

**Institutionalizing global genetic-resource commons:
Towards alternative models for facilitating access in the global biodiversity regime**

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Abstract

The proliferation of intellectual property rights has led to increasing restrictions and commercial pressures on access to and use of genetic resources. These changes present a formidable challenge for the incipient commons-based sharing practices for genetic resources on a global scale amongst scientists, breeders, and between *ex-situ* collections of microbial genetic material, which have been made possible by new technological breakthroughs. This paper presents a comparative analysis of three cases of global genetic-resource commons, in the fields of microbial, plant and animal genetic resources, with the aim to contribute to the understanding of the challenges faced and to analyze possible institutional solutions. The analysis in this paper shows that, under conditions of appropriate quality control, the use of standard contracts against misappropriation and an initial investment in the creation of social networks, global genetic resource commons can be a desirable and effective solution to provide essential knowledge assets that contribute to conservation and sustainable use of biodiversity with major benefits both for developing and industrialized countries.

Keywords: Microbial genetic resources, Plant genetic resources Animal genetic resources, Biodiversity, Access and benefit sharing, Intellectual property, Open source licensing.

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1. Introduction

Historically, commons-based management of natural resources in well-delimited communities has offered a sustainable alternative to both private ownership and state-based governance of resources (Ostrom, 1990). Well-studied examples of long-lasting and successful natural-resource commons are irrigation management in Spain and in Nepal, and the Alps in Switzerland. Access to and exploitation of these commons is restricted to and regulated by a well defined group of local users, even though the property regime governing the resource can vary from private, to common or state ownership. However, for a long time it was difficult to image commons-based management and production of goods and services on a wider scale, due to factors such as the costs of exchanges and the lack of global institutional frameworks (Keohane and Ostrom, 1995).

The first major instance of commons-based management on a global scale was the organization of modern scientific research during the 17th century (David, 2008). Learned societies and scholarly publications started to operate in international networks of peers which managed the production and quality control of scientific knowledge as a global public good. In recent decades, however, digital networks have dramatically expanded the opportunities for building and sustaining commons on the global scale, both in the field of networked information in digital environments and in the field of genetic resources (Benkler, 2006; Boyle, 2008; Hess and Ostrom, 2007; Lessig, 2001). Genetic-resource commons in particular have 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 (e.g. freezing, freeze-drying) and shipping of genetic resources enhanced interest and international cooperation in global life-science research. On the other hand, the information technology revolution dramatically expanded the possibilities of distributed coordination, as well as diminishing the search costs for locating genetic resources held in collections throughout the world.

The positive impact of these technological changes on the development of the global genetic-resource commons has, however, been attenuated by a set of counterbalancing factors, which could jeopardize the whole enterprise (Reichman et al., 2009). 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 legal frameworks, which raises the costs of designing appropriate institutional rules which can operate on a global scale. A major obstacle in this respect is divergent national access and benefit-sharing legislation across countries, and a lack of international coordination in the implementation of these legal provisions in a way which is

consistent with the needs of public science in developing and industrialized countries (Jinnah and Jungcurt, 2009 ; Roa-Rodríguez and van Dooren, 2008).

In recognition of these obstacles, science policymakers and genetic-resources 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 various user communities' research needs. In particular, a report of the Ad Hoc Open-Ended Working Group On Access and Benefit-Sharing (2005) recommends that an international regime on access to genetic resources and benefit-sharing directed towards conservation, health, agriculture, and related goals needs to be developed in a more equitable way than the patent system and that alternative *sui generis* models such as "open source" style models should be developed (cf. also Jeffery, 2008, p. 87). The need for such alternative models has already been acknowledged in the field of genetic resources used in food and agriculture, where it became clear and accepted that, in contrast to the case of medicinal plants, a purely bilateral system would not be possible, because the plant breeding process calls for a broad range of genetic resources as inputs into any one product (Burhenne-Guilmin, 2008). This paper aims to show that, more generally, when the research and innovation process is based on screening or off-breeding from 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 both the barriers of case-by-case contracting over every single entity in a system of exclusive property rights (Dedeurwaerdere, 2005), and the rigidity of centralized governmental and intergovernmental organizations (Halewood, 2010) to be overcome, without compromising downstream commercial applications (Reichman et al., 2009 ; Benkler, 2006). Therefore it seems relevant to explore whether and how the principles of commons-based production can also be applied to the specific case of global genetic-resource governance.

