named "likely" estimate). For the "conservative" estimate we first used records with clear storage behaviour documented (e.g. "orthodox") from SID, then from the exceptional species list, then from the literature review, and then *pR* estimated at species or genus level, with everything else documented as "unknown". For the "likely" estimate we did the same as with the "conservative estimate", and then also added records with less certain storage behaviour documented (e.g. "probably orthodox") from SID, then from the exceptional species list, then from the literature review, and then *pR* estimated at any level, with everything else documented as "unknown".

Access and benefit sharing

Following best practice seed conservation standards (FAO 2014; CPC 2020; Way 2021), the risk of loss of an *ex situ* seed collection can be mitigated by duplicating part of the collection to a second independent seed bank. Where facilities are not available locally, seeds can be stored in another country and be available to replenish collections if lost at another location.

However, the international transfer of seed collections between seedbanks is governed by national and international access and benefit sharing (ABS) measures. Namely, the Nagoya Protocol on "Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization" regulates the transfer of genetic material (and therefore seeds) between parties (CBD 2025). To assess the potential for sharing CR seed collections for conservation purposes between MSBP partners, we counted the collections from countries and nations with (i) "Party status to the Nagoya protocol", (ii) publication of access and benefit sharing "National Focal Point" (NFP), (iii) publication of a "Competent National Authority" (CNA) and (iv) records of "Internationally Recognized Certificates of Compliance" (IRCC; data downloaded from absch.cbd.int, accessed 2 December 2024). For more information, NFP is "a designated contact point for each party, responsible for facilitating information, liaising with the CBD Secretariat, and supporting access and benefit-sharing measures related to genetic resources". CNAs are bodies established by governments and are responsible for granting access to users of their genetic resources and representing providers on a local or national levels. IRCC provide "proof that genetic resources have been accessed and utilized in accordance with the Nagoya Protocol and the national laws of the provider country".

Results

Data sources and name matching

The September 2025 version of the IUCN Red List database consisted of 6,520 entries of CR_{iucn} plant taxa names including genus, species, subspecies and varieties at the time of download. IUCN taxon names were compared to those accepted in WCPV. Most taxon names used in the IUCN Red List (98.08%) matched WCVP (6,395 names of which 91.29% were accepted, 3.3% synonyms and 5.19% homotypic synonym). For the remaining 85 names, 66 names were accepted in WFO, with only 19 remaining unresolved. In total, 99.8% of IUCN names were matched to 6,432 taxon names at species, subspecies and variety level. These data include 291 assessments predating 2000, 463 from 2000 to 2010, 2,023 from 2010 to 2020 and 3,703 after 2020.

The list of taxa with IUCN predictions (Bachman et al. 2024) consisted of an additional 165 CR_{pred} taxa that were not listed by the IUCN, all of which were matched to 165 WCVP names. Therefore, the final dataset of critically endangered taxon names ($CR_{iucn} + CR_{pred}$) included 6,594 taxa (10 Marchantiophytes, 17 Lycophytes, 27 Bryophytes, 88 Gymnosperms, 96 Ferns and 6,357 Angiosperms; Appendix S1).

The September 2025 list of exceptional species (Pence et al. 2022a, b) included 23,792 names, of which 22,586 were matched to 22,588 names in WCVP (none in WFO), resulting 94.93% match rate. Similarly, the September 2025 version of the Millennium Seed Bank Partnership (MSBP) Data Warehouse database consisted of 223,876 accessions of 56,755 names. Of these names, 54,405 were matched to 52,637 names in WCVP (99.55%) and 348 against WFO (0.66%). Once taxonomic name changes are accounted for, the final number of names in collections held across the MSBP was 52,874 for 220,284 accessions (Appendix S2).

Collection gaps

Taxonomic gaps

Once name matches were performed, we were able to match the MSBP dataset against the IUCN (CR_{iucn}) and IUCN predictions (CR_{pred}) datasets. We found that in total, the MSBP contained 2,507 collections of 467 CR_{iucn} and seven CR_{pred} taxa, representing only 0.9% of the total number of 52,874 taxa banked in the MSBP and 1.14% of the total number of 220,284 MSBP collections. Only 7.19% of CR are banked by the MSBP. Those that are banked represent a wide taxonomic range across 96 plant families and 41 orders mostly belonging to angiosperms (456 taxa; Fig. 1), and a lower representation of gymnosperms (11), Lycophytes (2) and ferns (5 taxa). This represents 12.5% of CR Lycophytes banked across the MSBP, 12.5% of CR Gymnosperms, 7.17% of CR Angiosperms, and 5.21% of CR Ferns. Most CR taxa are scattered across the vascular plants (Fig. 1). Some plant families contained higher numbers of CR plants, such as Rubiaceae (428 CR taxa), Myrtaceae (343), Fabaceae (322), Lauraceae (315), Asteraceae (284) and Orchidaceae (274; Fig. 1).

Families with the highest numbers of banked CR are *Proteaceae* (113 banked CR taxa representing 55.75% of family banked), *Rosaceae* (101, 38.61%), *Asteraceae* (284, 12.68%), *Fabaceae* (322, 10.56%), *Orchidaceae* (274, 9.49%), *Myrtaceae* (182, 9.89%). Families that are 100% CR banked include *Byblidaceae* (1 CR taxon in family), *Cistaceae* (3), *Frankeniaceae* (1), *Kewaceae* (1), *Moringaceae* (1), *Nymphaeaceae* (1), *Onagraceae* (1), *Paulowniaceae* (1), *Stylidiaceae* (1) which are families with few CR. Overall, 50.62% of all families (244 families) have at least one CR taxon in them, and of these families with CR taxa 39.34% have at least one banked (and 19.92% of all families have at least one taxon banked; Fig. 1). Only 6.15% of families (15 families) with CR have 50% of their CR taxa banked, representing 3.11% of all families (Fig. 1). Finally, 148 (60.66%) families with CR taxa (30.71% of all families) remain entirely unbanked.

