




Tansley review

Plant genetic resources for food and agriculture: opportunities and challenges emerging from the science and information technology revolution

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Summary

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Over the last decade, there has been an ongoing revolution in the exploration, manipulation and synthesis of biological systems, through the development of new technologies that generate, analyse and exploit big data. Users of Plant Genetic Resources (PGR) can potentially leverage these capacities to significantly increase the efficiency and effectiveness of their efforts to conserve, discover and utilise novel qualities in PGR, and help achieve the Sustainable Development Goals (SDGs). This review advances the discussion on these emerging opportunities and discusses how taking advantage of them will require data integration and synthesis

and agriculture (PGRFA), Sustainable Development Goals (SDGs), synthetic biology.

across disciplinary, organisational and international boundaries, and the formation of multi-disciplinary, international partnerships. We explore some of the institutional and policy challenges that these efforts will face, particularly how these new technologies may influence the structure and role of research for sustainable development, ownership of resources, and access and benefit sharing. We discuss potential responses to political and institutional challenges, ranging from options for enhanced structure and governance of research discovery platforms to internationally brokered benefit-sharing agreements, and identify a set of broad principles that could guide the global community as it seeks or considers solutions.

I. Introduction

Technologies for generating and analysing large quantities of genotypic, phenotypic and environmental data are evolving at accelerating rates; so too are technologies and methods for synthesising genetic materials (Policy Science for Environment, 2016). New technologies for high-throughput assays and synthesis of genetic materials are revolutionising biology. The development of techniques for highly parallel, genomic sequencing has been followed by other methods for measuring the current molecular state of cells and organisms, for predicting classical phenotypes in an automated manner (Furbank & Tester, 2011), and even for re-engineering the content and function of living systems (Noman *et al.*, 2016). These technologies have led to the rapid generation of large amounts of data describing biological systems, and the analysis and interpretation of these data using statistical and computational expertise. These changes have transformed biology into an information-rich science, where the integration and interpretation of large quantities of data informs both the design and nature of new hypotheses and the application of existing results. At the same time, they are raising questions about the applicability of governance regimes for plant genetic resources for food and agriculture (PGRFA) that were established primarily to deal with the exchange of material genetic resources.

This review provides an overview of how plant gene banks, plant breeders, national programmes and farmers can potentially take advantage of these capacities to significantly increase the efficiency and effectiveness of their efforts to discover, conserve, and use new qualities in plant genetic resources.

As part of this enterprise, a range of actors will need to generate, access, integrate and synthesise data that is widely dispersed across organisational and international boundaries, and work through international partnerships that bring together complex portfolios of skills, sources of information and perspectives. To be successful, these partnerships will need to overcome a number of institutional and policy challenges that might otherwise affect the willingness of partners to cooperate in research and development activities, including generating and sharing digital genetic and trait data describing plant genetic resources (PGR). One such challenge is revising structures that currently incentivise people to treat data and information confidentially (e.g. due to competition for monetary rewards, intellectual property rights, grants, and publications), sharing it only among trusted friends or colleagues, or under restrictive licences. Another challenge concerns contested claims about how benefits derived from the use of data should be shared

among those that have contributed to the evolution and conservation of those resources. A range of collaborations and open-access data repositories have recently been criticised for facilitating uses of genomic data in ways that allow commercial users to take advantage of genetic resources without having to share their benefits as prescribed by international access and benefit-sharing laws (Hammond, 2016; The International Civil Society Working Group on Synthetic Biology, 2016). The laws in question require users to share monetary benefits in exchange for access to, and use of, material genetic resources in the development of new commercial products; they do not extend in scope to genetic sequence information. A growing number of developing countries and civil society organisations are calling on the United Nations to address this issue by developing new international obligations to share benefits derived from the use of genetic sequence data.

This review examines options for addressing these challenges through enhanced governance arrangements. This is timely in part because the 'omics' revolution in the biological sciences has considerable disruptive potential for changing the flows of information, the nature of partnerships, and the range of products and benefits that can be generated through PGR conservation and applied plant breeding. Meanwhile, the policy environment has lagged behind, with a concomitant shortage of shared norms to guide the resolution of contested claims related to how omics-driven research and development is conducted in relation to PGR. The kinds of governance arrangements eventually put in place, and the manner in which contested benefit-sharing claims are resolved, could have considerable impact on the way in which research and development in the agricultural sector is perceived and conducted.

II. Technological advances and their utility for gene banks and breeding, and longer-term contributions to SDGs

1. The impact of genetic technologies on germplasm repositories and seed banks

Historically, genetic variation was recognised and tracked based on visual assessment of phenotypic variation, but since the development of molecular marker technology in the 1980s, it can be assayed directly at the DNA level. There are many genotyping platforms (Goodwin *et al.*, 2016), but all are designed to do essentially the same thing: identify differences in the genetic sequences of individuals, and record the differences (polymorphisms) and monitor their presence or absence in specific individuals in a

systematic way, often using a reference genome coordinate system. In the context of germplasm repositories (here we refer to all collections held by private individuals, companies, national or international bodies), also known as 'gene banks', this has a number of obvious applications. First, it makes possible the extensive characterisation and traceability of the stocks that are currently held by gene banks. Genomic analysis allows the level of variation among individuals in a single seed pack, gene bank accession, or a number of accessions to be ascertained and accurately quantified. This can better inform the quality control, maintenance, distribution, and use of gene bank stocks. Moreover, extensive genotyping, linked to measured traits, allows repositories to be searched for strains containing desired genetic elements and/or trait characteristics, and the production of new products that improve the sustainability, diversity and resilience of crop plants, which is particularly important given the urgent need to feed and nourish a growing global population in the face of substantial change to the natural environment.

