



Genebanking plant genetic resources in the postgenomic era

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Abstract

Genebanking, the process of preserving genetic resources, is a central practice in the modern management of crop genetics, especially for the species used for food and agriculture. Closely interrelated networks of local, national and global actors are responsible for ex situ conservation. They all seek to make plant genetic resources accessible for all and now face new challenges arising from digitisation. Plant sciences are entering the postgenomic era, moving fast from initially providing a single reference genome for each species (genomics), to harnessing the extent of diversity within crop species (pangenomics) and among their relatives (referred to as postgenomics). This paper describes the extent to which ex situ collections have already undergone a digital shift, or are planning to do so, and the potential impact of this postgenomic-induced dematerialisation on the global governance of plant genetic resources. In turn, digitising material (seed) collection changes the relationship between genebanks and genomic databases. Comprehensive genomic characterisation of genebank accessions is ongoing, and I argue here that these efforts may provide a unique opportunity for genebanks to further embrace the moral, ethical and ultimately political principles on which they were built. Repurposing genebanks as decentralised digital biocentres could help relocate capabilities and stewardship over genetic resources. Empowering local farmers by providing access, promoting the use and unlocking benefits from state-of-the-art tools of modern plant breeding may allow bridging the breeding divide. However, to accomplish such a paradigm shift, genebanks require a strong political mandate that must primarily originate from the access and benefit-sharing framework. Only so may the global challenges associated with the loss of biodiversity and food insecurity be addressed.

Keywords Plant genetic resources for food and agriculture · Genebanks · Genomics · DSI · Biodiversity · Food security · Pangenomes

Abbreviations

ABS	Access and Benefit Sharing
CGIAR	Consultative Group for International Agricultural Research
DSI	Digital Sequence Information
FAO	Food and Agriculture Organization
ITPGRFA	International Treaty on PGRFA
NCBI	National Center for Biotechnology Information
PGRFA	Plant Genetic Resources for Food and Agriculture

Introduction

In 2011, the contemporary artist Ai Weiwei filled the Tate Modern Museum with millions of small hand-crafted porcelain sunflower seeds. While the artwork may allow several layers of interpretation, one could imagine those seeds as a metaphoric genebank: static for the centuries to come, while still paying a tribute to the individuals that produced them. Genebanking of plant genetic resources is a central practice of modern agriculture aiming at the ex situ conservation of crop and wild plant genetic diversity. It aims to limit the erosion of genetic diversity with the aid of a variety of global, national and local genebanks storing seeds, DNA, tissue cultures, germplasm and other reproductive propagules (FAO 2010; Belanger and Pilling 2019; Pilling et al. 2020). Globally, several commitments have been established to try to improve the quantity and quality of ex situ conservation: under the United Nations Sustainable Development Goal no 2, the aim of Target 2.5 is “By 2020, maintain the

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genetic diversity of seeds, cultivated plants and farmed and domesticated animals and their related wild species, including through soundly managed and diversified seed and plant banks” (UN 2015). Ex situ conservation is important not only for PGRFA but also as a tool to support the conservation of biodiversity at large: Target 8 of the Global Strategy for Plant Conservation of the Convention for Biological Diversity (CBD) aims for the conservation of at least 75% of threatened species by 2020 (CBD 2002). The recently agreed post-2020 Global Biodiversity Framework also mentions the role of ex situ conservation to achieve its “30 by 30”¹ objectives.

Ex situ conservation is generally complementary to in situ conservation, which comprises various protected areas and focuses more on the population and ecosystem levels (FAO 2010). Worldwide, some 1750 genebanks hold around 7.4 million samples (or 4.9 million accessions) from over 6900 species relevant to agriculture (FAO 2010; Paton et al. 2020). The largest genebank network, also responsible for most ex situ conservation efforts, is coordinated by the Consultative Group for International Agricultural Research (CGIAR). The CGIAR played a central role in policy design and provided technical inputs that framed the governance framework over ex situ conservation (Frison 2018). They apply the provisions of Article 15² of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA 2004). Significantly, a small number of key players in ex situ conservation—such as the Millennium Seed Bank and the Svalbard Global Seed Vault—hold a large proportion of all samples. While objectives and derived policies may vary from one site to another, genebanks are responsible for “collecting, maintaining, characterising, documenting and distributing” various plant varieties, which can be landraces, bred varieties or wild ancestors (FAO 2011; Anglin et al. 2018). Genebanks thus not only play a central role in the conservation of PGRFA but also determine the extent of access to and hence the potential for sharing of benefits derived from these resources. The structure of ex situ conservation underlies a precise normative ideal defining how, when and by whom PGRFA can be accessed, commodified and the modalities of their future use (Peres 2016; Curry 2017). They are indeed central both to the ITPGRFA and to the Nagoya Protocol of the CBD, which regulates the access to and benefit-sharing for a large proportion of terrestrial biodiversity (ITPGRFA 2004, CBD-NP 2010).