Spatial gaps

The countries with over 50% of their CR taxa banked are Australia (69 banked taxa), Spain (69), the United Kingdom (22), Namibia (8) and Saint Helena (23; Fig. 2A). The 6,429 CR_{iucn} and 165 CR_{pred} taxa were mapped to 166 and 37 countries respectively, totalling 6,594 CR taxa in 166 countries (Figs. 2A and S2; Appendix S5). On the lower limit, 48 countries had fewer than 10 unbanked CR_{iucn} and CR_{pred} taxa, while on the upper limit, 17 countries had over 150 CR unbanked taxa including Madagascar (8.36% of all CR taxa), United States (6.93%), the Indonesia (6.07%), Philippines (5.73%), Ecuador (4.87%), Brazil (4.52%), Mexico (4.31%), Colombia (4.25%), Papua New Guinea (3.79%), Cameroon (2.82%), Tanzania (2.71%) and China (2.65%) South Africa (2.65%, Peru (2.61%), India (2.53%), New Caledonia (2.53%) and Cuba (2.40%; Figs. 2A and S2; Appendix S5).

Collection quality indexes

We quantified the information available in the MSBP database into three main indices: an information index, a viability index and a genetic index (Fig. 3; Appendix S2). We found a mean of 0.81 (0.33–1.0.33.0) for the information index, 0.31 (0.0–1.0) for the viability

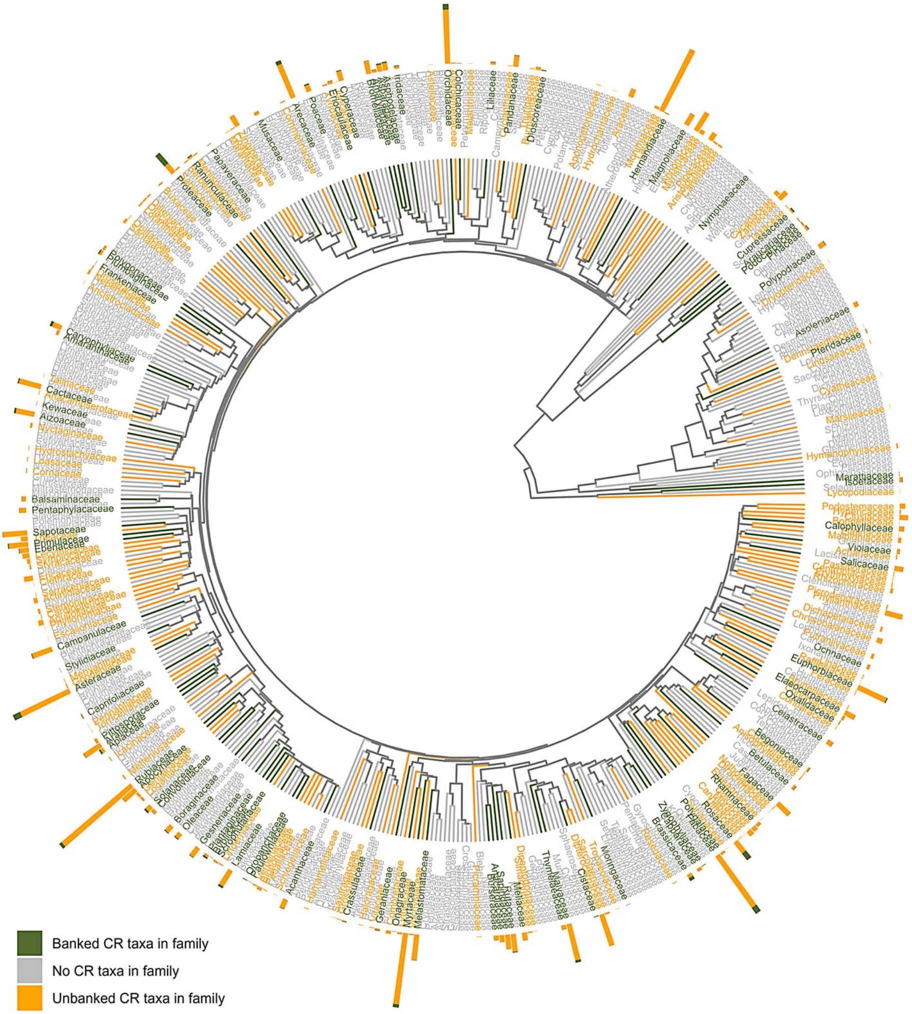

Fig. 1 Phylogenetic tree representing the numbers of banked and unbanked CR vascular plant taxa by family. Green represents the percentage CR taxa banked in each family, yellow the percentage unbanked, and grey the families with no taxa listed under the IUCN as CR, and taxa predicted as CR

index, and 0.31 (0.0–1.0) for the genetic diversity index. The mean overall index value was 0.48 (0.22–1.0.22.0), suggesting that although some data are present, many are still missing (Fig. 3).

