

# Institutionalizing global genetic resource commons for food and agriculture

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## INSTITUTIONALIZING GLOBAL GENETIC RESOURCE COMMONS FOR FOOD AND AGRICULTURE

Tom Dedeurwaerdere

### New challenges for the use and exchange of plant genetic resources for food and agriculture

The purpose of this chapter is to provide an overview of the development of new theories and case study material in the field of the evolving global commons in plant genetic resources for food and agriculture (PGRFA). The exploration of various emerging global genetic resource commons in fields such as animal genetic resources and microbial genetic resources is still in its infancy, compared to the global crop commons (Byerlee, 2010) or to the locally managed natural resource commons more generally (Ostrom, 1990). Nevertheless, the commonalities between these various forms of commons have caught the attention of a growing number of scholars and managers of common pool resources. Important common features, such as the role of social norms in complying with common rules and the presence of clearly defined boundaries, deserve to be analysed in a systematic manner with the aim of supporting the development of appropriate institutional and legal frameworks.

The first major instance of a formal commons on a global scale in the field of genetic resources for food and agriculture was the pool of PGRFA established and governed by various International Agricultural Research Centres (IARCs) under the leadership of the Collaborative Group on International Agriculture Research (CGIAR). Over the last 40 years, the IARCs have played a leading role in promoting open access to biological resources through the organization of a network of specialized *ex situ* conservation facilities throughout the world. However, legal uncertainty over the status of the collections in the early 1990s, and the growing recognition of the specific nature of PGRFA, called for the development of a specific legal instrument to regulate the conservation and use of these resources. Lengthy negotiations eventually led to the adoption of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) on 3 November 2001, which provided further

support for the collections' open access policy.<sup>1</sup> This open access policy is clearly reaffirmed in the 2003 CGIAR's policy guidelines:

The germplasm [that is, the seeds or the parts of a plant that enable reproduction] designated by the Centres is held in trust for the world community in accordance with the agreements signed with the FAO ... Based on the conviction that their research will continue to be supported by public funds, the Centres regard the results of their work as international public goods. Hence full disclosure of research results and products in the public domain is the preferred strategy for preventing misappropriation by others.

(SGRP, 2003)

The recent history of the global crop commons, however, increasingly shows the limits of an approach that is solely focused on plant genetic resources. New challenges have led public and private research entities, farmers and industry to consider pooling genetic resources together beyond only PGRFA. Examples of these challenges are the management of global infectious diseases affecting food crops, animals and sometimes humans, the development of crop and non-crop biofuels and the opportunities arising from biotechnology for increasing the nutritional value and safety of food products. The creation of such common pools has also benefited from the combination of technological progress in life sciences and the information sciences (Parry, 2004). On the one hand, the development of innovative methods for the identification, long-term conservation (for example, freezing and freeze-drying) and shipping of genetic resources has enhanced interest and international cooperation in global life science research. On the other hand, the information technology revolution has dramatically expanded the possibilities of distributed coordination as well as diminished the search costs for locating genetic resources held in collections throughout the world.

The positive impact of these technological advances on the development of the global genetic resource commons, however, has been attenuated by a set of counterbalancing factors, which could jeopardize the whole enterprise (Reichman et al., 2011). The important commercial value of a small subset of genetic resources, especially in the field of pharmaceutical product development, has put pressure on the sharing ethos that is at the basis of the exchange of resources within the commons. In particular, communalism and norms against secrecy have been eroded by delays in publication and restrictions on the sharing of research materials and tools, which, in turn, have often been caused by concerns about intellectual property rights (Rai, 1999). Another hurdle is the heterogeneity of the legal frameworks, which raises the costs of designing appropriate institutional rules that can operate on a global scale. A major obstacle in this respect consists of divergent national access and benefit-sharing legislation across countries as well as a lack of international coordination in the implementation of these legal provisions in a way that is consistent with the needs of public science in developing and industrialized countries (Jinnah and Jungcort, 2009; Roa-Rodríguez and van Dooren, 2008).

In recognition of these obstacles, science policy makers and genetic resource managers have increasingly focused on devising new methods for organizing and

integrating vast and diverse collections of resources, with a view to better securing the research needs of the various user communities. The need for institutionalizing the common pools of genetic resources used in food and agriculture was already acknowledged during the negotiation of the Convention on Biological Diversity (CBD) in 1992.<sup>2</sup> At this time, it became clear, and was accepted, that a purely bilateral system between single providers and users of given genetic resources, such as what is used in the case of medicinal plants, would not be possible for the food and agriculture sector due to the fact that the plant-breeding process calls for a broad range of genetic resources from many different providers to be input into any one product (Burhenne-Guilmin, 2008).

The choice of a commons-based governance of genetic resources, however, should be justified in terms of its costs and benefits compared to other institutional modalities for governing genetic resources (such as private intellectual property rights or exclusive use license contracts) as well as its success in addressing the specific needs in each of the sub-sectors. Much is to be learned in this respect from a systematic comparative assessment of over two decades of experimentation with genetic resource commons, in terms of their commonalities and differences, the specific patterns of use and exchange in the various sub-sectors, the features of the regulatory environment dealing with specific sets of resources (microbial versus animal, for example) and the importance of the pre-existing social norms. Further, where there is evidence of similar challenges and policy needs in the various sub-sectors (especially in regard to intellectual property rights and access to genetic resources for pre-competitive research purposes), these should be systematically explored to support the introduction of common strategies for the access and sustainable use of genetic resources.

This chapter shows that, when the research and innovation processes are based on screening or breeding from common pools with multiple inputs from various sources, commons-based innovation offers an interesting institutional option, as an alternative to both private proprietary and state-based solutions. Indeed, commons-based innovation in genetic resources allows for both the barriers of case-by-case contracting over every single entity in a system of exclusive property rights (Dedeurwaerdere, 2005) as well as the rigidity of centralized governmental and intergovernmental organizations (Halewood, 2010) to be overcome, without compromising downstream commercial applications (Lessig, 2008; Reichman et al., 2011). Therefore, it seems relevant to explore whether, and if so how, the principles of commons-based production can also be applied to the specific case of global and regional genetic resource governance.