¹ “30 by 30” refers to the latest engagements of the Convention of the Parties of the UN Convention for Biological Diversity in December 2022 to agree on 30% of Earth’s land and oceans being protected by 2030.

² Article 15 of the ITPGRFA provides a legal mandate to the CGIAR centers to hold and manage ex situ collections of plant genetic resources for food and agriculture.

To address major challenges such as food security, climate change and loss of biodiversity, crop breeding is under strong pressure from the current global governance frameworks to deliver adapted crops for future resilient agroecosystems. To access the diversity of genebanks for improving crops, some have advocated systematic genotyping and phenotyping of all conserved accessions³ (McCouch et al. 2013; Halewood et al. 2018a; Bohra et al. 2022).

To make use of the genebank’s diversity, crop breeders, researchers and farmers need to describe the accessions that are stored. This process aims eventually at predicting how DNA variability is associated with plant phenotypes (in other words, everything that links the plant to its environment). Now, genebank’s curators and administrators considered the promise of genebank postgenomics,⁴ i.e. using high-throughput genomics on genebank accessions to promote plant breeding. This is also a way to improve the cost-efficiency and effectiveness of collections (McCouch et al. 2012). For example, the Second Report on the State of the World’s PGRFA estimates that about a third of all PGRFA accessions are duplicates (FAO 2010; Curry 2022). In addition, the digitisation⁵ of collections would be an appropriate response to ongoing calls for improvement in the standardisation of genebanks’ sampling, storing and regeneration procedures (FAO 2014). Interestingly, the role of duplication in ex situ collections has been recently questioned (Curry 2022). Digitizing genebanks can be considered as some sort of additional layer of duplication and raises similar questions towards the actual consequences on crop genetic resources conservation.

In this paper, I argue that the comprehensive digitisation of PGRFA collections may also ultimately lead to a major shift in the stewardship role of genebanks and their relationship to scientists, breeders and farmers. First, through collecting and merging plant genomics data, I describe the ongoing shift from genomics to post-genomics. I then

³ The basic unit of the genebank is the “accession”: a unique sample that has been collected and recorded in the genebank. The amount and quality of the information can vary between accessions and can be sometimes even duplicates of the same plants.

⁴ Genomics is a subset of genetics that concentrate on analysing large (high-throughput) data that describes large portions of genomes. Omics is a term used to refer to other domains of biology that have also been scaling up the amounts of data they produced (and digitised), like for example transcriptomics or metabolomics. The increase in available data from a unique reference genome per species to the sequencing of intraspecific diversity (pangenomes) is referred to here as the postgenomic shift.

⁵ Here, I refer to digitisation in a relatively narrow sense that applies for genebanks: the action to sequence and collect genome’s sequence of physical materials (so called accessions: seeds, propagules...). Being de facto high-throughput data, these data are stored digitally, often in repositories that are separate entities from genebanks.

gathered the current plant genomics literature and my experience as a genebank curator and national representative involved in various negotiations concerning genetic resources, to draw over the implications of this shift for genebanks. I also argue that the digitisation of PGRFA collections will have a major impact on genebanking.

Genebanks' activities may shift from the general management of genetic resources (seeds) to the distribution of (digital) information (van Treuren and van Hintum 2014; Wambugu et al. 2018; Mascher et al. 2019). Sharing data will mechanically increase their involvement in post-banking activities: pre-breeding and breeding (for example to allow genomic selection⁶). But to embrace their new role fully, several challenges remain: like data governance, North/South imbalance, capacity building and standardization. In turn, I try here to evaluate how digitizing genebanks will have consequences on the global politics of genetic resources. Ultimately, empowering farmers and favouring their role as primary data producers (being genomic or phenotypic) will be central to future agricultural systems (MacPherson et al. 2022), and genebanks can be essential tools in that respect. Future developments in the access and benefit-sharing framework will hopefully avoid increasing an omics-driven breeding divide.