2. Integrating big data into breeding programs

Generating sequence information *per se* is no longer a bottleneck to crop improvement. Phenotypic characterisation has historically been more problematic, but increasingly, molecular phenotypes (e.g. gene expression and ion content) can be used as indicators of physiological or performance phenotypes, while quantitative imaging techniques using remote sensing can directly measure plant architectural and stress response characteristics in a variety of experimental set-ups (e.g. automated glasshouse and field settings under drone surveillance). Statistical models can be constructed to predict the breeding value of an individual, given its genomic composition (genomic selection); and an optimal breeding scheme can be designed in the light of such predictions. Genomic selection has been associated with major performance gains in livestock species, and it has similar potential in plant species. Accurate prediction is enhanced not only by access to *more* data, but to more variation in the available data – which means sampling the gene pool as extensively as possible, and assaying under the widest range of environmental conditions. If information can be collected, it is possible that the method will develop sufficient power to accurately predict genotype \times environment ($G \times E$) interactions, allowing for the development of specific crops tailored to particular environmental conditions. Dedeurwaerdere (2013, p. 369) notes that, the 'information technology revolution has dramatically expanded the possibilities of distributed coordination . . .' in the use of genetic resources. Indeed, the increasing generation and use of big data by farmers themselves (both as inputs into and outputs generated by agronomic decisions) could potentially create a huge reservoir of knowledge about plant performance (including stress tolerance, nutritional quality and overall yield) in a far wider range of climates, soils, and management regimes than could be tested by a single breeder, research team or organisation (Satizábal *et al.*, 2012; van Etten *et al.*, 2016, 2017). This information, if made available to breeders and biological engineers, has great potential to feed back into further improvement programmes. A more formal and extensive partnership between farmers, researchers and other

actors to facilitate the flow of information stands to substantially enhance benefits to the variety of plant genetic resources stakeholders.

3. Technologies for identifying and creating genetic variation

Molecular marker (genomics)-assisted germplasm curation, research and breeding All crop improvement practices aim to capture (within elite lines) genetic variants that confer desirable traits. The ability to accurately identify and track genome-wide genetic variation or individual molecular variants across generations of individuals offers a powerful tool for germplasm managers, basic researchers, and plant breeders (Collard & Mackill, 2008; McCouch *et al.*, 2012). For example, gene bank managers utilise molecular markers to establish and validate the identity of accessions in their collections, to determine genetic relationships among individuals, to perform gap analysis to guide collecting efforts, and for allele mining to identify accessions that carry particular alleles (traits) of interest. Basic biological researchers use genomic and other 'omics' analyses to characterise the structure, function and evolutionary significance of genes and alleles, to study plant development and response to environment, and to understand speciation and the implications of diversity at the individual, population and ecosystem levels. Applied breeding programs use molecular marker data to identify parents for crossing, to select offspring carrying favourable or deleterious alleles in segregating populations, and to perform genomic prediction.

Genetic and genome engineering Since the 1980s it has been possible to randomly insert new genetic material into the genomes of plants. The first genetically modified crops to be commercialised were tomatoes with extended shelf life (1994), insect resistant potatoes (1995), herbicide (glyphosate) resistant soy (1996) and virus resistant papayas (1998). Genetically modified crops are now grown on 181.5 million hectares of land, by 18 million farmers (Stevenson *et al.*, 2013; James, 2014). In the past decade or so, emerging technologies (such as programmable nucleases, e.g. zinc finger nucleases and RNA-guided Cas9 (i.e. CRISPR-associated protein 9) from bacterial CRISPR systems) have enabled so-called precision genome engineering (or genome editing): the induction of targeted modifications to the genome, its contexts (e.g. epigenetic marks) or its outputs (e.g. transcripts) (Petolino *et al.*, 2016; Schiml & Puchta, 2016). Targeted genome modifications include the induction of mutations at preselected loci to disrupt the function of one or more specific genes; the editing of existing sequences to reproduce ancient alleles or to introduce novel alleles; or the introduction of new genetic material into specific loci or regions of the genome. It is also possible to change DNA modifications, such as methylation, in order to modulate gene expression. When coupled with the ability to chemically synthesise DNA molecules at ever diminishing costs, genome engineering may enable multiple novel variations to be designed and tested at any desired genetic locus, including in multifactorial combinations (Puchta, 2017).

Although some of these technologies are still inefficient and difficult to execute, they are being developed for numerous food

and nonfood crops, and progress continues apace. Genome engineering and synthetic biology technologies have the potential to vastly reduce the time taken for knowledge generated in the laboratory to transition into marketable products by allowing the direct introduction of favourable alleles into agronomically valuable germplasm, thus reducing the number of breeding cycles required. One day, this may mean that it is possible for a farmer to request that a targeted set of changes be made to a highly valued cultivar as part of the breeding process. In response, a new genetic trait or combination of genetic characteristics could be rapidly designed and introduced into a cultivar to improve its resilience to stress, nutritional quality or architectural characteristics, making it a better fit for either the traditional cropping system or the modern agricultural landscape. These applications have the potential to bypass the direct use of specific *physical* host plants that may have played an important role in identifying the novel traits, with wide ranging implications for owners, managers and users of PGR.

4. Information technologies underpinning plant genetic resources

Information technology has played just as important a role as genomic technology in the evolution of crop improvement strategies. Ongoing improvement in the performance of computers, driven by the ever-increasing miniaturisation of transistors, was noted by Moore as long ago as 1965 (Moore, 1965). Subsequently, the development of many other aspects of computer hardware (parallelisation, storage, networking, etc.) has enabled, and also been driven by, the data revolution in almost every field of study. In particular, the development of the Internet, the World Wide Web, and the explosive growth in mobile communications networks, have put much of this computing power and the data that lies behind it in the hands of citizens world-wide, including those interested in PGR (scientists, breeders, farmers and consumers). However, much of the relevant data is highly dispersed, has limited compatibility, and is in practice hard to interpret except by specialists.

'Apps' are computer programmes that have been optimised for a particular purpose, and commonly used on mobile computing devices. Compared with traditional tools, apps are often simple to use, and each one developed to address a specific, limited, well-defined use case, frequently by opportunistic entrepreneurs and social entrepreneurs (the barriers to entry in the app development market are relatively low). Increasingly, such apps are in use by farmers, even in low and middle-income countries, to source seeds and other agricultural inputs, improve agronomic and pest management practices, and optimise market decisions. The provision of information about the genetics and performance of crop varieties in particular environments through apps could assist farmers in the selection of varieties appropriate to their conditions and cropping systems. Moreover, the collection, by farmers, of detailed measurements of the actual environments in which crops are grown could enable the development of more precise and sophisticated modelling of G×E interactions. The potential for such advances, while holding tremendous promise, is still largely untapped.