2. Emerging models of global genetic-resource commons

In the context of research on the life-science and information commons, the word "commons" has been defined as a general term to refer to any resource that is shared by a group of people at the local, community or global level (Hess and Ostrom, 2007, p. 4). Two major commons-based models for the exchange and management of genetic resources have successfully been developed on the global scale: the building of global pools of biomaterials, such as in the network of the Collaborative Group on International Agricultural Research (CGIAR) (Byerlee, 2010), and the building of digital information infrastructures, based on on-line databases and webportals providing access to an ever-widening collection of genetic information and related knowledge (Schauer et al., 2009).

Global pools of biomaterials emerged in response to research infrastructure needs in the context of 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 interest and cooperation in the collection of genetic resources. As a result, vast amounts of human, animal, plant and microbial genetic material are 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 mealy bug (Hammond and Neuenschwander, 1990). Through

research in Latin America on the natural enemies of this bug, a predator was identified, imported into Africa and successfully used in a major biological control program. As a result, millions of dollars of food crops were saved. Other well-known examples of the worldwide sharing of biological resources involve microbial materials. For instance, soy-bean production throughout the world has been improved through the use of nitrogen-fixing bacteria, the root nodule bacteria. Based on the worldwide exchange of some well-characterized and high-performing isolates of these bacteria, they are used in public and private research, for training and education, and commercially produced in large quantities in various countries (Dedeurwaerdere et al., 2009).

The increase in the exchange of genetic materials in relatively open global networks has, however, 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, and to human health (Doyle et al., 2005), and quality management (Stern, 2004). The importance of these and other problems has led to initiatives to promote the further institutionalization of the exchange networks in truly globally distributed pools with common quality standards, clear rules for entry into the pool and coordinated management (e.g. through the creation of a prototype for the Global Biological Resources Centers Network (GBRCN) in the microbial field (Smith, 2007), or the new proposed coordination structure of the Collaborative Group on International Agricultural Research in the field of crop genetic resources (CGIAR, 2009).

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 the distributed network of repositories into a virtual collection (Dawyndt et al., 2006). Further, digital networks make it possible to directly improve the global exchange of materials, by disseminating and coalescing around common machine readable Material Transfer Agreements (Nguyen, 2007). Finally, by systematically documenting the source and history of the materials deposited in genetic-resource collections, and releasing this information on line, 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 physical collections into global digital data and information infrastructures. The aim of this paper is to analyze the contribution of these new models and mechanisms from the digital-information commons to the further institutionalization of the exchange networks into truly globally distributed pools. The paper is structured as follows. Section 3 explores the contribution of theoretical models from the digital commons to the design of global genetic-resource commons. Section 4 applies these models to analyze 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, section 5, finally, summarizes some key features of genetic resource commons which can guide the efforts for putting these emerging global commons on a sound legal and institutional basis.

3. Theoretical models for designing genetic-resource commons on a global scale

The design of global genetic-resource commons should take into account the specific characteristics of genetic resources. Genetic resources are complex goods, with both a biophysical (the biological entity) and an informational component (the genetic information and information on the biochemical pathways). As biophysical entities, most genetic resources are widely dispersed, whether originally in nature (Beattie et al., 2003), 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 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 they exhibit against certain targets. Once a new property or function has been discovered, genetic similarity searching can identify the genetic sequences which are involved in the expression of these properties. This may in turn lead to further research on these genes or properties, without having to access the specific organism that lead to the discovery of the new informational inputs. Nevertheless, accessing specific entities becomes important at the end of the research and innovation chain, when biological entities are developed for 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 and 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 stocks (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 present options for regulating global genetic resources however only take these features of global genetic-resource networks imperfectly into account. One set of regulations, embodied in the access and benefit sharing regime established through the Convention on Biological Diversity, focuses on genetic resources as material goods (“natural resources”) (CBD, 2002). Most of the discussions around these regulations have been triggered by the need to regulate those natural resources that are exchanged for their known or likely commercial value (Safrin, 2004; Reichman et al., 2009). Another set of regulations, embodied in the global intellectual property regime established through the Trade Related Intellectual Property Rights agreement, addresses the informational components, but mainly with the aim of creating incentives for private investment in these resources at the end of the innovation chain (Dedeurwaerdere et al., 2007 ; Jeffery, 2008). In both cases, the specific features of research based on the screening and analysis of the informational components of large pools of resources is not considered.