Making sense of sequence diversity: the rise of plant genomics

With an estimated 391,000 species worldwide, plants (of which 85% are seed plants) are among the most diverse and genetically complex biological phyla on Earth (Antonelli et al. 2020; Marks et al. 2021). Several ambitious genomic projects aim at comprehensive sequencings of plant diversity, such as the Earth Biogenome project (Lewin et al. 2018), the 10KP project (Cheng et al. 2018), or more focused initiatives, such as the sequencing of an entire botanical garden (Liu et al. 2019). As of the end of 2022, the NCBI genome database (<https://www.ncbi.nlm.nih.gov/genome/>) includes 1028 reference genomes of varying depth and quality, which are published in various open-access repositories (including NCBI, Ensembl Plants, and Phytozome). The field of plant genomics remains largely dominated by China, the USA and Europe, accounting for about three-quarters of genomes published to date (Marks et al. 2021; Kersey 2019).

⁶ Genomic selection is the process taking advantage of the comprehensive genetic variability of genomes (after high-throughput sequencing) of a population to associate in a quantifiable manner to certain traits: it defines the breeding value of individuals in a population. Genomic selection is meant to facilitate/speed up the breeding process.

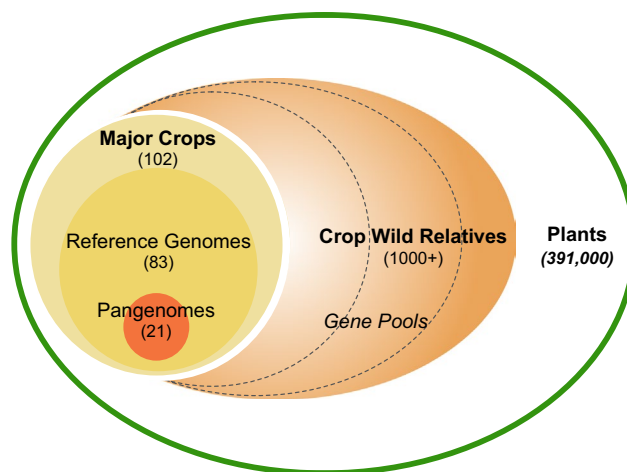
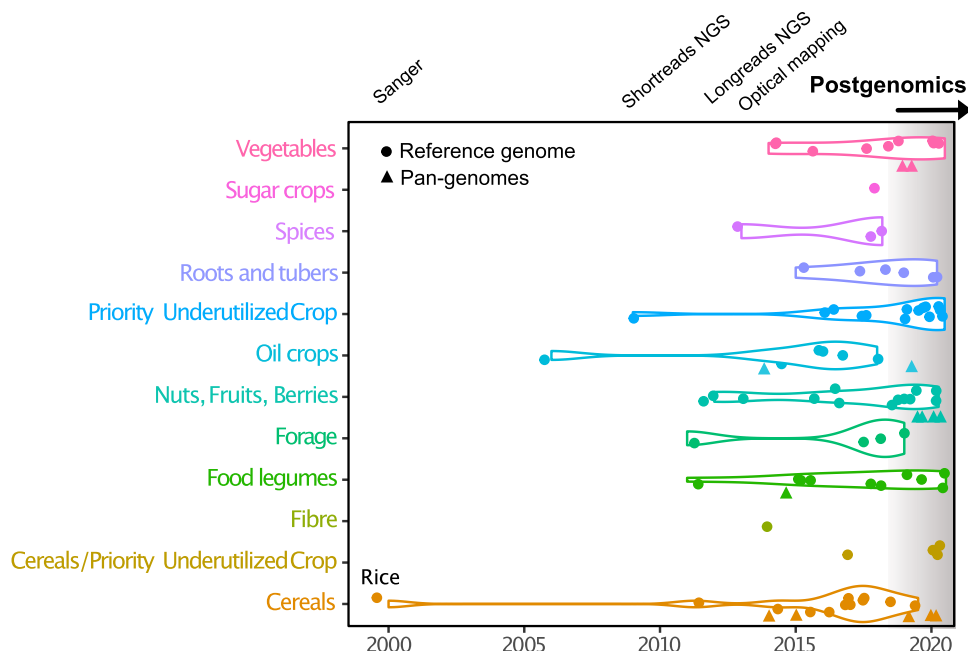