The chapter is structured in the following way. The first section briefly presents the recent history of global genetic resource commons, followed by an examination of the commonalities between the various theoretical models, ranging from the global genetic resource commons to the digital commons, with a view to enhancing our understanding of how commons-based design principles can offer an alternative to the private and state-based control of genetic resources. The next section applies these insights to analyse a focused set of case studies on the institutional design of global exchanges with microbial, animal and plant genetic resources. On the basis of this

analysis, the final section summarizes some key features of the genetic resource commons that can guide efforts in developing appropriate legal and institutional frameworks.

### Emerging models of global genetic resource commons

Global collections of genetic resources emerged in response to the needs of research infrastructure faced with the challenges of food security, global health issues and the biodiversity crisis more generally. Similarly, the genomics revolution and the broader impact of the globalization of research in the life sciences enhanced the interest and cooperation in the collection of genetic resources. As a result, vast amounts of human, animal, plant and microbial genetic material were collected throughout the world from various regions and habitats and exchanged in collaborative research networks. For instance, in the 1980s, Africa faced the destruction of a major crop, cassava (also known as manioc), by a scale insect, the mealybug (Hammond and Neuenschwander, 1990). Through research on the natural enemies of this bug, which took place in one of the IARCs in Colombia (the International Center for Tropical Agriculture (CIAT)), tiny wasps were identified as an effective predator. They were imported into Africa and successfully used in a major biological control programme that took place in collaboration with the International Institute for Tropical Agriculture. As a result, millions of dollars of food crops were saved. More recently, the CIAT, with the support of the Nippon Foundation, coordinated a similar biological control programme in Thailand and other countries in Southeast Asia. Other well-known examples of the worldwide sharing of biological resources involve microbial materials. For instance, soybean production throughout the world has been improved through the use of nitrogen-fixating bacteria, known as the root nodule bacteria. Some well-characterized and high-performing isolates of these bacteria, derived from the worldwide exchange of materials, are currently used in public and private research, for training and education, and commercially produced in large quantities in various countries around the world (Dedeurwaerdere et al., 2009).

The increase in the exchange of genetic materials in relatively open global networks, however, has also raised a set of new collective action problems. One of the main problems is the increase in practices that potentially create new threats to food and agriculture as well as to human health (Doyle et al., 2005) and quality management (Stern, 2004). The regional and international shipment of agriculture products means that pathogens do not necessarily require natural dispersion. Further, intensive agricultural practices bring with them a set of undesirable consequences, which are likely to increase these threats, such as resistance due to the overuse of antibiotics and pesticides or new variants of zoonotic animal diseases. The importance of these and other problems has led to initiatives to promote the further institutionalization of exchange networks in globally distributed common pools with common quality standards, clear rules for entry into the pool and coordinated management, such as the creation of the Global Biological Resources Centres Network in the microbial field (Smith, 2007).

In this context, digital infrastructures create a new set of mechanisms for restructuring the collaborative enterprise. More specifically, the use of computational methodologies within the life sciences makes it possible to build large knowledge repositories and to develop data-mining tools for integrating the huge accumulation of data in these repositories into a virtual collection (Dawyndt et al., 2006). Further, digital networks make it possible to directly improve the global exchange of materials by implementing machine-readable material transfer agreements directly into the digital catalogues of the collections (Nguyen, 2007). Finally, by systematically documenting the source and history of the materials deposited in these genetic resource collections, and releasing this information online, the digital information infrastructures also become a tool for making the reciprocity of exchanges clearly visible (Fowler et al., 2001).

At present, most genetic resource collections are taking advantage of the proliferation of these new mechanisms, by networking the existing infrastructure of the physical collections into global digital data and information infrastructures. As they stand, however, the measures that have been taken so far do not go far enough in implementing the kind of infrastructure that would be needed to realize the full potential of a digitally networked genetic resource commons. Moreover, existing initiatives remain fragmented, incomplete and limited in scope, with the risk that they may succumb to adverse legal, economic and political pressures over time.

For the design of a worldwide microbial commons, however, a more systematic approach, based on an analysis of the structure of the exchange practices and the terms and conditions of exchanges between the collections, and between the collections and the provider countries, is needed. In particular, in order to improve the current state of affairs, a better understanding is needed of the costs and benefits of the alternative institutional frameworks, which would serve to harmonize the conditions of exchange and put the emerging worldwide microbial commons onto a solid legal and institutional basis. The objective of this chapter is therefore to conduct a comparative assessment of the use and exchange practices in the various sub-sectors of the genetic resource commons (microbial, animal and plant) and to identify commonalities, differences and user community needs under different social, institutional and technical conditions.

### Theoretical models for designing a genetic resource commons on a global scale

The design of a global genetic resource commons should take into account the specific characteristics of the genetic resources. Genetic resources are complex goods, with both a biological (the biological entity) and an informational component (the genetic information and information on the biochemical pathways). As biological entities, most genetic resources are widely dispersed, whether originally in nature (Beattie et al., 2005) or as a result of human domestication (Braudel, 1992). As a result, it is often costly (or simply difficult) to exclude users from accessing these resources *in situ*.

In many cases, however, biological entities are accessed not for direct exploitation of the entity itself but, rather, for access to the informational components (Dedeurwaerdere, 2005; Goeschl and Swanson, 2002b). For example, large quantities of biological entities are collected in order to screen the biological functions and properties that they exhibit against certain targets. Once a new property or function has been discovered, the search for genetic similarity can identify the genetic sequences that are involved in the expression of these properties. This search may, in turn, lead to further research on these genes or properties without having to access the specific organism that led to the discovery of the new informational inputs. Nevertheless, accessing specific entities such as microbial isolates with unique properties for bioremediation, enzyme production or to produce food additives becomes important at the end of the research and innovation chain when biological entities are used in commercial applications. Therefore, any regime for regulating access to these resources should take into account both the broad informational features of the pool of resources as well as the potential commercial uses of specific biological entities.