III. The challenges that must be overcome to realise emerging R&D opportunities

Access to large-scale sequence and phenotype information at unprecedented scales is providing new opportunities to accelerate the application of basic research. This includes the ability to formulate testable hypotheses about the genetic architecture of quantitative variation, the genes and biological pathways involved, and the causal variants responsible for the inheritance of complex traits in diverse species (Hamblin *et al.*, 2011; Lipka *et al.*, 2015; Sardos *et al.*, 2016; Yano *et al.*, 2016). It should be noted that raw sequence information, if it is to be correctly interpreted and exploited, needs to be integrated with an intimate knowledge of the biology of the species under consideration, the phenotype or performance of the individuals or population that has been sequenced, and the agro-ecosystem in which they have been grown, including the cultural context and farmers' management practices. Furthermore, when experiments are implemented appropriately, taking into account experimental and mating design (Cavanagh *et al.*, 2008; Ersoz *et al.*, 2009), there are opportunities to unify discovery biology with breeding. In other words, breeding programs can become 'test beds' for hypotheses about G × E interaction as well as platforms for the development and deployment of new varieties (Poland, 2015). Realising this potential will require the ability to work at different scales, extending from molecules to landscapes within a quantitative biology framework (Cooper *et al.*, 2014), and will require greater collaboration between breeders, growers and the biological research community. A potential model describing such a framework is shown in Fig. 1.

1. Technical impediments to sharing, tracking, annotating and linking data

Some of the technical impediments that need to be overcome to facilitate data-integration and the potential for data-sharing include: (1) data are fragmented and dispersed across organisations and international borders and are not managed following the FAIR principles of Findability, Accessibility, Interoperability and Reusability (Wilkinson *et al.*, 2016); (2) inadequate systems exist for logging and tracking PGR as well as metadata related to PGR, for example there is no universally agreed-upon system for permanently and uniquely identifying PGR (e.g. publications do not provide traceable, permanent unique identifiers for PGR); and (3) radically different approaches to data management and sharing within and across public and private sectors due to fundamentally different objectives and low levels of mutual trust.

These challenges are further complicated by the fact that a number of different kinds of data need to be integrated, including genetic sequence, phenomic, environmental and GIS (geographical information system) data. Some have suggested that data on PGR in gene banks should be deposited in digital data repositories (mirroring the physical repositories they describe), and made available, consistent with national and international agreements, through standard application programming interfaces (APIs) to scientists, breeders, farmers and entrepreneurial tool developers. Several initiatives have been established to promote this

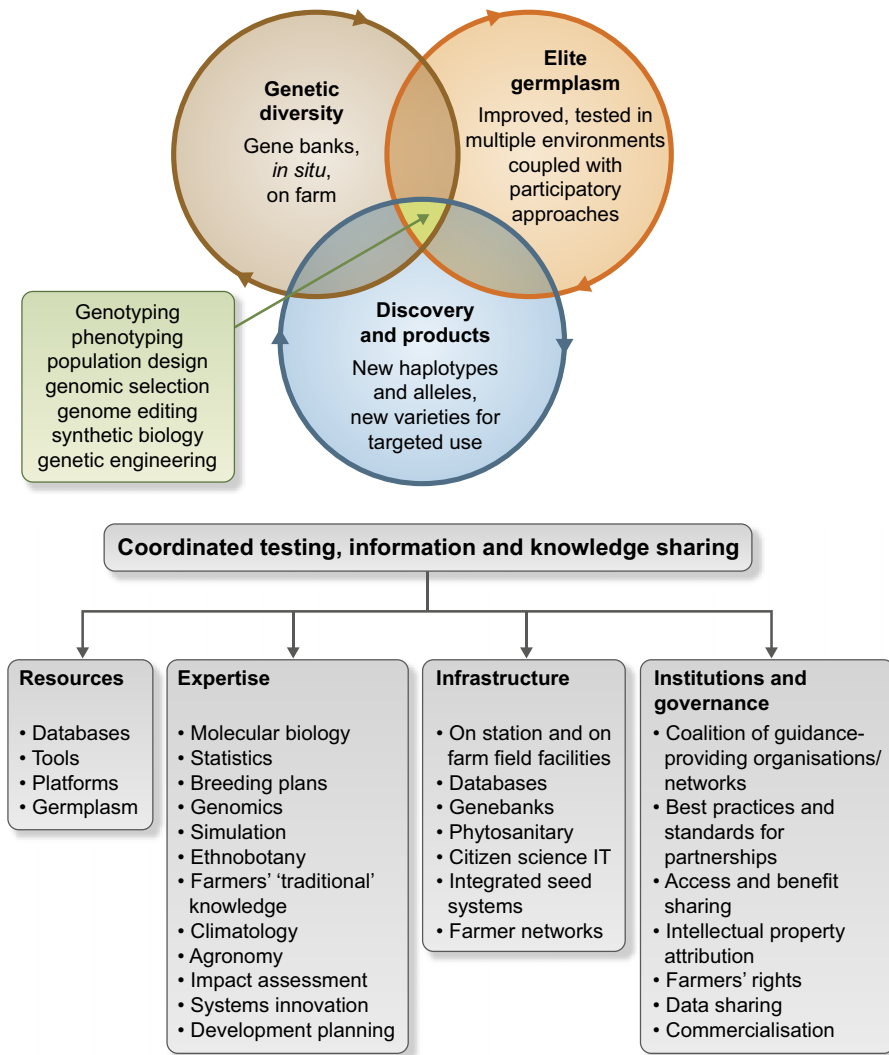


Fig. 1 Schematic presentation of a model for discovery and breeding platforms. Multi-environment testing and information or knowledge sharing underpin systematic assessment and improvement of plant genetic resources to produce elite germplasm and new products.

interoperability, including DivSeek (www.divseek.org), Global Open Data for Agriculture and Nutrition (GODAN: www.godan.info), the Research Data Alliance (RDA: www.rd-alliance.org) and the Breeding API (BrAPI: <https://brapi.org>).