To take the specific informational features of the networked genetic resources into account, it might be more fruitful to look at the institutional solutions and models developed in the related field of 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). Here a “hybrid” regime has developed, addressing both commercial and non-commercial uses of multiple contributions to the development of knowledge goods (Benkler, 2006, pp.122-127; Lessig, 2008). Moreover, there is already considerable experience with these global commons, and systematic research on generic design principles has been conducted. This 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 which 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. Because of the difficulty of putting 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 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 to the move from social to monetary rewards. These include the costs related to a clear delineation of the tasks to be paid for (Deci, 1976) and 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 resources used as inputs for collaborative research in global exchange networks have 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; its theoretical monetary value as assessed at the beginning of the innovation 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 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, p. 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 global exchange networks 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 is clearly also present in major successful collaborative projects in the field of the 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, 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 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 co-exists with 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.

4. Results of case studies of institutional choices

4.1 Materials and methods

In addition to the analysis of some specific initiatives (Beck, 2010; Hope, 2008; Halewood and Nnadozie, 2008), a few case studies have addressed the institutional characteristics of commons-based production with bio-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 as regards the characteristics of the innovation process and their common concern with agricultural biodiversity. In all three fields, a substantial part of the innovation process is based on access to multiple inputs in order to produce a single output, whether that be for screening for interesting entities in a pool of resources (in all three fields) or for off-breeding new entities by combining multiple inputs from the pool (in the animal and plant fields). Institutional modalities have been developed in all three fields, in order to gain facilitated access to the multiple research inputs. In particular, commons-based innovation is one of the emergent institutional modalities of these sectors, although it increasingly has to cope with the pressures from the global intellectual property regime described above and the competition from vertical integration and centralization of the inputs within global companies.

The analysis of the case studies is based on the original surveys and semi-structured interviews conducted in 2005 and 2009 with the members of World Federation of Culture Collections, by a research group at Cambridge University (Stromberg et al., 2006 ; 2007) and at Université

catholique de Louvain (Dedeurwaerdere et al., 2009), and 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 of the Food and Agriculture Organization. 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 cases studies of major collections; and (3) evaluation of the contribution of non-market motivations and modular organization to effective commons-based innovation practices.

4.2. 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 preservation and the 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. More than half a million microbial isolates are distributed each year by the public *ex-situ* collections that are members of the World Federation of Culture Collections alone (Dedeurwaerdere et al., 2009). Each of these collections contains a very substantial set of unique materials (an average of 40% of the strains in the WFCC culture collections that are referenced on StrainInfo (www.straininfo.net) are unique). Intense collaboration and exchange amongst culture collections is a necessary consequence of this situation. It is difficult to estimate how many *ex-situ* materials are exchanged between 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).

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 Stromberg et al. (2006) surveyed the 499 public collections that were members of the WFCC (119 completed survey forms). In 2009, Dedeurwaerdere et al. (2009) undertook a quantitative assessment of the entire accession database of a geographically representative set of 9 major collections (totaling more than 15,000 single accessions), conducted semi-structured interviews with administrators of these collections, organized a short complementary email 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, the effect of which is to prevent 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 amongst 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 below.

At the same time, many resources are still distributed on an informal basis, especially within the US 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, the effect of which is to permit all uses of the material and further distribution 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., 2009). These include the absence of a clear tracking procedure for the microbial resources, which is present in the formal arrangements, and the limitation of the benefits of the commons to small groups of well-connected scientists. 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 Convention on Biological Diversity.