In general, genetic resources act as informational inputs in the process of research and innovation, both as stock (in the form of accumulated traits of known usefulness in natural environments) and as generators of new flows of information (the discovery of new useful features) (Swanson and Goeschl, 1998). The current literature on natural resource commons, however, only partially takes these features of global genetic resource networks into account. To take the specific informational features of the networked genetic resources into account, it might be more fruitful to look at the commonalities that they have with the institutional solutions and models that have been developed in the digitally networked information commons. Digital information commons have been proven to offer a set of robust and successful models for the production of informational goods and services (Benkler, 2006; Boyle, 2008; Hess and Ostrom, 2007; Lessig, 2001). In their case, a 'hybrid' regime has been developed that addresses both the commercial and non-commercial uses of multiple contributions to the development of knowledge goods (Benkler, 2006, 122–27; Lessig, 2008). Moreover, there is already considerable experience with these global commons, and systematic research on generic design principles has been conducted. This research can provide elements for a systematic comparative analysis with the genetic resource commons. This section focuses on two key common design principles of successful commons that came out of this research, which are the role of non-market motivations and the modular character of the organizational architecture.

The main institutional feature that is common to all successful digital information commons is the design of complex incentive schemes that are driven more by social and intrinsic motivations than by monetary rewards (Benkler, 2006). Mixed motivations are common in a heterogeneous set of initiatives such as open-source software communities, global genetic sequence databases and distributed peer-to-peer computational infrastructures. Since it is difficult to put a precise monetary value on the creative inputs of a vast and distributed network of contributors, it has proven to be more effective to rely on non-market motivations for organizing the networks (Deek and McHugh, 2008). Moreover, extensive empirical research has shown that, when social

motivations are involved, such as increasing recognition in a collaborative group or increasing the satisfaction of intrinsic motivation with respect to furthering general interest objectives, monetary rewards can decrease the willingness to contribute to the global pool (Frey and Jegen, 2001). Further, there are hidden costs involved in moving from a social to a monetary reward. These costs are related to a clear delineation of the tasks to be paid for (Deci, 1976) as well as a monetary evaluation of the value of each and every contribution to these tasks (Benkler, 2006).

The exchange of genetic resources in the global commons is clearly a case where social and intrinsic motivations will play an important role. Indeed, the attribution of a monetary value to each entity is especially hard, or simply impossible, when the genetic resource that is used as an input for collaborative research in a global exchange network has to be assessed. Many innovations result from the combination and comparison of information gained from a wide variety of genetic resources from different sources, which all play a certain varying role in the progress of the research. Furthermore, the value of the resources only becomes apparent late in the research and innovation process, while its theoretical monetary value at the beginning of this process is likely to be extremely low (Simpson et al., 1996). Finally, in some cases, the initial value of the resource is increased by the presence of informational components that are difficult to quantify, such as associated know-how and traditional knowledge, but which can make a major contribution to research into environmental, food or health-related properties (Blakeney, 2001).

The second feature, which plays a role in the success of the commons-based production of knowledge in the digital commons, has been the adoption of modular technical and organizational architectures. Modular architectures have allowed efforts and contributions from many human beings, which are diverse in their quality, quantity, focus, timing and geographical location, to be pooled in an effective manner (Benkler, 2006, 100). Modularity presupposes the presence of a set of independently produced components that can be integrated into a whole. The fine-grained character of the modules determines the number of potential contributors to the network. If there is a large set of relatively small contributors, each of whom only has to invest a moderate amount of additional effort and time in the network, the potential benefits of taking part in a global exchange network is likely to be high. However, if even the smallest contributors are relatively large and if they each require a large investment of additional time and effort to take part in the collaborative network, the potential reciprocity benefits of being part of the network, and the cost-effectiveness of doing so, will diminish, and the universe of potential willing contributors will probably decrease.

Modularity was clearly also present in the major successful collaborative projects in the field of genetic resource commons, such as the collaborative sequencing of the worm genome by a network of teams distributed around the world in the early days of the genomic revolution (Sulston and Ferry, 2003) or the networks of crop improvement established by the various members of the CGIAR (Byerlee, 2010).

The importance of non-market motivation is a necessary condition for the emergence of effective commons-based production, but it is clearly not sufficient. It is the combination of the potential of non-market production of collective goods and the effectiveness of

an organizational form that allows widely dispersed contributions to be integrated and that makes effective commons-based innovation possible on a global scale. Research on these general design principles shows that, under conditions of appropriate quality control and through an initial investment in the creation of social networks (Benkler, 2006), commons-based production and management of informational goods can be a desirable and effective institutional modality, which can co-exist with a market or state-based production of knowledge goods. This is especially true in the early stages of research on the innovation and product-development chain, when access to multiple inputs is required.

## Results of case studies of institutional choices

### *Materials and methods*

Except for the analysis of some specific initiatives (Beck, 2010; Hope, 2008; Halewood and Nnadozie, 2008), few case studies have addressed the institutional characteristics of commons-based production with genetic resources. This section presents a comparative analysis of three such case studies, in the fields of microbial genetic resources, plant genetic resources and animal genetic resources. These cases have been selected because of their broad similarity in regard to the characteristics of the innovation process and their common concern with agricultural biodiversity.

The methodology of this comparative assessment builds upon the well-established literature on the natural resource commons, by acknowledging that the biophysical characteristics of the resource, the governance arrangements and the characteristics of the users all impact upon the management of the commons (Agrawal, 2001; Ostrom, 2005). Therefore, the discussion of commonalities and differences between the three cases will address the variations along these three dimensions (see also Table 19.1). However, at the outset, it is necessary to point to some broad similarities that justify the treatment of these cases under the common category of the genetic resource commons. First, with respect to the biophysical characteristics of the resource, a substantial part of the innovation process in all three cases is based on access to multiple inputs in order to produce a single output, whether this process is for screening for interesting entities in a pool of resources (in all three fields) or for breeding new entities by combining multiple inputs from the pool (in the animal and plant fields). From a governance perspective, institutional modalities have been developed in all three fields, in order to gain facilitated access to these multiple research inputs. In particular, commons-based innovation is one of the emerging institutional modalities of these sectors, although it has to cope increasingly with the pressures from the global intellectual property regime, as described earlier; the recourse to restrictive contractual practices; the adverse impact of national access and benefit-sharing legislation on scientific research; the competition from vertical integration; and the centralization of the inputs within global companies, among others (Reichman et al., 2011). Finally, in these three cases, the user communities are driven by a mix of market and non-market motives, even if in some sectors the commercial pressures have led to an erosion of some of the non-market components.