The Global Information System of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) seeks to link existing information systems on PGRFA. It has established a new mechanism to facilitate this by identifying PGRFA using Digital Object Identifiers (DOIs: www.fao.org/plant-treaty/areas-of-work/global-information-system/en). The goal is to promote the networking of high quality data repositories (and data access channels) with efficiently designed data input systems. If successful, the deployment of DOIs should increase the quantity and diversity of PGR-related data, reduce utilisation barriers to the plant material conserved by germplasm repositories, and facilitate their use by growers, plant breeders and biological engineers. Adoption of standardised protocols would facilitate the pooling of such data across organisations for comparative analyses and collaborative work, and could lower entry barriers that currently

limit farmer involvement in translational agricultural research and development.

Experience from other areas of biological research provides some clear models for how this need for data integration can be addressed. The transformative effect of bioinformatics on many biological questions owes much to open-access data. A key decision was made in the early 1980s to operate three international repositories for the storage of nucleotide sequences, that is: GenBank at the National Center for Biotechnology Information (NCBI) in the USA, the European Molecular Biology Laboratory – EMBL Data Library (today the European Nucleotide Archive), and the DNA Database of Japan (DDBJ) (Lawson & Rourke, 2016). This unprecedented degree of collaboration among members of the international research community paved the way for persuading the leading scientific journals to require data publication as a precondition of article publication. This new ideal has resulted in large quantities of nucleotide sequence data being made publicly available without any claims of intellectual property passed on by the data providers or the database operators (see

Supporting Information Notes S1). These data now include the sequences of humans, other mammals, birds, fish, insects, microbes, and over 120 000 flowering plant species. More recently, newer models for the pre-publication of data and manuscripts (deposition in advance of formal acceptance by a refereed journal) have been suggested, following the work of other communities (Toronto International Data Release Workshop, 2009). Furthermore, alliances of interested parties have formed to develop data models and appropriate structures for interfacing between public and private data. One such example in the context of medical bioinformatics is *The Global Alliance for Genomics and Health* (<http://genomicsandhealth.org>).

2. Political and institutional impediments

Bioinformatics capacities have not evolved in a political and institutional vacuum. They have gained prominence during a period of considerable discord within the international community concerning the proper balance of incentives for the development of advanced agricultural technologies (in the form of intellectual property rights) on the one hand, and for the conservation and sustainable use of genetic resources (in the form of access and benefit sharing laws) on the other.

Until the late 1960s, plant genetic resources were generally treated as 'global public goods'. In the decades that followed, technologically advanced countries pushed for the international recognition of intellectual property protection for living materials, through the UPOV (International Union for the Protection of New Varieties of Plants) Convention and the Uruguay Round of GATT (General Agreement on Tariffs and Trade) negotiations. This led to disquiet, particularly among developing countries that were the historic sources of much of the genetic diversity of the crops being commercialised and protected. Developing countries pushed back, through negotiations under UNEP leading to the Convention on Biological Diversity 1993 (CBD: www.cbd.int). They insisted on the recognition of their sovereign rights to regulate access to genetic resources within their borders, with the expectation of negotiating access and benefit sharing agreements with foreign access-seekers (or 'bioprospectors').

Discontent with the impact of the CBD on benefit sharing led to the negotiation of the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization (Nagoya Protocol), which came into force in 2014. Under the Nagoya Protocol, contracting parties agree to put mechanisms in place for the monitoring and enforcement of bilaterally negotiated access and benefit sharing agreements. At the moment, it is too early to predict how the Nagoya Protocol will impact stakeholders' willingness to share genetic resources for use in agricultural research.

Meanwhile, the 2004 International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) created a multilateral system of access and benefit-sharing (MLS) for contracting parties and international organisations. The MLS provides facilitated access to the genetic diversity of 64 crops and forages for the purposes of conservation and use for agricultural research, training and plant breeding. Commercial users of

material accessed under the multilateral system are obliged to make financial payments to an international benefit-sharing fund under prescribed circumstances. To date, no obligatory payments have been made under this system. In turn, some potential material providers are not following through on commitments to make genetic resources available through the system. These lapses led to the launch, in 2013, of a process for enhancing the multilateral system of access and benefit sharing through renegotiation of its basic terms. If and when agreed, these new terms will be reflected in a revised Standard Material Transfer Agreement (SMTA).

It is important to note that the CBD, its Nagoya Protocol, and the ITPGRFA, link benefit-sharing obligations to the access and use of physical *material* containing functional units of heredity (e.g. seeds and cuttings). They do not specifically regulate access to digital data, for example genomic sequence or phenotypic data (see Notes S2). All three agreements refer to digital research data as a potential benefit to be shared in return for access to genetic resources. In fact, all three agreements were negotiated without much discussion or debate about how ongoing technological breakthroughs (e.g. sequencing, phenotyping and bioinformatics) might eventually make it possible to take advantage of genetic resources without the need to access these physical resources. Thus, even if the agreements were to operate as intended, they would not directly address concerns that the use of open-access sequence data (and other related big data) will make it possible to profit from the use of genetic resources without benefit-sharing obligations (see Notes S3).

In light of this recent history, it is perhaps not surprising that some country and regional representatives, civil society and farmers' organisations have voiced concerns that technological breakthroughs in genomic breeding, gene editing, and gene synthesis will widen the technology gap, and concomitant economic disparities, between the developed and developing countries. They worry that these breakthroughs will exacerbate tensions associated with the unrealised expectations of monetary benefits accruing from access and benefit sharing laws. These stakeholders note that at present the requisite technological capacities principally reside in elite research institutions in the global north. They are sceptical that these new capacities will be used to develop technologies targeted at resource-poor farmers working in vulnerable agricultural systems. This has led to demands (by some civil society organisations and developing countries) that research organisations stop providing unregulated open access to genetic sequence data until benefit sharing issues can be addressed (Hammond, 2016; The International Civil Society Working Group on Synthetic Biology, 2016). If efforts are not made to enhance trust and inter-stakeholder cooperation, these controversies might ultimately undermine the development of an open-science culture, slowing the rate of the scientific advance and crop improvement. On the other hand, there are also reasons to view the development of legally binding solutions at the level of the United Nations with caution. Reichman *et al.* (2016, p. 81) summarise the overriding institutional challenge:

'the resulting fears of . . . "biopiracy" if left unchecked, [threaten] to destabilize the pre-existing system of formal and informal exchange of

both *ex situ* and *in situ* genetic resources on which . . . agricultural research and applications have traditionally depended. By the same token, overzealous regulatory measures to defend sovereign rights to these genetic resources could perversely shut down that same system of exchanges, with potentially serious consequences for global scientific research.'