Information index

The information index is broken down into a geographic, taxonomic and year index. For the geographic index, 50.34% of accessions of CR taxa have coordinates (score = 1), 36.68% have locality information but no coordinates (score = 0.75), 10.63% have country information only (score = 0.5) and 2.35% have no information (score = 0). The mean geographic

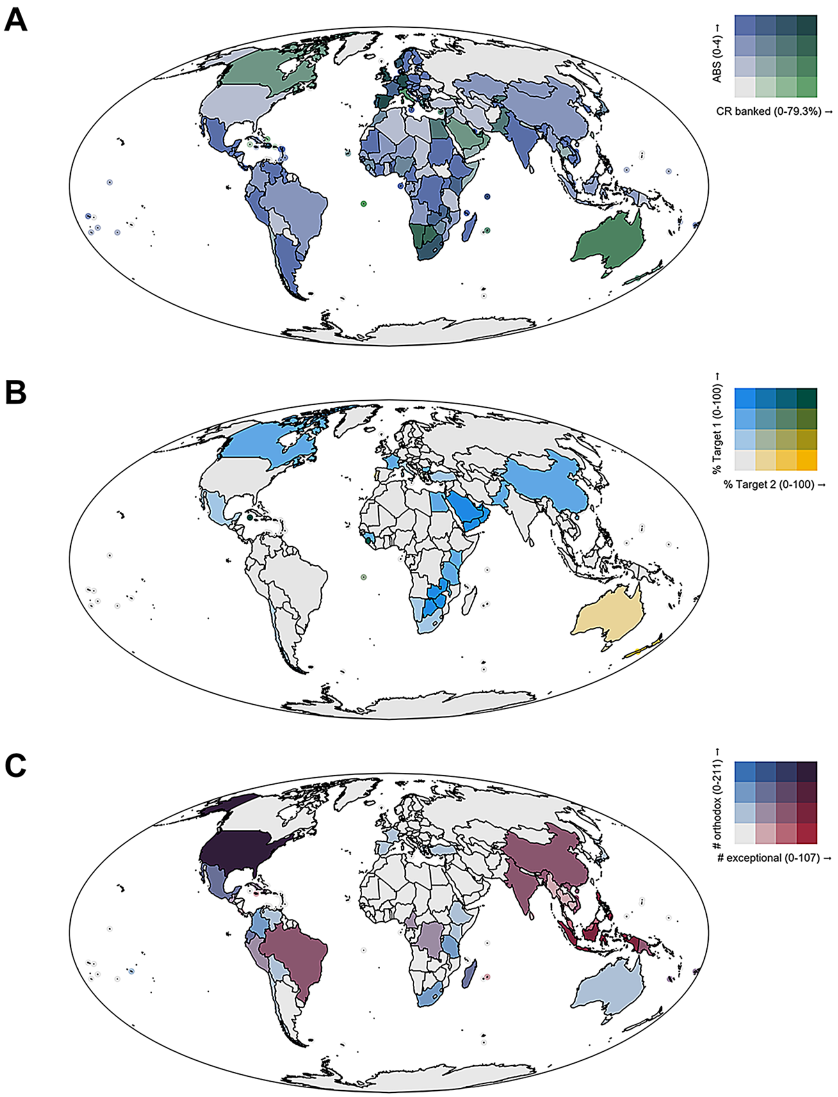

Fig. 2 Three maps. (**A**) Bivariate map of the percentage banked CR taxa against the number of Access and Benefit Sharing (ABS) measures per country (National Focal Point, Competent National Authority, Internationally Recognized Certificates Compliance and/or Interim National Reports Implementing Nagoya Protocol). Countries in green have a high percentage banked CR (>40% United Arab Emirates, Australia, Botswana, Germany, Spain, United Kingdom, Italy and Namibia), in blue all 4 ABS measures are present (Mexico, Guatemala, Panama, Peru, Dominican Republic, British Virgin Islands, Guyana, Argentina, Uruguay, Ivory Coast, Benin, France, Cameroon, Belarus, Bulgaria, Ethiopia, Kenya, India, Laos and Vietnam), and therefore dark green indicates a high proportion of banked CR taxa that can be shared and used in conservation projects (Spain). (**B**) Bivariate map of the percentage of banked CR taxa meeting the recovery (blue) and geographic (yellow) targets per country. Target 1 (the recovery target) is met when a taxon has over 1,050 seeds banked from 50 individuals while target 2 (the geographic target) is met when a taxon has been collected in 100% of its range from 5 populations and 50 individuals in country. (**C**) Bivariate map of the number of unbanked CR taxa that are orthodox (blue) or recalcitrant (red) based on the "conservative" estimate. The largest numbers of orthodox CR seed taxa to be collected are in United States, Madagascar, South Africa, Ecuador, Mexico, Colombia and Tanzania (>50 taxa), while most recalcitrant CR taxa that need collecting are in Indonesia, Philippines and the United States (>50 taxa)