Fig. 1 Number of plant species and the various crop genome sequences available. While a very small proportion of species are used in agriculture (102 major crops), the list could be extended if Crop Wild Relatives are being considered and sequenced in so-called “super-pangenome” studies

Perhaps fortunately for plant geneticists and breeders, a relatively small subset of species is relevant to agriculture. To assess the extent of genomic advances in these species, I have compiled a list of 102 major crops, including 72 key crops covered in the Second Report on the State of the World's PGRFA (FAO 2010) (Supplementary Table 1). However, this is a limited proportion of the estimated 7039 edible plants identified (Ulian et al. 2020). This short list largely coincides with a previously published list of common commodity crops (Castañeda-Álvarez et al. 2016) and the species listed in Annex 1 to the ITPGRFA. In addition, 30 key neglected and underutilised crops were also considered. The number of accessions in gene banks correlated well with the extent of genomic description (Supplementary Table 1). Of the 102 species selected, 83 have reference genome sequences of varying degrees of completeness, with about a third of these genomes completed to the chromosome level. Notably, 16 of the 19 species without publicly available genomes are part of the African Orphan Crops Consortium and are partially completed, together with another 100 species relevant to Africa (Hendre et al. 2019; Ulian et al. 2020; Ye and Fan 2021). The chronology of sequencing is closely related to technical advances, with an increasing number of increasingly diverse crops sequenced as sequencing techniques improved from Sanger and short-read to long-read Next Generation Sequencing and optical mapping (Figs. 1, 2).

The simultaneous increase in throughput and decrease in prices recently allowed a surge of resequencing, moving

Fig. 2 The rise of postgenomics in crop species. A chronology of crop genome's publication according to data from NCBI (<https://www.ncbi.nlm.nih.gov/genome/>) shows a recent rise in pangenomes and sequencing of underutilized crops. The shift from a unique reference genome per species to the sequencing of intraspecific diversity (pangenomes) is referred to here as the postgenomic shift. The data used to draw this figure are summed up in Supplementary Table 1



from unique reference genomes to larger pangenomes.⁷ As first observed after the Human Genome Project (Thacker 2005; Shaw 2016), as more and more whole genomes are completed and technology evolves, there is a natural movement towards the characterisation of allelic diversity performed by studying pangenomes of varieties within one species (Golicz et al. 2016; Bayer et al. 2020). In other words, after comparing variations across species (with only a single reference genome for any given species), sequencing allows now for comparing genomes within species (for example for presence/absence of genes). At least 21 pangenomes have been published—i.e. species with multiple reference genomes available (Guignon et al. 2020; Della et al. 2021), mostly from major crops such as rice (Schatz et al. 2014; Wang et al. 2018; Zhao et al. 2018), wheat (Montenegro et al. 2017; Walkowiak et al. 2020), maize (Lu et al. 2015), canola (Hurgobin and Edwards 2017), grapes (Liang et al. 2019), barley and chickpea (Monat et al. 2019; Gao et al. 2020; Jayakodi et al. 2020)—with a lot more still to come (Supplementary Table 1). Three groups of crops were distinguished with decreasing levels of description: first, cash crops with many accessions available in genebanks, and whole genomes as well as pangenomes described (rice, wheat and canola, but also banana and grapes); second, intermediate crops, with diversity reasonably well covered, but with a single reference genome available (typically vegetables); and third, some crops with few accessions and

partial or ongoing genome sequencing, which are mostly orphan crops (Supplementary Table 1).

Thus, for the vast majority of key crops, whole genome sequences are available, though of varying quality and depth (Yuan et al. 2017). Modern breeding and plant sciences are generally increasingly data-rich and are now entering a postgenomic era, with a “rising deluge of data” (Stephens et al. 2015; Kelly 2019). Description of pangenomes by resequencing within varieties of the same crop—from single nucleotide polymorphism detection up to larger structural variants—will be highly beneficial for allele identification in breeding programs and genomic selection (Tao et al. 2019; Williamson and Leonelli 2023).