IV. Renewed governance structures for PGR (and related big data)

'In the future, if the multiple source [innovation] model is used, we will see a switch from the transfer of institutional models and blueprints for research methods from centers to clients to an approach where emphasis is on seeking out, understanding, and learning from innovators in their local context. An implication for resource allocation in agricultural research will be a major increase in the funds given to information exchange and networking activities whereby local institutions are in direct contact with each other and "centres" are no longer seen as the hub. A further implication of the model would be that increasing access to, and control of, these networks would be in the hands of the poorer groups.'

Biggs (1990)

The forgoing analysis underscores the need for enhanced governance of the generation and use of genetic sequence data and related information about PGR. This enhanced governance is necessary in order to promote trust and transparency amongst different stakeholders, and encourage the development and use of knowledge and technologies that ultimately advance the sustainable development goals. The questions we examine in this section are: 'what forms of governance are needed? What kinds of interventions would be necessary to enhance the overall operation of the existing patchwork of organisations, institutions and practices in furtherance of the SDGs (see Fig. 2)?'

On one hand the new bioinformatic capabilities risk exacerbating many of the unresolved issues related to the governance of agricultural research generally and genetic resources more specifically. On the other hand, we are hopeful that, these new 'disruptive technologies' have the potential – if properly governed – to transcend some of these long-standing tensions. This is partly because they make it possible to engage a broader range of interested parties in the research and development process in ways that are economically efficient, practical, and attuned to non-market considerations. For example, they can radically lower the costs of local level needs assessments and facilitate crowd-sourced farmer evaluation of materials across a broad range of agro-ecosystems.

Of course, these are not entirely new questions. Over the course of the last 30 years there have been a number of studies, from a range of theoretical perspectives, analysing the influence of organisational structures on agricultural research and development in general, and more particularly on efforts to conserve, add value to, share and exploit PGR. Many of these studies were conducted before the recent increases in technological capacities outlined above; nonetheless, they can still provide useful insights.

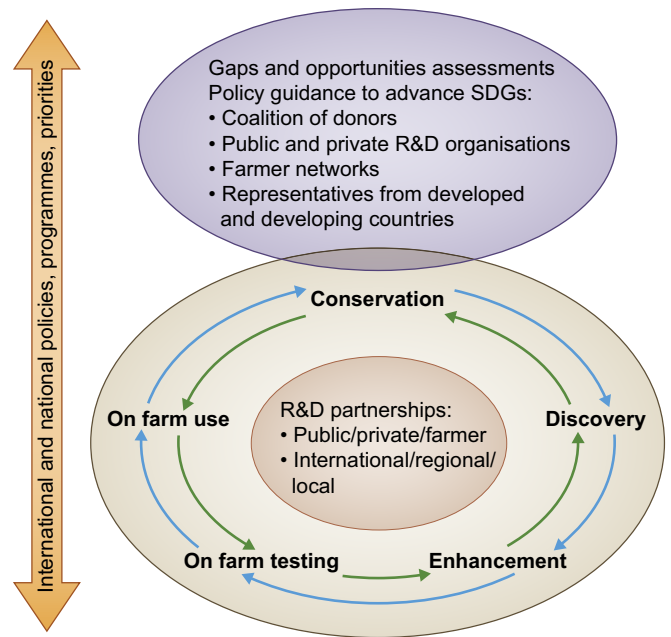


Fig. 2 Generalised governance structure. Blue arrows, knowledge-driven forward flow of materials, technology and information to benefit the farmer. Green arrows, reverse-flow of data and information to enhance earlier steps in the impact pathway. SDG, Sustainable Development Goals.

1. Modular architecture for commons-based production

Dedeurwaerdere (2013) considers a range of case studies of 'commons-based production' of public goods in whole genome sequencing, wheat breeding, animal breeding programmes, and research on root nodule bacteria for use in soy bean production. He concludes that many of the most successful programmes have been characterised by 'modular architectures' which allow the pooling of input from many individuals from diverse backgrounds, focus and geographical location. By extension, the innovation systems through which these goods are produced necessarily require the inputs of many actors, none of whom can act alone. Dedeurwaerdere notes a second common feature in successful case studies: a critical density of the actors participating in the commons-based production efforts are motivated by nonmarket incentives, for example: recognition by scientific peers, access to funding, commitment to sustainable development, biodiversity conservation, or other broader social goals. Furthermore, the goods produced through these modular architectures of commons-based production, for example improved breeding lines and whole genome sequences, tend to be treated as precommercial. That is not to say that information commons are exclusive of private interests or linkages to the further development of appropriable, commercial goods; indeed, such linkages frequently exist, but the goods are not generated exclusively for this purpose.

Dedeurwaerdere's work fits within an emerging field of analysis of 'new commons' focusing on purely culturally created goods (Madison *et al.*, 2010; Ostrom & Hess, 2010). It builds on Elinor Ostrom's institutional analysis of factors contributing to the sustainable management of common-pool natural resources

(Walker *et al.*, 1990). Common-pool natural resources, for example, forests and watersheds, are defined as rivalrous (i.e. one person's use of a resource detracts from others' use of the same resource), and non-excludable (i.e. it is difficult or impossible to prevent others from accessing the resource). The natural resources and users studied by Ostrom were necessarily limited in number and geographic space. On the other hand, the new cultural commons pertaining to PGR that are emerging as a result of new information technologies and capacities may be distributed around the world, with potential to dramatically scale-up the number of participants. In the case of digital information, one person's use does not impinge on others' use of the same resource. Thus, information is nonrivalrous. It is also virtually impossible to exclude others from accessing it. Perhaps the biggest difference between cultural and natural resources commons is that the former have to be created through commons-based production systems, while the latter already exist. As a result, the 'social dilemmas' to be addressed with respect to both commons are very different. Madison *et al.* (2010) state that:

'...unlike resources in the natural world, resources of information and expression must be created before they can be shared. Because of the public goods character of these resources, a cultural commons must manage both use and production of cultural resources. [...] This characteristic of cultural commons produces a more intertwined set of exogenous variables because separating the managed resources from the attributes and rules-in-use of the community that produces them is impossible.'