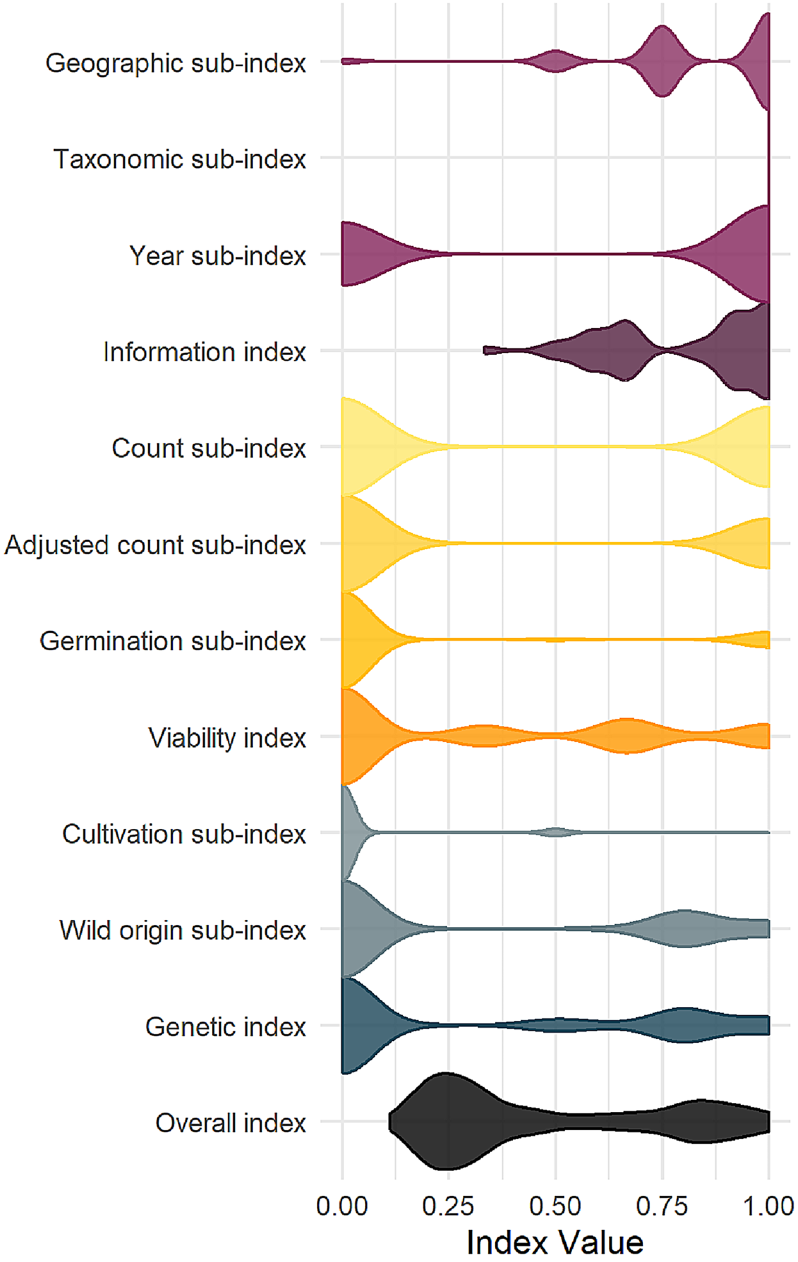

Fig. 3 Violin plot visualising the distribution of accessions for each data quality score across the Millenium Seed Bank partnership. We use indices to separate the quality of the data out into an Information index (calculated from Geographic, Taxonomic and Year sub-indices), a Viability index (calculated from Count, Adjusted Count and Germination sub-indices) and a Genetic index (calculated from Cultivation and Wild origin sub-indices). Each index is estimated individually, and the overall index is calculated from the mean of all indices

index is 0.83. For the taxonomic index, 100% of accessions of CR taxa are matched to WCVP or WPO (score = 1). For the year index, 60.49% of CR accessions have data on year of collection (score = 1) and 39.51% have none (score = 0). The mean year index is 0.6 (Fig. 3).

Viability index

The viability index is broken down into a count, adjusted count and germination index. For the count index, 45.16% of banked CR had a current count available (score = 1) and 54.84% do not (score = 0). The mean count index is 0.45. For the adjusted count index (estimated from the proportion of full seeds in collections based on x-rays), 33.77% have adjusted counts available (score = 1) and the remaining 66.23% have none (score = 0), with a mean count index of 0.34. For the germination index, 13.26% of banked CR have recently been germination tested (score = 1), 1.71% have been germination tested over 15 years ago (score = 0.5), and the remaining 85.03% have not been germination tested (score = 0). The mean germination index is 0.14.

More specifically, only 15% of the 2,507 collections have been germination tested. Of those tested, 74.6% have germination values > 75% for their best test, including 128 collections with 100% germination. The remaining 183 collections had a germination percentage varying between 1 and 99% with a mean of 68.52%, indicating they may not all be viable, or that the right germination conditions have not yet been identified.

Genetic diversity index

The genetic diversity index is broken down into a cultivation and wild origin index. For the cultivation index, 190 (7.57%) accessions came from cultivated collections. Of these cultivated accessions, only 7.37% had data on the relation to parent and isolation technique information (score = 1), but 92.63% had information on either data on relation to parent or on isolation technique available (score = 0.5). However, because only a small proportion of collections were from cultivation sources, we found that overall, only 0.56% have data on the relation to parent and isolation technique information are available (score = 1), 7.01% have either data on relation to parent or on isolation technique available (score = 0.5) and 92.43% have no information available (score = 0). The mean cultivation index is 0.04. For the wild origin index, 10.12% have data on the number of plants that were collected from (hereafter "sampled"), the total number plants in the population ("total") and the total number of individuals with seeds in the population ("seed"; score = 1), 23.34% have "sampled" and "total", or "seed" (score = 0.8), 1.51% have "sampled" (score = 0.6), 0.68% have "total" or "seed" (score = 0.2) and 64.36% have no information (score = 0). The mean wild origin index is 0.3.

Seed banking targets

Recovery target (Target 1)

Of the 474 banked CR taxa, only 34 (7.17%) taxa with 44 individual collections met the recovery target (≥ 1,050 seeds collected from ≥ 50 individuals; Appendix S2). However, once multiple collections were merged per taxon, 45 (9.49%) taxa met the recovery target. More specifically, 152 (32.07%) taxa had over 1,050 seeds and 55 (11.6%) were recorded as sampled from at least 50 different individuals, with 234 (49.37%) taxa with no seed counts available, and 346 (72.78%) with no information on how many individuals were collected from in the wild. Overall, 6,120 CR taxa still need to be banked, with 6,560CR taxa still needing 1,050 seeds from at least 50 different plants stored *ex situ* to achieve the recovery target, including 440 banked CR taxa.