In addition, the portion of genetic diversity accessible by sequencing can be expanded by an order of magnitude with a third level of complexity: mining diversity outside the crop genus, in what has been referred to as the super-pangenome (Khan et al. 2020). In other words, sequencing the gene pools of crop wild relatives (Brozynska et al. 2016). Indeed, during domestication and breeding, a vast proportion of naturally occurring genetic variability has been lost. There are several examples of successful use of crop wild relatives in (pre-)breeding programs, such as Pm21 from the wheat relative *Haynaldia villosa*, which conferred resistance to powdery mildew in some wheat cultivars, or resistance to late blight (*Phytophthora infestans*) derived from the wild potato *Solanum demissum* (Dempewolf et al. 2017; Gao et al. 2020). It may be interesting to consider crop wild relatives from a PGRFA perspective, as it blurs the boundary between conventional biodiversity conservation and utilitarian mining of diversity for breeding purposes (Montenegro de Wit 2017).

⁷ The pangenome is defined as the entire set of genes within a species: it entails not only one reference from one organism, but the entire variability contained within that clade.

Meanwhile, the gradual increase in the complexity and diversity of genomic data, resulting from improvements in sequencing technologies (Bevan et al. 2017; Yuan et al. 2017) and in data analysis (Schneeberger et al. 2009; Chaudhari et al. 2016; Sun et al. 2017; Brinton et al. 2020; Khan et al. 2020), will require dedicated new frameworks, which can be very challenging. Some databases have already tried to address challenges associated with comparative genomics (Guignon et al. 2020). For example, a rice pangenome study allowed the identification of 12,000 new genes that were initially absent from the rice reference genome (Schatz et al. 2014). Similarly, significant variations in gene numbers among 22,000 barley accessions were observed (Jayakodi et al. 2020). These two examples illustrate the significant differences observed between single reference genomes and their actual variability within species. Ultimately, this progress will possibly translate into more/better traits to be integrated into crop breeding programs. Maybe one of the most compelling cases illustrating the capacities of large-scale sequencing and subsequent digitisation is the chickpea, a relatively poorly documented crop until recently, where a single study sequenced more than 3000 accessions and wild relatives (Varshney et al. 2021). This study aimed to directly use the data for streamlining high-throughput phenotyping, allele identification and genomic selection (Varshney et al. 2021; Bohra et al. 2022). Many genebanks, including CGIAR, genotype their collections to better harness the genetic potential they contain (Halewood et al. 2018b). For example, the collection of grapes accessions of the Swiss national genebanks has been recently sequenced to allow a better understanding of their complex relationship with the rest of the continent. Better characterization of rice accessions from the International Rice Institute allowed identifying among rice accessions, traits for flood resistance or enhanced micronutrient contents (Halewood et al. 2018b). The examples of the successful harnessing of digitization in breeding are numerous (Aubry 2019; Aubry et al. 2022; Gaffney et al. 2022). The discovery of new alleles is central to crop breeding, and the study of pangenomes is surely the next logical step and signals entry into the postgenomic era.

So far, the very large majority of the data published in the literature are stored outside genebanks in dedicated omics repositories (like the INSDC databases). Meanwhile, as it becomes standard, it remains to be seen whether and how existing genebanks will have to accommodate these data and their constant increase in volumes. Some scholars anticipate a switch from germplasm collections to “biological digital centres” (Mascher et al. 2019). The ultimate step for genebanks, yet to be performed, will be to build the necessary links between causal alleles and phenotypic traits, like layers from phenomic, epigenetic, proteomic and metabolomic studies (Gebhardt 2013; Anglin et al. 2018; Nguyen and Norton 2020). This is potentially transformative for breeders,

who will simply have to browse these databases to obtain an estimate of the genetic value of any given accession, a proper genebank-to-phenotype link (Mascher et al. 2019). Therefore, digitisation of germplasm collections can improve collection efficiency, in terms of both resource management—tracking accessions, avoiding duplication, and building a core collection (Glaszmann et al. 2010; McCouch et al. 2012)—and utilisation. But the real impact of this profound shift in genebank functions has yet to be seen in a more global context, not only for direct users (plant breeders⁸) but also more generally for all other stakeholders involved: farmers, researchers and civil society organizations.