TABLE 19.1 Biophysical, institutional and community characteristics of the genetic resource commons

	Microbial genetic resources	Plant genetic resources	Animal genetic resources
Biophysical properties	High genetic variation within a species and high mutation rates	Well-defined varieties and a high degree of genetic stability	Relatively well-defined breeds
Characteristics of the user groups	Type of users Main non-market motivations	Mix of public and private Contribution to scientific research ethos and conservation of biodiversity	Mostly private sector Animal health and conservation of genetic variety
Features of the governance arrangements	Governing bodies Organization of distributed collaboration Forms of exchange Main challenges to the commons-based exchange	Global and regional federations Shared resources among a distributed network of microbial collections Mix of formal and informal Restrictive license policies in high commercial value collections	National and local breeding organisations Shared resources among farmers of the same breed Mix of formal and informal Vertical integration of breeding operations in transnational companies

Source: Capgènes, www.capgenes.com.

The analysis of the case studies is based on the original surveys and semi-structured interviews by a research group at Cambridge University conducted in 2005 and 2009 with members of the World Federation for Culture Collections (WFCC) (Stromberg et al., 2007; Stromberg et al., 2006) and at Université catholique de Louvain (Dedeurwaerdere et al., 2009) as well as on expert interviews with officials at the Policy Research and Support Unit at Bioversity International and the Commission on Genetic Resources for Food and Agriculture at the Food and Agriculture Organization (FAO). The findings of these surveys and interviews were combined with information taken from the notes of internal meetings and official reports and compared to the results of previous studies.

For each of the three cases, the analysis will focus on three elements: (1) analysis of the institutional arrangements governing the exchange practices in that field; (2) synthesis of the data on commons-based production obtained through in-depth case studies of major collections; and (3) evaluation of the contribution of non-market motivations and modular organization to effective commons-based innovation practices.

### Microbial genetic resources

The study and commercial exploitation of microbial genetic resources requires the systematic authentication of pure micro-organisms in *ex situ* collections and the preservation and exchange of certified biomaterials for cumulative follow-on research (WFCC, 2010). As a result, many countries are actively involved in collecting and exchanging micro-organisms on a global scale.

Well-known examples of the worldwide sharing of biological resources involve microbial materials in the field of food and agriculture. For instance, soybean production throughout the world has been improved through the use of a nitrogen-fixing bacteria, known as the root nodule bacteria. Through the exchange of some well-characterized and high-performing isolates of this bacterium, soybeans can now be used in public and private research, for training and education, and commercially produced in large quantities in various countries (Genetic Resources Policy Committee, 2007). Another example is related to the management of the threats from pathogenic micro-organisms for agriculture and food production systems such as fungi-causing root rot and stem rust diseases or mycotoxin-producing fungi, which are harmful for animal and human health. Some of these fungal pathogens can be transported by the wind, while others move with the international shipment of agricultural products. Through international collecting efforts, diagnostic and identification tools have been developed that can be used in the early detection of these pathogens (Smith et al., 2008) as well as in the detection of contamination in agriculture and food commodities (Doyle et al., 2005). Another case that is more centred in one region is the use of microbial ferments in food processing, such as yoghurt. For decades, these microbial strains have been exchanged and managed through farmers' markets as a common heritage of the local farmers (see Figure 19.1). However, commercial interest from Japanese companies who are selling this local yoghurt variety in Japan under their own brand name has placed pressure on these local collections to limit such exchange in order to ward off



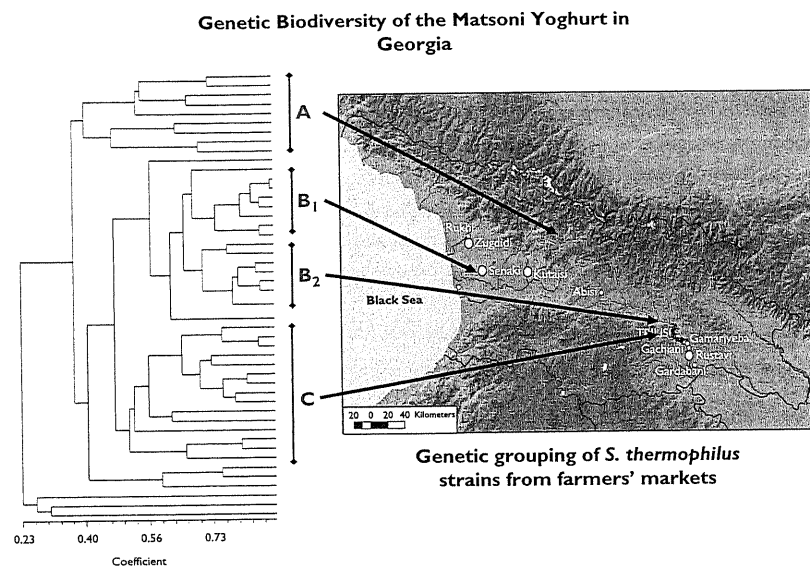


FIGURE 19.1 Genetic biodiversity of the Matsoni Yoghurt in Georgia.

misappropriation. Thus, these new restrictions might work against the open exchange practices that have produced the local diversity in the first place.<sup>3</sup>

Currently, more than half a million microbial samples, which have been collected from various countries, are distributed throughout the world every year by the public *ex situ* collections that are members of the WFCC, mostly for the marginal costs of distribution (Dedeurwaerdere et al., 2009). Each of these collections contains a very substantial set of unique materials (an average of 40 per cent of the strains in the WFCC's culture collections that are referenced on StrainInfo are unique).<sup>4</sup> Intense collaboration and exchange among these culture collections is a necessary consequence of this situation. It is difficult to estimate how many *ex situ* materials are exchanged between the research collections outside the WFCC collections on an informal basis, but it is fair to say that the volume of materials exchanged between these collections is probably even greater (Dedeurwaerdere et al., 2009).

Nevertheless, the exchange of biological materials within a global commons, which prevailed during the early days of the modern life sciences, now seems to be reversed. More and more biological materials are enclosed behind national and privatized fences or only accessible under very restrictive license conditions. For instance, recent research on avian bird influenza has been hampered by countries such as Indonesia that refuse to provide access to samples of the H5N1 virus.<sup>5</sup> In this case, the Indonesian government feared that foreign companies would acquire the rights to any vaccine that might eventually be developed, without proper guarantees of low-cost access to this vaccine for developing nations. After an agreement in 2007 to start

negotiations to define the terms of references for fair and equitable sharing in any possible profits, Indonesia resumed sharing the H5N1 avian influenza virus samples.