Genetic resources for food and agriculture lie somewhere between cultural and natural resources commons (Halewood, 2013). The original raw materials were naturally occurring plants; they have since been dramatically altered over the course of millennia through combinations of both natural and human selection pressures. One social dilemma unique to cultural commons (and hybridised natural and cultural commons such as Plant Genetic Resources for Food and Agriculture) is that underuse, not overexploitation, threatens their creation and continued existence. Farmer-bred crop varieties that are not maintained through continued selection will degrade and cease to exist. If they are not actively reproduced, they will be subject to genetic drift and recombination with other populations until they eventually cease to be what they were (see Notes S4). The same is true of most varieties bred by professional plant breeders.

Before the bioinformatics boom, the range of actors involved in the generation, conservation, improvement and use of plant genetic resources was already extensive. It involved farmers in centres of genetic diversity; public and private sector researchers and plant breeders; and community, national and international gene banks, with the Svalbard Global Seed Vault as the 'safety back-up of last resort'. Halewood's (2013) observation that, 'given this complexity, it is perhaps not surprising that the modular organization of PGRFA commons have evolved into separate tiers, involving like-minded and like-situated [...] communities of actors, with various levels of connection between them' highlights the pervasive tendency toward homophily within social networks. That is, the infrastructure for the conservation and production of PGRFA

integrates and rewards some tiers better than others. One tier is organised around gene banks throughout the world. Actors within this tier are generally preoccupied with and rewarded for the conservation of existing genetic resources, rather than the production of novel genetic resources. This may change if pre-breeding activities become the remit of gene banks, particularly with increased sequencing and data processing capacity. Primary responsibility for innovation and the production of PGRFA rests with plant breeders and farmers, both of whom have well-established reward systems. Professional plant breeders tend to occupy a different tier than farmers (who were the original plant breeders), one in which market forces, at least for some crops, are playing an increasingly important role. There are also functional links between gene banks and breeders. The situation with farmers is very different, particularly resource-poor farmers in centres of crop genetic diversity. Resource-poor farmer networks are generally small and local, with poor connections to national and international gene banks, and few links to professional plant breeders. Planting decisions for these farmers are nonetheless often largely market driven, and/or for private consumption. Their collective contributions to crop diversity over several millennia have been made without established mechanisms of reward or recognition for individual farmers or even farmers' collectives as innovators or as producers of PGRFA beyond the reward of the crop harvest itself. Hodgkin *et al.* (2013) draw similar conclusions with respect to their analysis of the state of the 'Global System for the Conservation and Sustainable Use of PGRFA' developed under the auspices of the United Nations. Over the last 40 years, considerable effort has been made to support *ex situ* conservation (gene banks) and professional plant breeding; comparatively little has been done to support on-farm (*in situ*) conservation and local breeding efforts. To date, efforts to integrate these modular architectures into cooperative networks have not been successful in fostering new collaborations or greater trust among disparate interest groups.

2. Brokerage platforms to enhance innovation systems

The literature on innovation theory, particularly on the role of research in agricultural innovation, provides insights about the influence of organisational structure and the importance of enhanced linkages between the key actors involved. The starting point for much of this literature is a rejection of the idea that agricultural innovation follows a predictable, politically neutral, linear pathway controlled by research centres that transfer beneficial technologies to passive recipient farmers in a 'trickle-down' framework (see Notes S5). Instead, it is argued that agricultural innovation derives from multiple sources, follows unpredictable paths, and is highly influenced by (if not inseparable from) institutional, economic and political factors (Chambers, 1983, 2008; Biggs, 1990; Hall *et al.*, 2003, 2005). Douthwaite *et al.* (2003) characterise this duality as positivism vs constructivism. Regardless of the fact that the narrative of the linear innovation pathway does not accurately reflect reality, it is perpetuated because, among other things, it is appealingly simple: it reinforces the dominant position of scientific research centres and their access to funds; responds to donors' need for predictable, measurable

returns on investments; and cannot be easily challenged by those outside the major research centres who are actively contributing to innovation processes.

One focus of innovation systems research is the analysis of empirical evidence of different groups' contributions to the development, diffusion and adoption of agricultural technologies to establish the extent to which those processes are centralised or decentralised. Another focus is the identification of ways of increasing innovation capacity by enhancing engagement between stakeholders in the development and use of technologies, with a focus on institutional learning, and strengthening the linkage of previously marginalised stakeholders to the innovation process. Various studies have confirmed the utility of such interventions in helping previously unorganised groups, or groups disconnected from formal research scientists, to articulate their interests or demands; in lowering levels of uncertainty in the preliminary stages of innovative processes; in forging alliances for new innovation agendas between actors that would not or could not risk engaging in new activities on their own; and in mediating conflicts among partners regarding funding allocation and intellectual property ownership (Klerkx *et al.*, 2009). Examples of interventions that have enabled such progress include the creation and empowerment of innovation intermediaries (Howells, 2006), innovation brokers (Klerkx *et al.*, 2009), multi-stakeholder platforms (Adekunle & Fatunbi, 2012), and education and training networks (Spielman *et al.*, 2008). These studies have also shed light on circumstances that can lead to the failure of such interventions, including perceptions that the broker: (1) is not sufficiently independent and too closely tied to the objectives of his or her own organisation, (2) may eventually enter into competition with other stakeholders in the innovation processes concerned, or (3) has too much influence as a source of expert knowledge and ends-up occupying the position of a consultant providing expert opinions, undermining the group dynamic and reducing contributions from others.