Challenges of repurposing gene banking for big data

Given the complex relationship between genebanks and food systems (Pistorius and van Wijk 1999), genebanks may be considered a good example of “hybrid objects” (Latour 1993). Latour describes hybrids as complex networks between science, economy and politics. Governance of hybrids is often challenging, as it is hard to consider these aspects comprehensively. For a long time, genebanks have been considered solely a pool of resources. However, their integration into various international legally binding instruments (Art. 15; ITPGRFA 2004) and global objectives (SDG, Target 2.5; Commission on Genetic Resources for Food and Agriculture, Second Global Plan of Action for PGRFA) closely link their function to political, social and ethical values (Esquinas-Alcázar 2005). This hybridity makes genebank management and policy complex, involving a wide variety of stakeholders (e.g. scientists, breeders, farmers, indigenous communities...).

The challenges associated with the digitisation of genetic resources and their progressive dematerialisation⁹ bring a new set of stakeholders into play (e.g. database managers, sequencing firms, bioinformaticians), somehow destabilising the existing political consensus (Aubry 2019; Hartmann Scholz et al. 2021). Given the rise of fully dematerialised ubiquitous (cheap, portable and quick) sequencing (Erlich 2015), the current governance and operations of genebanks may have to be reassessed. A perfect example of fully decentralised data generation is the use of portable sequencers, such as Oxford Nanopore devices, which not only allow

⁸ Plant breeders refer here to a broad representation: from individual breeders, local networks, SMEs, up to large transnational breeding companies.

⁹ Dematerialisation is referring here to the fact that specific genetic resources contained in genebanks (accessions) could be sequenced and later accessed without the actual need for their “physical” shell (being a seed or a propagule).

sequencing in the field but also offer a cloud-based analytic pipeline (Kono and Arakawa 2019; Cozzuto et al. 2020). The spread of such tools may have a strong impact on the economics of digital sequence information (DSI), especially in the context of growing genome editing capacities (Zhu et al. 2020), and genebanks will therefore need to adapt.

Meanwhile, it is not clear to what extent the few key providers of sequencing devices and data analysis (Illumina, Oxford Nanopore and PacBio have the largest market share) could influence conservation policy at large. There are well-known examples of hardware industries progressively shifting their business model to embrace big data, and there is no reason why the development of genomics should be any different. Digitisation of genebanks may profoundly change their position within food systems and will be confronted with similar challenges that affect other digital assets managers in a digital economy (Stuermer et al. 2017; Rohden et al. 2019). It may thus be necessary to evaluate the influence of all the stakeholders concerned by digitising the seed banks: the old ones (farmers, breeders, indigenous communities) as well as the new (bioinformaticians, data scientists and managers). New policies are needed to ensure that some of the most fundamental objectives of genebanks are met: protecting crop genetic diversity for the environment, food security and sustainable development. While repurposing genebanks to match the standards of modern science (and breeding) sounds logical and probably irreversible, in the next section, I try to assess the possible consequences of that shift and who is the most likely to profit from it.

Digitising genebanks or banking digital assets?

The growing reliance on genomic and phenotypic data in plant conservation and breeding has created some uncertainty regarding the management of plant genetic resources. In the late 2010s, some ambiguity arose within the legal framework for the information derived from various germplasm (CBD 2016; Aubry 2019). This controversy coincided with the rise of genome editing techniques, which opened up unprecedented possibilities for writing/synthesising DNA and modifying genomes (Chari and Church 2017). Referring again to the chickpea example (von Wettberg et al. 2018; Bohra et al. 2022), sequencing (i.e. digitisation of the genomes) of wild parents identified alleles responsible for low shattering important for chickpea cultivation. While these wild parents do not necessarily cross with cultivated chickpeas, it could be technically possible to genetically modify this locus.