Geographic target (Target 2)

We found that only 16 (3.38%) banked CR taxa with 37 individual collections met the geographic target (collected in 100% of the countries of their range, from ≥5 collections and from ≥50 individuals). When target 2 is broken down, we find that 344 (72.57%) of collections are collected over their native range and 122 (25.74%) have at least 5 collections inside at least part of their native range. Once collections were pooled by taxon, 26 banked CR taxa (5.49%) meet the geographic target. More specifically, 344 CR taxa (72.57%) are collected from 100% of the countries in their range and 122 CR taxa (25.74%) were had at least 5 collections in their native range. Although very few collections meet target 2, the average proportion of countries collected from across the range of a banked CR taxa is 87.33%. Overall, 96.62% banked CR taxa still need additional collections to meet the geographic target. Thus, a total of 6,578 CR taxa does not meet the geographic target, including 458 banked CR taxa.

Spatial distribution of recovery and geographic targets

The countries with over 90% of banked CR taxa meeting the recovery target were Botswana, Cayman Islands, Oman, Saudi Arabia, Sierra Leone, United Arab Emirates, Yemen, Zambia, Zimbabwe (Fig. 2B; Appendix S5), with as many as 202 countries with less than 10% of their banked CR taxa meeting the recovery target (Fig. 2B). In contrast, countries with over 10% of banked CR taxa meeting the geographic target included Australia, Cayman Islands, New Zealand, Portugal, Saint Helena and Sierra Leone (Fig. 2B), with 225 countries with fewer than 10% of their banked CR taxa meeting the geographic target (Fig. 2B). Only the Cayman Islands and Sierra Leone had 100% of banked CR meeting both recovery and geographic targets.

Seed storage behaviour

Seed storage behaviour data were compiled for 6,455 CR taxa overall, of which 120 from the exceptional species list, 350 from the Seed Information Database (SID 2025), and 425 from literature review. Additionally, we estimated storage behaviour for 6,319 CR taxa using the desiccation sensitivity predictor tool (Wyse and Dickie 2017). Multiple estimates per taxon from different sources were compiled into a single “conservative” (Fig. 4A) and “likely” (Fig. 4B) estimate of storage behaviour based on the certainty of the prediction.

The “conservative” estimate included 2,202 unbanked CR of which 85 (3.86%) came from the exceptional species list, 33 (1.5%) came from SID, 234 (10.63%) from the literature, and 1,850 (84.01%) from the predictor tool, of which 1,835 (83.33%) were estimated

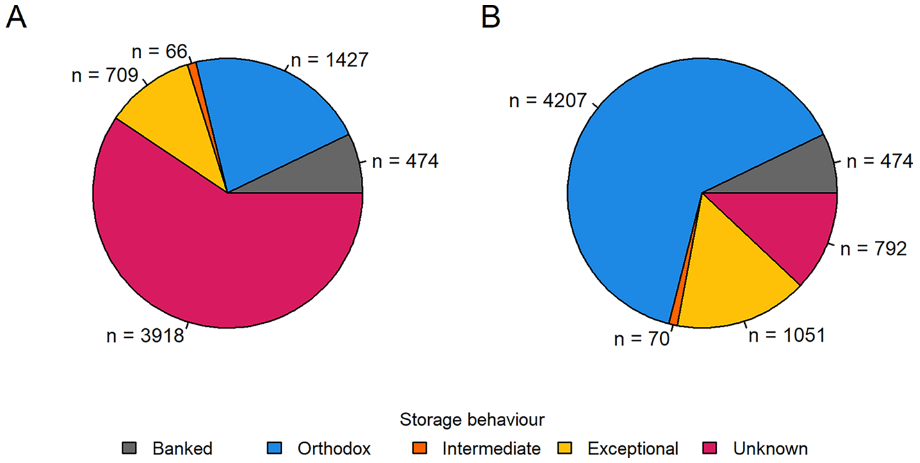

Fig. 4 Proportion of CR taxa that are banked, orthodox, intermediate, exceptional or unknown. Panel A represents a "conservative" estimate of seed storage behaviour, while panel B represents a "likely" estimate. Note that we do not present the seed storage behaviour predictions of taxa already banked.

at genus level and 15 (0.68%) at species level. The "conservative" estimate therefore suggests that at a minimum we have 1,427 (23.32%) orthodox, 66 (1.08%) intermediate, 709 (11.58%) exceptional unbanked CR, leaving 3,918 (64.02%) unbanked CR taxa of unknown storage behaviour. However, the "likely" estimate allowed the inclusion of storage behaviour for 3,126 additional unbanked taxa. At the upper limit we could potentially have 4,207 (68.74%) orthodox, 70 (1.14%) intermediate, 1,051 (17.17%) exceptional and 792 (12.94%) unknown CR taxa.

Even considering all predictions in the "likely" estimate, the desiccation sensitivity predictor tool (Wyse and Dickie 2017) was unable to predict the storage behaviour of 275 (4.17%) taxa, primarily because the taxa were not vascular plants. For the predictions that were made, probabilities of recalcitrance calculated varied for different taxonomic ranks (Appendix S3). At species level, all probabilities assigned were 0.0 or 1.0 for likely orthodox or likely recalcitrant taxa, respectively ($n = 114$). As the precision of prediction decreases to genus, family and order, pR becomes more uncertain and approaches 0.5 meaning the taxon has an equal likelihood of being recalcitrant/exceptional or orthodox. Overall, 2,348 taxa were predicted at genus-level, 2,956 at family-level and 901 at order-level.