3. Strengthening network ties for innovation and policy development

The 'modular architectures' described above are conceptually similar to what is known in network theory as a 'collaborative innovation network'. Networks come in many forms, but are fundamentally comprised of actors and relations. Actors, referred to as 'nodes' in network theory, are differentiated by influence (e.g. power, prestige) and relationships vary along an informal–formal continuum.

Properly functioning, participatory networks foster trust, largely through the formation of social capital. Local actors, particularly farmers and community organizations, currently enjoy relatively little social capital in existing PGRFA networks. Access to influential nongovernmental organisations (NGOs), scientific knowledge networks and direct linkages to financial stakeholders could substantially expand the social capital of local stakeholders and, importantly, enhance trust within the network.

Overcoming barriers to trust, and the divergence of interest between the different actors interested in PGRFA is central to accelerating the development of improved crops. However, it will

require new models of scientific practice that redefine the traditional top-down (hierarchical) models that have dominated the field. Greater engagement with stakeholders who have traditionally been implicitly or explicitly viewed as passive, peripheral participants in the larger innovation process is critical if we are to break out of the current situation where material-sharing is in decline and benefit-sharing is not apparent.

We briefly mention two types of networks that could inform the structure and *modus operandi* of new genetic resources or bioinformatics-based innovation platforms. Peer network academies (Klerkx & Leeuwis, 2009) represent a high-value collaborative network hub due to their focus on networks of stakeholders that share common interests (e.g. corn, rice, dairy, and poultry in the agricultural industry). Two key features of a peer network academy organised around PGRFA are an online databank, which can serve as a clearing-house for essential information, including germplasm input systems linking to larger data repositories, and a collaborative structure in which farmers are active participants in knowledge discovery by virtue of their fields functioning as demonstration farms (citizen scientists).

A second type of network model to be considered in this context is that of Collaborative Innovation Networks (CoINs). CoINs facilitate inter-network collaborations that span traditional social, economic, and cultural hierarchies and boundaries to encourage direct communication between actors that have traditionally had little or no direct communication and collaboration (Gloor, 2006). They are characterised by a widely dispersed but interdependent membership working toward common goals in an environment of trust. A hallmark of CoINs is their lack of central management, which allows broadly-based transparent interactions among network actors. However, new innovation platforms will likely (at least initially) require investment in more centralised governance mechanisms to identify and promote shared goals and trust among the range of actors that we underscore need to be involved. Of course, some of the 'modules' of the innovation platform could embrace CoINs-inspired structures and *modus operandi*, and over time the proportion of such activities related to the innovation platform could increase.

To address hierarchical organisational structures and concentrated power among the elite actors involved in genetic resources or bioinformatics-based innovation platforms, we suggest two possible approaches. Farmers, especially those in developing countries, will need a seat at the table that is not merely symbolic, but functional. Redefining farmers as citizen-scientists filling an integral role in field experimentation and data generation as part of a modular, commons-based innovation system holds tremendous potential for overcoming the historical backdrop of mistrust between local stakeholders and elites working in agri-business, science and public policy. In addition, data generating systems could and should link field data, germplasm information and relevant metadata in a manner that moves farmers from the end of the conventional agricultural research extension pipeline (Klerkx *et al.*, 2009) to a central, equal role in the PGR collaborative innovation network. Farmers (and the system as a whole) should benefit from being able to develop new, collaborative linkages with scientists, civil society organisations, and agri-industry groups.

Such a data network would require feedback loops that facilitate not only the transmission of information into large-scale data repositories (e.g. genetic sequence, phenomic, environmental and GIS data) but also cycle information back out to the field in an open and transparent manner that engenders trust, furthers cooperation, and produces equitable benefits across the network. Complementary capacity strengthening is necessary to promote the ability of farmers' organisations and resource-poor national agricultural research and extension services to take advantage of these networks.

V. Access and benefit sharing and big data

As highlighted above, much of the support for international access and benefit sharing (ABS) laws came from developing countries that were (and are) concerned about existing inequities in the distribution of benefits derived from the commercial use of genetic resources. If institutionalised, the modular, inclusive, governance mechanisms described above could help allay concerns that the new bioinformatics capacities will exacerbate those inequities. To increase the likelihood of this positive outcome, organisations seeking to catalyse new genetic resources/bioinformatics-based innovation platforms should promote best practices and develop voluntary standards explicitly addressing ABS issues. Demonstrable compliance with these standards could be a precondition of endorsement by the innovation platform(s) of project proposals prepared for donors, or projects in which platforms engage directly. The advantage of this approach to developing ABS standards and best practices, is that they can be developed organically, building on existing practices and reciprocal interests of the actors involved. In this way, they could be sufficiently flexible to take into account the very different motivations of the very different groups of actors, and the wide range of both nonmonetary and monetary benefits that can be generated.

Meanwhile, as discussed above, the issue of sharing benefits derived from the use of genetic sequence data has already made its way onto a number of international agendas, with developing regions calling for new, internationally negotiated benefit-sharing rules. The ITPGRFA Governing Body, Conference of the Parties to the CBD, and FAO (Food and Agriculture Organisation) Commission on Genetic Resources for Food and Agriculture have all initiated fact-finding processes to consider the effect of genome sequencing and synthesis on the conservation and sustainable use of genetic resources, and the equitable sharing of benefits. The issue is also being considered under the framework of the WHO (World Health Organisation) Pandemic Influenza Preparedness (PIP) framework. The PIP Framework Advisory Group and a specialized technical working group are considering options for benefit sharing linked to the sharing and commercial use of gene sequence data of influenza viruses with human pandemic potential (see Notes S2). On one hand, there is clearly a need for novel approaches to promote both monetary and nonmonetary benefit sharing. On the other, we are concerned that discussions at the level of the United Nations have historically tended to focus almost exclusively on monetary benefit-sharing (largely overlooking ways to promote valuable forms of nonmonetary benefit-sharing).