As omics progress, the legal definition of plant genetic resources appears more and more ambiguous, with a two-components: physical (e.g. seeds, propagules) and

informational (DSI) (Aubry et al. 2022). This (possibly) new dichotomy has created obstacles for most fora dealing with genetic resources, especially the internationally legally binding instruments dealing with access and benefit-sharing (ABS). Many scholars commented on this controversy, which appeared to reveal some underlying fragilities in the ABS framework design (Halewood et al. 2018b; Aubry 2019; Laird et al. 2020; Bond and Scott 2020; Nehring 2022). CGIAR centres took a proactive stance, seeking to integrate big data into their collections—for example, by generalising the use of digital object identifiers (DOI) in the global information system of the ITPGRFA (Halewood et al. 2018b). While many research programmes are using genebank infrastructure to access, extract and mine data (DSI), it appears that, without a quick and comprehensive integration of contemporary genomics practices, not only the treaties but also the public collections may become obsolete. Noteworthy, in the early days of human sequencing, (which could be considered the very first omics data wave), some questions were raised: about data access, databases governance, and the extent to which genomics databases could be considered as global public goods or protected commons (Chadwick and Wilson 2004). While the human data field does not consider access and benefit sharing per se, the ethical considerations that drove the governance of biobanks and their associated databases could be inspiring the management of digital data from non-human biodiversity.

Uploading the vault: from *ex situ* to *in silico* conservation

Interestingly, not long after the inception of the CBD, the challenges of digitisation were already apparent, as noted by Pistorius and Van Wijk (1999): “the collection and storage of genetic information in the form of data on DNA sequences is much more attractive than in the form of seed”. From a historical perspective, genebanks originated with the efforts of the Soviet plant geneticist Nikolai Vavilov to build a “universal store of genes” (Bonneuil 2019), a move subsequently revitalised by Otto Frankel to become an essential part of modern agriculture (Harlan 1975; Hawkes 2002; Scarascia-Mugnozza and Perrino 2002; Curry 2017). As socio-scientific hybrids, genebanks are embedded in food systems and are therefore strongly dependent on policy changes, levels of funding and parallel waves of privatisation in the plant breeding sector (Pistorius and van Wijk 1999; Nehring 2022). Notably, this may have a long-term impact not only on breeders or farmers but also on food security.

In a broader context of the biodiversity crisis, the regime complex governing genetic resources, in the first place the FAO Seed Treaty (ITPGRFA 2004), calls for improvement of the efficiency of gene banking (Curry 2022). Considering

digitisation as part of the default gene banking process also underlies preexisting political views and values for the future of food systems (Alpsancar 2016; Fenzi and Bonneuil 2016; Peres 2016). In the long run, an inherent risk of mass-scale digitisation of genebanks might be that, if they are considered exclusively as instruments for the rational development of plant science, there is ground for gradually making genebanks redundant. Genebanks are costly and complicated structures while building new biological digital centres (*i*-genebanks) would presumably be cheaper (and therefore more efficient). The value of DNA information long-anticipated by Pistorius and Van Wijk could thus be considered as the ultimate stage of depoliticisation (and subsequent commodification) of PGRFA: when removed from their physical shell, genetic resources as “building blocks of biological crop diversity” (Bonneuil 2019) are more easily stored and managed, but they are also even more unlikely to be related to the farmers that initially grow and breed them (van Dooren 2009). Without further pursuing this extreme, prospective *in silico* scenario, it remains that genebanks still need to respond to the legal and ethical commitments from which they originate. Could genebank’s digitisation bring more equity to the food system?

Genebanks may indeed take advantage of the genomic revolution to embrace the human component constitutive of crop breeding and its resulting seeds/resources/accessions. The rise of omics technology could then possibly enhance participatory breeding (Jarvis et al. 2008; Williamson and Leonelli 2023) and in turn, help consider genetic resources more holistically: as constitutive elements of specific social and cultural organisation (Leclerc and Coppens d’Eeckenbrugge 2011). The future of bio-digital resources and their repositories are also tightly linked to scientific development: the relatively broad consensus over open access to genetic data in the biosciences (Amann et al 2019) and the developments of data sharing standards (e.g. FAIR: Findable, Accessible, Interoperable, Re-usable and CARE: Collective benefit, Authority to control, Responsibility, and Ethics, Reiser et al. 2018; Carroll et al. 2021), will influence the way digital data (DSI) originating from PGRFA could be managed, and mechanically impact on genebank practices. However, openly circulating data is not necessarily free of any economic interests, and open access is not fair access (Bezuidenhout et al. 2017; Aubry 2019). To move from the axiom “breeding uniformity and banking diversity” (Curry 2017), genebanks will need to actively integrate all stakeholders involved in PGRFA conservation and carefully consider their respective interests. But moving from physical genebanks as we know them, to participatory bio-digital bio-centers is a paradigm shift that does not naturally align with the concept of genetic resources as it historically developed (Curry 2017; Bonneuil 2019). This will therefore require ambitious organisational and governance adjustments. This

transformation requires first moving away from big centres and vaults towards polycentric farm networks managing local genetic commons (Ostrom 1999; Nehring 2022), which would ultimately be more focused on farmers. Again here, digitisation allows facilitated access to postgenomic-derived (big) data, which in turn can be translated into added value for breeding programs. Meanwhile, to make that possible, a strong effort towards capacity building and standardization across collections and datasets will be needed.