When we look at predictions of desiccation tolerance at the family level (Figs. S3 and S4), for the "conservative" estimate we find that 73 (33.33% of families with CR taxa in them) are composed primarily of orthodox taxa, with only eight families primarily predicted to have exceptional taxa (*Fagaceae*, *Elaeocarpaceae*, *Dipterocarpaceae*, *Meliaceae*, *Myrtaceae*, *Myristicaceae*, *Araucariaceae* and *Hymenophyllaceae*) and seven primarily intermediate (*Aspleniaceae*, *Dennstaedtiaceae*, *Pteridaceae*, *Lindsaeaceae*, *Marattiaceae*, *Lycopodiaceae*, *Isoetaceae*; Fig. S3). For the "likely" estimate we find that 175 (79.91%) of families with CR taxa in them are composed primarily of orthodox taxa, with only 12 families primarily predicted to have exceptional taxa (with *Sapotaceae*, *Rhizophoraceae*, *Chrysobalanaceae* and *Lauraceae* added when compared to the conservative estimate), and seven primarily intermediate (Fig. S4).

Finally, when we separate out the 474 CR taxa banked in the MSBP, under the “conservative” estimate, 247 (52.11%) taxa were classified as orthodox, six (1.27%) as intermediate and 209 (44.09%) were classified as unknown. Only 12 (2.53%) taxa were classified as recalcitrant (*Aquilaria malaccensis*, *Elaeocarpus bojeri*, *Wilkesia hobdyi*, *Grammitis ascensionensis*, *Persoonia acerosa*, *Persoonia pauciflora*, *Eucalyptus dolorosa*, *Eucalyptus imlayensis*, *Eucalyptus recurva*, *Quercus camusiae*, *Syzygium maire* and *Calamus inermis*). Under the “likely” estimate, 416 (87.76%) taxa were classified as orthodox, seven (1.48%) as intermediate and 27 (5.7%) were classified as unknown. Only 24 (5.07%) taxa were classified as exceptional and further viability testing is recommended to ascertain the status of these exceptional collections.

Spatial patterns in seed storage behaviour

The largest numbers of orthodox CR taxa from the “conservative” scenario to be collected are in United States (211 taxa), Madagascar (122), South Africa (104), Ecuador (90), Mexico (68), Colombia (65) and Tanzania (63), while most exceptional CR taxa that need collecting are in Indonesia (107 taxa), Philippines (96) and United States (91; Fig. 2C; Appendix S5). From the “likely” scenario, the largest numbers of orthodox CR seed taxa to be collected are in Madagascar (363 taxa), United States (268), Ecuador (256), Mexico (219), Colombia (215), Philippines (208) and Indonesia (201), while most recalcitrant CR taxa that need collecting are in Indonesia (155 taxa), Philippines (118), Papua New Guinea (96), United States (92), Malaysia (69), Madagascar (60), Brazil (58) and Vietnam (52; Fig. S5; Appendix S5).

Access and benefit sharing

The lack of ABS measures available in countries affected the number of collections per country conserved by the MSBP (Fig. 2A), with only 9 collections (0.36%) of CR taxa belonging to countries without ABS measures. When studying the number of ABS indicators, we find that 1,039 (41.44%) collections were made in countries with one ABS measure; 160 (6.38%) with two; 362 (14.44%) with three; and 869 (34.66%) with four measures. Looking into the differences between different ABS measures, NFP emerged as the most essential indicator for banking of CR plant material with 96.93% of the collections (2,430 collections from 66 countries) in the MSBP coming from countries with NFP in place; followed by 55.44% under Nagoya (1,390 collections from 49 countries), 49.18% with CNA (1,233 collections from 29 countries), and 34.66% with IRCC (869 collections from 13 countries).

ABS measures are therefore important drivers of collections as they facilitate storage and transfer of seeds between countries. Overall, we found 177 countries with National Focal Points (NFP), 79 countries with a Competent National Authority (CNA), 27 with one or more Internationally Recognised Certificate of Compliance (IRCC) and 141 countries with Interim National Reports on the Implementation of the Nagoya Protocol (NR; Figs. 2A and S6), indicating differences in how countries can collect and share plant materials. The countries with all four ABS measures in place are Antigua and Barbuda, Argentina, Belarus, Belgium, Benin, Bhutan, Bulgaria, Cameroon, Côte d’Ivoire, Dominican Republic, Ethiopia, France, Guatemala, Guyana, India, Kenya, Laos, Malta, Mexico, Panama, Peru, Republic of Korea, Saint Kitts and Nevis, South Africa, Spain, Uruguay and Vietnam (Figs. 2A and S6).

Discussion

Collection gaps

Critically Endangered (CR) plants face imminent risk of extinction in the wild if no urgent conservation action is delivered. *Ex situ* conservation approaches, particularly seed banking, play a crucial role in preserving genetic diversity over the long term and ensuring the availability of seeds for future restoration and reintroduction efforts. Here, we assessed the quality of CR seed collections across the MSBP, the world's largest collaborative seed banking initiative (Data Warehouse 2025). Our findings indicate that only 0.9% of the 52,874 taxa banked in the MSBP are CR taxa, representing only 7.21% of all taxa assessed and predicted to be CR. This marks only a modest increase of 1.21% since 2018 (Liu et al. 2018); however, in absolute terms, the number of CR taxa conserved has tripled (from 156 in 2018 to 474 in 2025, Fig. 4), highlighting both an acceleration in CR taxa listing and an increase in their collection and storage.

While most collections of CR taxa include basic information such as taxon name, collection year, and geographic coordinates (mean information index = 0.81), they often lack critical data on seed viability (counted, x-rayed and germination tested; mean viability index = 0.31) or genetic diversity (information about parent population; mean genetic diversity index = 0.31; Fig. 3). Only 9.49% of banked CR taxa have seed numbers that meet the threshold for restoration research (recovery target), and just 5.49% have at least 5 collections across their native countries (geographic target). These gaps underscore the need for improved collection strategies to maximise the conservation value of seed banks for CR taxa.