In order to get a better picture of the institutional arrangements within the microbial commons, a set of original surveys and interviews were conducted in 2005 and 2009. In 2005, P. Stromberg, U. Pascual and T. Dedeurwaerdere (2006) surveyed the 499 public collections that were members of the WFCC (119 completed survey forms). In 2009, T. Dedeurwaerdere, M. Iglesias, S. Weiland and M. Halewood (2009) undertook a quantitative assessment of the entire accession database of a geographically representative set of nine major collections (totalling more than 15,000 single accessions), conducted semi-structured interviews with administrators of these collections, organized a short complementary e-mail survey on access and benefit-sharing measures with 238 WFCC collections (43 completed questionnaires), and completed 16 in-depth phone interviews with scientists from both public and laboratory culture collections.

The most advanced institutional arrangement for formal commons-based innovation and research is the viral license adopted in February 2009 by the 61 members of the European Culture Collection Organization, which permits distribution to other culture collections and collaborating scientists under the condition that recipients use the same license when further distributing the microbial strains. The open-access license thus travels with the micro-organisms, which prevents misappropriation of the resource by other players in the network (in a similar way to open-source licensing of computer software). Many developing countries' culture collections, such as the All-Russian Collection of Micro-Organisms in the Russian Federation and BIOTEC in Thailand, have also adopted formal licenses that permit non-exclusive use and further distribution by other culture collections for non-commercial uses. Nevertheless, in spite of these examples of coordinated and standardized formal arrangements for facilitated access among culture collections, which are used both in developing and industrialized countries, many culture collections still use ad hoc formal arrangements or even have recourse to more restrictive license conditions, as discussed later in this chapter.

At the same time, many resources are still distributed on an informal basis, especially within the United States where, with some major exceptions such as the Agricultural Research Collection, there is only a loosely organized network of public culture collections. Informal exchanges occur without written contracts, which serve to permit all uses of the material as well as the further distribution of the material to collaborating scientists or other third parties. In spite of the obvious advantages, in terms of costs and rapid dissemination, the informal system has some major disadvantages (Reichman et al., 2011). These include the absence of a clear tracking procedure for microbial resources, which is present in the formal arrangements, and the possibility that scientists will limit the distribution of the resources to a small group of close collaborators, on the basis of informal case-by-case arrangements, instead of providing a set of standard conditions that make the materials easily available to all possible users. Moreover, in the absence of formal agreements, it is unclear how cross-border exchange can be organized in compliance with the access and benefit-sharing provisions of the CBD.

The microbial commons is a clear case where non-market motivations and modular organization play a key role in contributing to the effectiveness of distributed collaboration in the management and conservation of microbial material, both in the formal and informal exchange regimes. Strong norms of reciprocity and a general shared conception that the collections hold the materials in trust for humankind as a whole underlie the exchange practices (Dedeurwaerdere et al., 2009). This conception is especially strong in taxonomic research, where a copy of every type of strain – the official reference strain used in the definition of the species – is present in, on average, seven different collections worldwide (based on the WFCC collections that are referenced on StrainInfo). The community also invests in strengthening social norms – for example, by regularly revising the common guidelines for operating the culture collections drawn up by the WFCC (WFCC, 2010). However, there have been some breaches in these social norms, which were communicated in the interviews. These include the competitive pressures for rapid publication (which has led to an increase in secrecy), a lack of compliance with the norm of depositing microbial strains once the research is published, and concerns about biopiracy when collecting microbial strains from developing countries. On the positive side, however, the vast majority of deposits are still made without attaching any specific conditions.

The modular organization, based on collaboration and specialization in the worldwide network of culture collections, is mainly a response to the high cost of conserving *ex situ* microbial genetic resources and to the fact that vast amounts of resources are still being collected from *in situ* sources and are being added to the existing pool. This distributed collaborative infrastructure has recently been digitally empowered, primarily by the establishment of the StrainInfo bio-portal. Initially conceived as a one-stop open-access portal for digitally linking and integrating the information content of the databases in different collections, StrainInfo has now also developed a common standard for interoperability – the microbial commons language and XML standard – which will allow automated knowledge generation based on the decentralized efforts of all of the individual data contributors (Verslyppe et al., 2010). At present, 62 collections (holding more than 300,000 strains) have joined the open-data portal, while 13 of these have moved towards using the new common XML standard and other collections have already shown an interest.<sup>6</sup>

The commercial pressures on life science research have, however, also led to an alternative system for exercising property rights, based on exclusive license contracts. One prominent example is the American Type Culture Collection, which distributes its holdings under a contract, thereby prohibiting the further distribution of its micro-organisms by recipients until a new license has been negotiated with the collection, even if the recipient is a public service collection with high quality management requirements for the handling and distribution of microbial material. Such exclusive licensing has had a negative impact on the effectiveness of microbial research and innovation. Since there are high mutation rates for micro-organisms, cumulative scientific research is only possible when it is based on access to, and distribution of, identical micro-organisms within a network of collaborating scientists. This is especially true within taxonomy. Tracking the further distribution of identical copies is

part of the overall aim of quality management and is a basic scientific procedure (OECD, 2007; WFCC, 2010). The rise of exclusive contracting poses a real threat to public microbial research.

Finally, exclusive ownership based on patents is also an important institutional modality within the field of microbial genetic resources. The impact of patents on the access to genetic resources, however, is much less than it is in other areas, such as plant genetic resources. Indeed, microbial species are characterized by high internal genetic variation between organisms in the same species complex as well as by high mutation rates upon reproduction (Staley, 2002). The patenting of one micro-organism within a species complex provides exclusive rights to that one microbe, which is selected for its balanced expression of a cluster of interesting properties. However, many other organisms within the species complex, which are not covered by the patent, may have a similar set of properties, and they can often be accessed for further research and innovation through the culture collection system.