Ultimately, I argue here that, with sufficient political support, digitising genebanks could be a unique opportunity to significantly enhance the role of farmers in maintaining diversity and future-proof breeding.

Conclusion

With an estimated less than 1% of PGRFA genebank accessions used for crop improvement (Sharma et al. 2013), there is a general call for the genebanks to surf the wave of omics data to improve conservation efficiency and facilitate access to and use of their resources. However, as illustrated by the tense debates over the digitisation of genetic resources in the ABS instruments, digitisation is not merely improving genebank practice, but rather producing a major shift in their position within the food systems. They are considered not only as simple providers of seeds, cryogenic tissue cultures or propagules but rather as bio-digital centres, more effectively meeting the needs of breeders and farmers. Digitisation will improve their capacities for prediction in breeding. While most crop genomes are being sequenced and plant science is now entering the postgenomic era, the benefits that will emerge and the actors most likely to profit from them remain open. The observed bias in sequencing towards cash crops indicates that global industrialised economies are leading the postgenomics revolution and most probably feeding the breeding divide. Genebanks are at a crossroads: either driving the path to what could be referred to as digital biopiracy (Nehring 2022) and ultimately enhancing both breeding (Aubry 2019) and digital divide (Bezuidenhout et al. 2017) or using this probably unique opportunity to adapt practices, promote capacity building and ultimately improve access to their resources. This may, in turn, empower local and smallholder farmers to participate actively in storing, sharing and breeding local agrobiodiversity.

The key questions are: what happens when all crop diversity has been sequenced? To what extent could the genomic revolution help close the current gap in conservation and sequencing between cash and neglected crops? Will contemporary genebanks help to bridge the breeding divide, and what role can they play in conserving or extending genescapes? Interestingly, calls for a more inclusive plant genomic

community are starting to rise from the research side (Marks et al. 2021).

The digitisation of genetic resources may offer a unique opportunity to reshape genebank-centric PGRFA conservation. Notably, there is a strong need to broaden the scope of conservation to promote and finance in situ and on-farm conservation. However, in situ conservation is significantly more complex and in direct tension with agricultural practices. Although it could also allow the maintenance of functioning agroecosystems which contain, among other elements, many crop wild relatives. Similar issues concerning the extent of digitisation of collections arise for (non-agricultural) biodiversity—e.g. in the development of the Extended Specimen Network in the US, which interestingly considers DSI on a much broader basis than purely genomic sequences (Lendemer et al. 2020). Other scholars evolving within the Commons conceptual framework, suggested alternative crop diversity management systems (Louafi et al. 2021). In this framework, shifting relationships between farmers, multipliers, breeders and genebanks are proposed to help address the stewardship and capabilities imbalance in the seed systems (Wynberg et al. 2021). Addressing the postgenomic digital shift can be central to promoting a new relationship between farmers and genebanks.

For genetic resources considered within the scope of the ABS framework, without waiting for hypothetical trickle-down benefits of the use (and commercialization) of digitised information derived from their accessions, genebanks could grasp the unique opportunity created by the genomic revolution. Like Ai Weiwei's porcelain sunflower seeds, moving away from the representation of an impressive collective investment, genebanks may convey a particular vision for the seed systems, and their digitisation is a unique opportunity to enforce this vision, particularly the equity and fairness it conveys.

While a shift toward a hybrid of gene bank/genomic database might be perceived as a change in the division of labour: departing from their initial physical storage function to a more proactive role in the food systems, digital genebanks will help tackle the global loss of biodiversity and food insecurity. This will certainly only become a viable option if dedicated funds are allocated to scale up infrastructures, mobilise experts and deploy inclusive research programmes dealing with state-of-the-art conservation and sustainable use of PGRFA. But ultimately, empowering genebanks depends on political choices that are deeply rooted in how our seed/food systems are structured.

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