Taxonomic gaps

At the family level (Figs. 1 and S1), only 6.15% of families containing CR taxa have at least 50% of their taxa banked, and just 3.11% of families with CR have achieved 100% banked. A total of 148 families with CR taxa remain entirely unbanked, suggesting that some plant lineages have been disproportionately overlooked. Broadening the taxonomic scope of seed collections is therefore a priority, particularly for families with a high proportion of bankable taxa.

Between 33.33% (conservative estimate) and 79.91% (likely estimate) of families containing CR taxa are composed primarily of orthodox-seeded taxa, indicating substantial potential for conventional seed banking. Both the predictions of red list status (Bachman et al. 2024) and storage behaviour (Wyse and Dickie 2017) suggest that family-level traits and phylogenetic distances can be useful proxies for determining storage potential when direct experimental data are lacking. Target families with over 30 unbanked orthodox CR taxa include *Aizoaceae*, *Asteraceae*, *Boraginaceae*, *Bromeliaceae*, *Campanulaceae*, *Caryophyllaceae*, *Cyperaceae*, *Euphorbiaceae*, *Lamiaceae*, *Malvaceae*, *Melastomataceae*, *Orchidaceae*, *Phyllanthaceae*, *Piperaceae*, *Poaceae*, *Rubiaceae*. While most CR are difficult to collect due to their restricted distributions and small population sizes, some families (e.g., *Bromeliaceae*) may also be under-collected due to their often-epiphytic growth form, which present additional practical challenges for seed collection.

Seed storage behaviour

Considerable effort is still required to achieve comprehensive *ex situ* conservation of CR taxa. Currently, 6,120 CR taxa remain unbanked (Fig. 4). Among these, 23.32–68.74% are expected to have orthodox seed storage behaviour and can therefore be stored using standard MSBP protocols. Conversely, 11.58–17.17% are categorised as exceptional, requiring alternative storage methods such as cryopreservation. However, the wider implementation of cryopreservation is hindered by its technical complexity, high costs, and limited infrastructure across seed banks (Pence et al. 2022a, b; Leddington 2023). Research is needed to optimise cryopreservation protocols and identify the most appropriate tissues (e.g., cells, seeds, embryos, pollen, spores or shoot tips) for long-term storage (Breman et al. 2021). Beyond cryopreservation, exceptional taxa may also require in-vitro cultures, propagation, or maintenance in living collections (Pence et al. 2022a, b). Additionally, 1.08–1.14% of unbanked CR taxa have intermediate seed storage behaviour, and 12.94–64.02% have unknown storage traits, meaning that 14.02–65.16% of unbanked CR taxa will require a combination of conventional and non-standard seed banking techniques. Given the variability in predictive models for seed storage behaviour Wyse and Dickie (2017), further validation with empirical data from MSBP is essential.

Recent advances in *ex situ* conservation strategies for exceptional taxa are promising (Pence et al. 2022a, b). Cryopreservation has the potential to secure a broader range of plant taxa and tissues compared to conventional seed banking, and its adoption is expanding. However, strategic investments are necessary to make this technique more widely accessible across MSBP partner institutions. Propagation and living collections, which fall outside the MSBP's primary remit, are instead managed by botanic gardens (Breman et al. 2021). Given their importance for conserving taxa that cannot be stored in seed banks, closer collaboration between seed banks and botanic gardens is needed to ensure a holistic approach to *ex situ* conservation.

Access and benefit sharing and the global biodiversity framework

Ex situ conservation through seed banking operates within a complex legal framework shaped by Access and Benefit Sharing (ABS) measures, ensuring compliance with the Nagoya Protocol under the Convention on Biological Diversity (CBD 2025). The MSBP has actively worked to align its collections with national ABS measures, ensuring that seed banking contributes to equitable benefit-sharing. Currently, 96.87% of collections (2,430 collections from 66 countries) originate from countries with at least a National Focal Point (NFP) in place, facilitating access while promoting fair collaboration between source countries and seed banks.

Duplicating seed collections across multiple institutions provides an additional safeguard against loss and enhances the accessibility of genetic resources. However, legal constraints sometimes limit the transfer of germplasm between institutions, restricting research and conservation potential. The Kunming-Montreal GBF, adopted in 2022, aims to strengthen biodiversity conservation efforts and includes several targets relevant to seed banking, particularly Targets 2, 4 and 13. More specifically the geographic target focusses on how to "Restore 30% of all Degraded Ecosystems" while targets 4 and 13 focus on preserving genetic diversity with focus on how to "Halt Species Extinction, Protect Genetic Diversity, and Manage Human-Wildlife Conflicts" and "Increase the Sharing of Benefits From Genetic Resources, Digital Sequence Information and Traditional Knowledge" respectively.

Despite these global commitments, the lack of specificity in current biodiversity targets presents challenges for assessing conservation progress. The Aichi Biodiversity Targets, including Global Strategy for Plant Conservation (GSPC) Target 8 (securing "at least 75% of threatened plant species in *ex situ* collections, preferably in the country of origin") were not met (Green et al. 2019), with only a fraction of the world's threatened flora banked. We did not assess all threatened taxa (including VU, EN and EW) but given that only 7.21% of CR taxa are currently stored in seed banks, achieving 75% was a distant goal and illustrates the consequences of insufficient investment (Green et al. 2019). While the GSPC was updated at CBD COP16 with complementary voluntary actions (CBD COP 16 2024), these actions lack specific, measurable, achievable, realistic, and time-bound (SMART) goals for seed banking and still require specific indicators. Substantial financial commitment is required to scale up conservation efforts, improve storage infrastructure, and support research into cryopreservation and seed viability testing.