As the summary of the last 30 years of international policy-making above underscores, it is challenging to develop globally applicable, legally binding ABS norms that are a custom fit for emerging areas of scientific practice. There is a risk that new efforts at the level of the United Nations to develop a one-size-fits-all, ABS policy solution with respect to genomic sequence data could inadvertently end-up perpetuating disincentives for sharing, accessing, and using genetic resources and information (including genomic sequence data). New rules, if inappropriately crafted, could inadvertently create barriers to the development of innovation platforms and enhanced governance arrangements as described above. In the following paragraphs, we briefly consider a range of options regarding new ABS policies that are, have been, or could be, considered by these intergovernmental bodies. This is not meant to constitute a thorough analysis of ongoing negotiations; only to provide an introductory insight into the kinds of benefit sharing 'solutions' that are actively under consideration in those fora.

Perhaps the lightest-weight option would be for one, or some combination, of those international bodies to opt for a 'soft' norm approach, without the creation of new, legally binding obligations. This approach could involve identifying and endorsing best practices, developing voluntary guidelines and model ABS agreements. It could also include self-reporting mechanisms through which new innovation platforms could report on their management structures, guiding principles, partnerships and activities, and seek endorsements from relevant international bodies.

Another approach would entail extending the scope of the Nagoya Protocol and the ITPGRFA to apply to genome sequence and other types of digital data related to PGR, in addition to material genetic resources. Under the ITPGRFA, this would entail data owners and curators agreeing to provide facilitated access to data sets subject to the condition that if that information was 'incorporated' (or used) in the development of new, commercialised PGRFA products, the data user would have to make payments to the Benefit-Sharing Fund (BSF). Under the predominant model for national implementation of the Nagoya Protocol, parties seeking access to a database containing genome sequences or other PGR-related digital data would need to negotiate an ABS agreement, which could include any number of conditions. The same mechanisms for monitoring and enforcing compliance with ABS agreements for material genetic resources would be extended to trace and enforce agreements related to digital PGR-associated data. Unfortunately, as highlighted above, these contract-based, track-and-trace ABS systems are already proving to be very difficult to implement given the nonrivalrous and nonexcludable nature of material genetic resources. Controlling access to information – given that it is already so diffused, easily copied, and easily moved through the Internet – would be even more difficult, as would be tracking and tracing the use of that information in the development of a discrete, new, commercialised crop variety or patented trait. One can imagine the adoption of such a model eventually leading to a collapse of the ABS systems that the international community has been working to develop since the CBD came into force. On the other hand, perhaps the technological breakthroughs that have created enhanced interest and value for genetic sequence

information could also be deployed in enhanced systems for monitoring and verifying uses of those data.

A more pragmatic variation of the contract approach that is currently being considered under the ITPGRFA framework is to create a subscription system for accessing both genetic resources and sequence data, and for sharing related monetary benefits. Under this system, commercial users (or governments representing clusters of commercial users) would commit to making annual payments to the BSF, based on their annual seed sales, for a fixed period (e.g. 10 years). During that time, they would have facilitated access to both genetic resources in the multilateral system and also to genetic sequence data. Since the rate of payment would be based on seed sales generally, there would be no need to track and trace the use of the material genetic resources or sequence data in the creation of new products. This model is attractive in that it could generate more predictable levels of funding. It would also simultaneously address ABS commitments for both genetic resources and digital sequence data, and in a way that significantly reduces transaction costs associated with the 'pure' contractual model currently in place for materials.

From the point of view of nongovernmental actors involved in conserving and using genetic resources and genomic data, the most straightforward option would be for national governments to undertake to make financial contributions to the BSF on a percentage of seed sales within their borders, without linking the actual incorporation of the genetic resource or the data in new commercialised products. In return, natural and legal persons within their borders could enjoy facilitated access to both crop genetic resources in the multilateral system of ABS and digital genetic sequence data. The system would also not require tracking or tracing of the use of materials or information. National governments could decide whether or not to recoup those costs from their own seed companies. There is a precedent for this model: Norway has adopted the policy of voluntarily making payments to the BSF based on 0.1% of seed sales. In the context of the ongoing renegotiations of the ABS conditions of the ITPGRFA's multilateral system, some developing countries and observer organisations have promoted this approach. A number of developed countries have rejected it. Ultimately, in order to avoid the extraordinary complexities that would be associated with a legally binding extension of the contractual model to genome sequence data, it is possible that the practical merits of this approach will be more widely appreciated.

Under the Nagoya Protocol, some have argued that it would also be possible to develop similar multilateral ABS arrangements for some classes of genetic resources and related information, though to date, there have not been any concrete initiatives to do so (see Notes S6).

VI. Conclusion

It will most certainly take several years for the international community to develop mechanisms to address the issues raised in this review, particularly if it is collectively decided that new legally binding agreements (or amendments or protocols to existing legally binding agreements) are necessary. In the meantime, there will be

opportunities for interested organisations and networks to develop inclusive forms of governance for the deployment of the new technical capacities discussed in this paper to realise the sustainable development goals. To succeed, broad coalitions of scientists, information technologists, gene bank managers, breeders, farmers and civil society organisations will need to find opportunities to articulate a set of common goals and develop inclusive, transparent, systems for working together. If they are successful, the governance mechanisms, best practices and benefit-sharing standards they develop could positively influence the tone of ongoing intergovernmental negotiations and the form and content of norms that are eventually developed under the aegis of the United Nations. The ball is now in the court of champions of these new technologies to foster innovation platforms and governance systems which will inspire trust and promote the most effective, equitable deployment of those technologies.

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Supporting Information

Additional Supporting Information may be found online in the Supporting Information tab for this article:

Notes S1 Expansion of the discussion on potential IP claims with respect to data made available on GenBank.

Notes S2 Further details about previous discussions concerning potential inclusion of information about PGR, for example genomic sequence or phenotypic data, in the Nagoya protocol.

Notes S3 Introduction to an example (from a WHO initiative) of an attempt to address concerns about benefit sharing obligations following commercial use of open-access genetic sequence data.

Notes S4 Some farmers in crop centres of diversity are seeking recognition for their roles in both the creation and further exploitation of PGR and related data.

Notes S5 Further details about an alternative view on the creation and dissemination of agricultural innovation.

Notes S6 An alternative view on how a multilateral access and benefit sharing arrangement for PGR and related information could be achieved under the Nagoya Protocol.

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