In sum, the field of microbial genetic resources is characterized by a strong and lively commons-based innovation sector, which has recently been empowered by new digital means for distributed collaborative research. Nevertheless, a large part of this sector is still informal, which poses serious threats to its long-term sustainability. Moreover, commercial pressures have also led to the adoption of exclusive-use contracts by a small number of collections, which present a major breach in the traditional sharing norms of the global microbial community. On the other hand, some collections are moving towards the adoption of formal non-exclusive licenses in order to safeguard the benefits of the pre-existing informal arrangements for the exchange of the bulk of resources, which still have unknown scientific and/or commercial potential but which are the building blocks for future scientific research and innovation.

### PGRFA

The impact of the intellectual property regime on access to genetic resources is much greater in the plant genetic resources field than in the microbial or animal genetic resources field (Chen and Liao, 2004; Tvedt et al., 2007). Plants have well-defined varieties and much greater genetic stability on reproduction than either micro-organisms or animals, which means that exclusive rights can be extended to direct offspring, and the results of all cross-breeding from these offspring will have sufficient genetic similarity (for protected varieties) or will contain a specific gene (for patented genes). On the one hand, the ease of transferring traits between crops makes it very hard to protect the proprietary information contained in the improved varieties or to stimulate private investment in the absence of intellectual property rights (Swanson and Goeschl, 2005). On the other hand, intellectual property rights favour the innovators who are already situated on the innovation frontier (Goeschl and Swanson, 2002a), under-represent the needs of poor countries (Benkler, 2006) and do not provide appropriate incentives for collaborative investment in the long-term informational values associated with the resource (Dedeurwaerdere et al., 2007).



These features of plant genetic resources, in conjunction with the commoditizing pressures of the last quarter of the twentieth century, have led to a conflict between the plant breeding industry and developing countries (Reichman et al., 2011). The former has succeeded in obtaining tough, patent-like *sui generis* protection of new plant varieties, without either a research exemption or the farmers' right to reuse their own seeds. Industry also continues to breed off the stocks that have been drawn – with or without permission – from developing countries. These latter countries, in turn, have asserted sovereign rights over their genetic resources through the CBD, which has jeopardized the viability of the heretofore internationally public collections. Only by a major effort undertaken under the auspices of the FAO has it become possible to rescue the public collections held by the CGIAR and entrust them to the oversight of an intergovernmental organization operating under the 2002 ITPGRFA. This treaty organization, which is affiliated with the FAO, has stabilized the CGIAR repositories and avoided the risk of chaos that threatened their survival. Its biggest success lay in the de facto creation of a legally formalized global commons for basic plant materials of primary concern for global food security and in stimulating ever-growing contributions to this basic resource. However, the implementation of the FAO treaty is still underway, and – as discussed in other chapters of this volume – many of its core features such as its Standard Material Transfer Agreement are still under scrutiny.<sup>7</sup>

Extensive research has been conducted on the institutional arrangements adopted within the global crop commons (Halewood and Nnadozie, 2008; Helfer, 2005). At the time of writing, the crop commons, formalized through the ITPGRFA, pools over 1.2 million accessions conserved in the collections and gene banks of contracting parties all over the world. The majority come from the 11 international collections of the CGIAR, some from other international collections, while more and more national public collections are officially joining the multilateral system of exchange as the Treaty is implemented.<sup>8</sup> The plant genetic resources that are within this pool are all exchanged with the viral license of the Treaty for research, breeding and education purposes. When commercial applications are developed, the Treaty offers two options: (1) commercialization with a non-exclusive-use license that permits further use for non-commercial research, breeding and education purposes or (2) commercialization with an exclusive-use license and the payment of a fixed royalty to a multilateral fund.

Non-market values and modular organization also play an important role in making the crop commons a sustainable institutional form. Strong bonds and trust among scientists from many countries involved in crop improvement programmes underlie the exchange practices and promote the sharing of information as well as the integration of regional efforts (Byerlee, 2010). The shared commitment to the common goal of increasing food production and reducing global poverty is a key driver of the whole system (*ibid.*). From the early days of the crop improvement programme, the community also invested in strengthening these social norms. The core activity has involved six months of field-based training for young scientists. In the field of wheat improvement alone, over 1,360 individuals from 90 countries have participated in these training courses, and 2,000 more have visited the International

Centre for Maize and Wheat Improvement (CIMMYT) in Mexico. In addition, participating countries are allowed to give their own names to the varieties they release, and this process produces a sense of ownership and ensures that the international seed banks are seen as honest brokers with respect to germplasm and information sharing (*ibid.*). Finally, the CGIAR has developed policy guidelines that broadly reflect these values, both before and after the entry into force of the ITPGRFA on 29 June 2004 (CGIAR, 2009; SGRP, 2003).

Experimental breeding is a clear example of a worldwide modular and distributed organization of research and innovation. One well-documented case is the international nursery network, which was organized by the CIMMYT. Every year, the CIMMYT dispatches improved germplasm to a global network of wheat research cooperators who evaluate wheat germplasm in experimental trials targeted at specific agro-ecological environments. From 1994 to 2000, the CIMMYT distributed 1.2 million samples to over 100 countries, corresponding to an average of 500 to 2,000 globally distributed field trials per year (Byerlee, 2010). Data from the field trials are returned to the CIMMYT for analysis, and the results are returned to the network of collaborating scientists. In this way, the crop commons builds an iterative collaborative platform that collects environmental and local feedback in a way that is similar to the system used by free software projects to collect bug reports (Benkler, 2006, 344).

In sum, the analysis of these institutional characteristics shows many similarities between the microbial commons and the global crop commons. In both fields, institutional arrangements have established a globally networked commons that is open to new users and contributors to the system under a standardized non-exclusive contract. Based on the quantitative data, the scope of the crop commons seems to be more limited than that of the microbial commons, which covers far more individual collections and has a larger number of holdings. Nevertheless, within the crop commons, all of the material is exchanged under a formal viral license because of the major threat of exclusion from key research resources in the form of patents. In the microbial commons, a mix of formal and informal contracts is used, depending on the circumstances and the commercial pressure on the collections.

### Farm animal genetic resources

Three major institutional arrangements are in use for the management and exchange of genetic resources in animal breeding. The first was developed in the hybrid-breeding sector. Hybrid breeding is based on crosses of very different parent or grandparent lines. Since innovators do not disclose the parent and grandparent lines that are used to produce the hybrid, unauthorized reproduction of animals can be effectively prevented by keeping the information on the parent lines and grandparent lines that are crossed secret. As a result, in areas where hybrid breeding is a well-developed technological option – mainly in poultry and pigs – an exclusive-access regime has developed within a centralized and large-scale breeding industry (Pilling, 2009).