Seed banking targets

Beyond merely increasing the number of taxa conserved in seed banks, it is critical to ensure that collections are both representative and viable for future use. To address this, we propose two key metrics to assess collection adequacy: a restoration target, evaluating whether collections contain sufficient seeds (> 1,050 seeds) to support restoration research; and a geographic target, assessing whether a taxon has been collected from 5 collections inside its native range. Both restoration and geographic targets must also meet the current MSBP target for genetic diversity, of collecting seeds from 50 individuals.

Ideally, a seed bank collection should contain 10,000 seeds to support multiple conservation goals (CPC 2020; Way 2021; MSBP 2022). However, CR taxa, which often have small, fragmented populations, excessive collection may pose risks to wild populations. Best practice guidelines recommend collecting from at least 50 individuals, which can in practice be difficult when a taxon is clonal, or when the population is very small (< 50 individuals) as is the case with most CR. In such cases, collections should be made from no more than 20% of the seeds available from all reproductive individuals of a given population, requiring multiple collection events across years to reach an adequate sample size (Way 2021; MSBP 2022). Where possible, for CR or small populations, the MSBP protocols recommend keeping seeds from individual plants separate to protect the genetic quality of the collection (MSBP 2022). The usability of the collections can often be improved through seed multiplication, by propagating seed from each maternal line and ensuring cross pollination, thus avoiding inbreeding (Van Der Merwe et al. 2023).

Capturing the geographic range of a taxon is also crucial for genetic conservation (Hoban and Strand 2015). Indeed, taxa can be spatially variable in their characteristics and genetic diversity. Capturing a wider variety of traits and genes means we can capture individuals from a population that may have adaptations that allow them to survive under conditions such as higher or lower temperatures, greater drought or flooding, allowing them to adapt to a changing environment (Schoen and Brown 1993; Hoban and Strand 2015). While the standard MSBP protocol is to make 5 collections per taxon, this criterion is difficult to implement for many CR taxa that are range restricted and occurring in a single population.

In such cases, overharvesting is a real risk, and similarly to the recovery target, only 20% of seeds can be collected, requiring several repeat visits to capture the overall genetic diversity of that taxon. However, with more broadly distributed CR, geographically separate populations need to be sampled across their native distribution to ensure we are capturing genetic alleles unique to different genetic groups. This target is difficult to achieve, as we find that only 5.49% of banked CR taxa currently meet the geographic target, emphasizing the need for expanded conservation efforts for CR taxa to ensure long-term survival of populations; by maintaining genetic diversity and gene flow, buffering the effects of population declines and facilitating responses to changes (Miraldo et al. 2016).

Many national authorities maintain their own CR status lists and priorities, often based on locally available data and expertise. In many cases, data may be insufficient at the global scale for an IUCN Red List assessment, yet locally adequate to evaluate extinction risk. As a result, taxa can be listed as threatened nationally even if they are not recognized as such globally. For instance, *Plantago princeps var. laxifolia* is recognised in Hawai'i as a CR variety endemic to Maui by the IUCN (Center for Plant Conservation 2025; IUCN 2025), whereas the current WCVP list only acknowledges *Plantago princeps*, which is listed as Vulnerable rather than CR by the IUCN. Extinction risk is therefore closely tied to taxonomic interpretation, which can vary between authorities, and such mismatches can present limitations in analyses such as ours.

Despite these challenges, the targets we develop here are simple and flexible, allowing application at any scale with any taxonomic backbone. They can help stakeholders identify what still needs to be done to achieve a genetically robust seed collections for restoration, thereby contributing to GBF target 4. While these targets are useful, further research is needed to assess the genetic structure of taxa conserved at the MSBP, to ensure genetic variation has been sampled and to provide future conservation recommendations (Ottewell et al. 2016). In the absence of such data, life-history traits and distribution range data can be used to predict genetic indicators and estimate risks of sampling genetic diversity and donor selection for conservation management plans (White et al. 2025).

Four main genetic indicators are being proposed to establish levels or targets of conservation for wild taxa: genetic diversity, genetic differentiation, inbreeding, and effective population size estimates (Hoban and Strand 2015; Laikre et al. 2020). However, these estimates will need adjustments for CR taxa, for example, conserving a population larger than an effective population size of 500 (Harmon and Braude 2010) will not be appropriate for most CR taxa due to their reduced population size and distribution range. Currently, the MSBP collections have an exceptionally low genetic diversity data index for CR plants, which we recommend as a priority for future collection to facilitate the calculation of genetic diversity indexes.

Conclusions

In situ conservation, through protection of species in the wild, is often considered the best conservation approach. However, given the current rates of habitat degradation from land use changes, invasive species spread and urbanisation, appropriate areas are becoming increasingly rare. While the GBF has committed to protecting 30% of the planet, it has also committed to restoring 30% of degraded areas. *Ex situ* collections will play an important role in ensuring we can meet our commitments towards restoration goals and conservation of genetic diversity. The current rate of CR species banking is insufficient to meet global conservation targets. Without immediate action to expand collections, improve storage infrastructure, and integrate genetic diversity considerations into seed banking strategies, many CR species may be lost before they can be effectively conserved. Urgent international collaboration, sustained financial support, and evidence-based policy adjustments are necessary to ensure that seed banks can fulfil their role in safeguarding plant diversity for future generations.

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Author contributions EB, IQ and JV conceived the initial idea of the manuscript, which was further shaped by all authors. IQ performed the initial analysis which was updated by KLDA with input from all authors. DB provided expert knowledge on bryophyte and fern storage behaviour. KLDA lead the writing of the manuscript with significant contributions from EB, UL, and JV, with all authors contributing towards writing, editing and commenting on the manuscript.

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Data availability Datasets generated during the current study are available as supplementary information. Code is available on https://github.com/KiranLDA/CR_gap_analysis.

Declarations

Competing interests The authors have no relevant financial or non-financial interests to disclose.

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