Most livestock breeding is, however, based on experimental breeding within a pool of animals that are managed in an open commons. On the one hand, when

animals are exchanged between livestock keepers, the assumption normally is that the owners of the breeding animals (or other genetic material) acquired through such exchanges can use the genetic resources involved for further breeding as they wish (Pilling, 2009). On the other hand, sustainable breeding requires a high level of coordination between the breeders in the pool, both for information exchange on the parent lines and for developing common health and sanitary standards, and the breeding objectives have to be adjusted to local consumption patterns and available feed resources. Therefore, the majority of experimental breeding programmes that are run by farmer-owned cooperatives and breeder organizations operate in the context of national breeding programmes or farmer-driven societies with a regional scope (*ibid.*). Such programmes are often developed by one country or one region alone, even if there is often an important level of cross-breeding with imported animals to improve the genetic quality of the pool. As such, the institutional arrangement for commons-based management is not a globally interconnected pool as in the case of plants and microbes but, rather, is better characterized as a global network of exchange among limited (national or regional) commons.

Commons-based experimental breeding is, however, coming under increasing pressure from international companies that are taking over farmer-owned cooperative schemes, especially cattle-breeding schemes (Mäki-Tanila et al., 2008). The growth of transnational commercial breeding operations has led to the development of a third institutional regime, based on the operations of centralized commercial-breeding companies, with high expectations for quick profits and a unilateral focus on productive traits. Centralizing breeding operations may raise new challenges, such as the reported decline in the reproduction and health traits of the Holstein breed (one of the most widely used dairy cows), possibly due to a long-standing emphasis on production yield (*ibid.*, 35). Other challenges posed by the global commercial-breeding companies are the introduction of new business practices, such as patents. However, these patents mostly concern certain genetic mutations that cause genetic defects, while patents on productive traits at present only have a minor impact because of the multi-locus nature of most economically important traits (*ibid.*, 24).

Non-market values play an important role in the organization of the traditional commons-based production sector in animal breeding, which is described earlier, although these values have to be combined with the productivity constraints of the private farms that are breeding the animals (CGRFA, 2009, 7 and 20; Mäki-Tanila et al., 2008, 21). Animal breeding is part of national food security, and cooperative breeding programmes are set up to promote collective goals such as animal health and the conservation of genetic variety within populations and breeds (which is essential to meet future challenges in the development of livestock). These non-market motives have to be shared by most of the members of the collective pool to be effective, which explains why most schemes are developing common guidelines for quality management and sustainable breeding. They are also actively promoting these guidelines among individual farmers, through information campaigns and quality-assurance contracts provided by the breeders' cooperatives. Finally, in many countries, legal rules have been adopted to strengthen the general interest objectives

of the breeders' organizations (FAO, 2007). For instance, under current regulations, existing breeding organizations cannot claim property rights on the basis of which they could breed the animal in question exclusively. Moreover, any new breeding organization has to be approved by the state, comply with a set of quality-management standards and undertake conservation-breeding programmes.

The modular organization of the experimental breeding programme has been developed as a solution to deal with the specific problems of animal breeding, such as the need to limit in-breeding and to maintain a sufficiently diverse breeding base for disease management. The goat improvement programme developed in France by Capgènes aptly illustrates this modular organization.<sup>9</sup> In this programme, a yearly selection of the 1,000 best-performing animals is made from a pool of 170,000 goats on 800 farms. From this 1,000, 40 male goats are selected after a lengthy process of quality checking and off-breeding. These males then serve as the starting point for the following year's artificial insemination programme for breed improvement. This collective breeding process is illustrated in Figure 19.2.

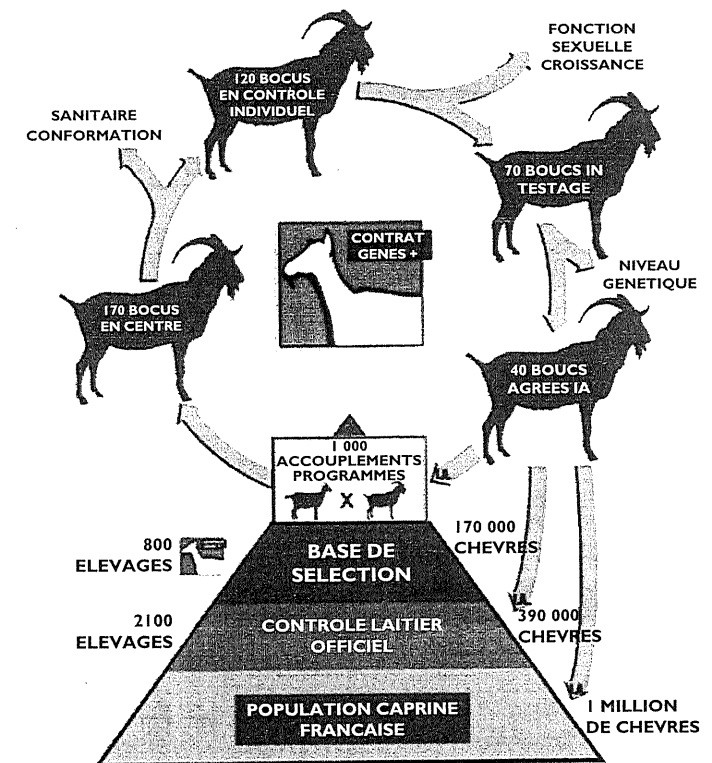


FIGURE 19.2 Example of a collective breeding process with collective ownership

As can be seen from this analysis, there are some major differences between the institutional characteristics of commons-based production with animal genetic resources and those using plant and microbial resources. The main differences involve the reliance on private actors (rather than public collections) whose resources are pooled in a collective breeding programme as well as the limited geographic scope of the commons-based improvement programmes. The geographical limitations of this sector remain the case despite the active international exchange of genetic material for the selective upgrading of domestic breeds, which creates a network of highly inter-related populations in various countries. The greatest institutional similarities are to be found between the animal and the microbial sector. In these two sectors, many exchanges still happen on an informal basis because the threat of possible misappropriation through patents or breeders' rights is relatively rare. However, the recent introduction of new business practices may cause this situation to change rapidly.

### Comparative assessment of the design features

As shown in this chapter, an emerging body of research has identified new and emerging genetic resource commons, which share many features with other already well-researched fields of commons-based production such as the digital information commons and the natural resource commons. These commons share important features such as non-market motivations (which contribute to compliance with common rules without state intervention) and decentralized problem solving (in the form of modularity in the digital information commons, distributed infrastructures in the genetic resource commons and community-based governance in the natural resource commons).

The hypothesis of this chapter is that these general features are also relevant to an understanding of the practices for sharing in the global genetic resource commons. The main similarities shown by our comparative analysis of three relatively homogeneous problem situations are the reliance on non-market motivations and the adoption of modular organizational architectures for distributed collaboration. Although the balance between non-market and market motivations has shifted in the last decade due to increasing commercial pressures, it is fair to say that in all three cases, there is a mixed set of motivations for the commons-based exchange practices. Of these, the scientific research ethos, biodiversity conservation, animal health and food security, along with monetary recompense, are the most important. Moreover, in all three fields, distributed collaboration has been shown to be an effective solution for dealing with innovation processes where multiple inputs are needed to provide single outputs, which are, in turn, the inputs for further research and innovation and which need to accommodate both commercial and non-commercial uses of the outputs. We have represented a summary of these features in Table 19.1.

This analysis has also shown some important differences between the genetic resource and digital knowledge commons. One difference involves the cost of the collections. The costs of creating genetic resource collections are substantial since they involve the long-term conservation of the resources. By contrast, the physical capital

required to participate in the digital information commons is mainly limited to an individual computer that is able to access the network (Benkler, 2006). In the field of microbial and plant genetic resources, part of this capacity problem is addressed since the distributed collections are already connected through global networking. Examples of such networks include the breeding programmes within the CGIAR network and the global network of culture collections coordinated by the WFCC. In the case of commons-based production in the field of animal genetic resources, the semen that is contributed to collective breeding improvement programmes is, to a certain extent, excess capacity, as local farm breeding would continue in the absence of the collective breeding programme. In this case, the analogy with the networking of the excess capacity of computing resources in peer-to-peer networks, as analysed by Y. Benkler (2006, 114), is much more straightforward.

Despite this difference, the importance of addressing non-market motivations in the design of a global genetic resource commons, once the initial investments in capacity have been made, should not be underestimated. As shown by the case studies, the sustainability of the various genetic resource commons always depends on a substantial investment in the strengthening of non-market values. Such an investment can be accomplished either through formal legal rules that modify the behavioural incentive structures for the participants or through informal means that act directly on the development of social and intrinsic motivations. An example of a formal means that applies to plant and microbial material is the use of standard viral licenses for preventing the misappropriation of the resource; an example from the animal resource field is the legislation that regulates the development of collective-breeding organizations in various jurisdictions. Examples of informal means are the guidelines for quality management schemes based on the broader social values developed by the collective animal-breeding organizations, the WFCC guidelines for the operation of culture collections and the CGIAR policy guidelines that pre-dated the ITPGRFA.

### Conclusion

There has been a dramatic increase in interest in commons in the last 10 to 15 years, from traditional commons that manage the use of exhaustible natural resources by fixed numbers of people within natural borders to a global information commons that deals with non-rival, non-excludible goods by a potentially limitless number of unknown users. The emerging global genetic resource commons fits somewhere in between, shifting in the direction of information commons as digital information infrastructures allow physically distributed commons to be networked in virtual global pools.

The analysis of a selected set of cases in this chapter shows that networking common pools of genetic resources in a global commons is potentially a workable alternative to market-based solutions, which have been shown to be unable to generate sufficient investment in the vast quantities of genetic resources that are neglected because of their unknown and/or unlikely commercial value or which have been shown to under-represent the needs of poor countries. These neglected resources are the building blocks for future scientific research and have enormous value for

sustaining biodiversity and local livelihoods in developing and industrialized countries. Research and breeding requires access to these multiple inputs, which can be combined into new compounds or screened to find organisms with new properties.

In the current legal environment, there are a range of obstacles that present a formidable challenge to fully realizing the new opportunities offered by global networks of genetic resources (Reichman et al., 2011). Such challenges demonstrate the need for appropriate organizational forms, legal arrangements and social practices that can help to better secure the global user community's need to address issues of common concern, such as global food security, global health, human development, biodiversity conservation and climate change. As discussed in this chapter, in response to this challenge, governments, non-profit organizations, global research communities and breeders have developed a range of initiatives for the exchange of materials and information, which have already delivered important outcomes. The key issue is how to build upon these initiatives and how to put the incipient global genetic resource commons on a solid institutional basis that will enable commons-based production to co-exist, whenever effective, with market-based and state-based contributions to collective goods.

## Notes

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- 1 International Treaty on Plant Genetic Resources for Food and Agriculture, 29 June 2004, [www.planttreaty.org/texts\\_en.htm](http://www.planttreaty.org/texts_en.htm) (last accessed 11 May 2011).
- 2 Convention on Biological Diversity, 31 ILM 818 (1992).
- 3 Interview with Nina Chanisvili, 25 March 2010.
- 4 For more information on StrainInfo, see [www.straininfo.net](http://www.straininfo.net) (last accessed 10 April 2011).
- 5 For more information on avian influenza, see the World Health Organization, [www.who.int/csr/disease/avian\\_influenza/en/](http://www.who.int/csr/disease/avian_influenza/en/) (last accessed 10 April 2011).
- 6 See StrainInfo at [www.straininfo.net](http://www.straininfo.net) (last accessed 10 April 2011).
- 7 Standard Material Transfer Agreement, 16 June 2006, [ftp://ftp.fao.org/ag/agp/plant-treaty/agreements/smta/SMTAe.pdf](http://ftp.fao.org/ag/agp/plant-treaty/agreements/smta/SMTAe.pdf) (last accessed 11 May 2011).
- 8 For more information on the International Treaty on Plant Genetic Resources for Food and Agriculture, see [www.planttreaty.org/inclus\\_en.htm](http://www.planttreaty.org/inclus_en.htm) (last accessed 10 April 2011).
- 9 Capgènes, [www.capgenes.com](http://www.capgenes.com) (last accessed 10 April 2011).

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