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 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 the social norms, for example through the regular revision of the common guidelines for the operation of the culture collections drawn up by World Federation of Culture Collections (WFCC, 2010). However some breaches in the social norms emerged from the interviews. These include the competitive pressures for rapid publication (which leads to an increase in secrecy), a lack of compliance with the norm of depositing microbial strains upon publication of research results, 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 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. The main example of this is the establishment of the Straininfo bioportal. 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 the individual data contributors (Verslyppe et al., 2010). At present, 62 collections (holding more than 300,000 strains) have joined the open-data portal; 13 of these have moved towards

using the new common XML standard (www.straininfo.net, accessed on 14th May 2010), while other collections already showed their interest.

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, which prohibits the further distribution of the micro-organism 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 a negative impact on the effectiveness of microbial research and innovation. Because of the high mutation rates of micro-organisms, cumulative scientific research is only possible when 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 overall quality management and is a basic scientific procedure (WFCC, 2010; OECD, 2007). 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 access to genetic resources is however much less than that in other areas, such as plant genetic resources. Indeed, microbial species are characterized by high internal genetic variation between the organisms in the same species complex, and high mutation rates upon reproduction (Staley, 2002). The patenting of one micro-organism within a species complex provides exclusive rights to that one microbe, selected for its balanced expression of a cluster of interesting properties. However, many other organisms within the species complex, that 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 the 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 it is still informal, which poses serious threats to its long term sustainability. Moreover, commercial pressures have led to the adoption by a small number of collections of exclusive-use contracts, 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.

4.3. Crop genetic resources

The impact of the intellectual property regime on access to genetic resources is much greater than in the plant genetic-resources field than in the microbial or animal genetic-resources field (Tvedt et al., 2007; Chen and Liao, 2004). Plants have well defined varieties and much greater genetic stability on reproduction than either micro-organisms or animals. This means that exclusive rights can extend to direct offspring and the results of all cross-breeding from this offspring that has sufficient genetic similarity (for protected varieties) or contains a specific gene (for patented

genes). On the one hand, the ease of transfer of traits between crops makes it very hard to protect the proprietary information contained in 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 favor 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).

The global crop commons seeks to address these and other problems that exclusive-rights regimes have created for innovation, especially in the experimental breeding sector (based on the systematic cross-breeding of selected plants). The global crop commons is based on facilitated access to materials and their derivatives within a common pool of the world's major crops and forage plants for research, breeding and training purposes (Byerlee, 2010). Initially this pool was built in the context of the international experimental breeding programs organized by the Collaborative Group on International Agricultural Research (CGIAR). This regime was further formalized, in response to the threats posed by the intellectual property regime, through the 2002 International Treaty on Plant Genetic Resources of the Food and Agriculture Organization.

Extensive research has been conducted on the institutional arrangements adopted within the global crop commons (Helfer, 2005; Halewood and Nnadozie, 2008). At the time of writing, the crop commons, formalized through the International Treaty, 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 (www.planttreaty.org/inclus_en.htm). The plant genetic resources that are within this pool are all exchanged with the viral license of the Treaty, for uses of these materials for research, breeding and education purposes. When commercial applications are developed, the Treaty offers two options: commercialization with a non-exclusive use license which permits further use for non-commercial research, breeding and education purposes, or 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 programs underlie the exchange practices and promote the sharing of information, and the integration of regional efforts (Byerlee, 2010). The shared commitment to the common goal of increasing food production, and global poverty reduction, is a key driver of the whole system (Byerlee, 2010). From the early days of the crop improvement program, the community also invested in strengthening these social norms. The core activity has been six months field-based training of young scientists. In the field of wheat improvement alone, over 1360 individuals from 90 countries have participated in these training courses, and 2000 more have visited the International Maize and Wheat Improvement Center (CIMMYT) in Mexico. In addition, participating countries are allowed to give their own names to the varieties they release. This produces a sense of ownership, and ensures that the international seed banks are seen as honest brokers with respect to germplasm and information sharing (Byerlee, 2010). Finally, the CGIAR has developed policy guidelines that broadly reflect these values, both before (CGIAR, 2003) and after (CGIAR, 2009) the ratification of the International Treaty.

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 organized by CIMMYT. Every year 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 CIMMYT distributed 1.2 million samples to over 100 countries, corresponding to an average of 500 to 2000 globally distributed field trials per year (Byerlee, 2010). Data from the field trial is returned to 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 similar way to that in which bug reports are collected by free software projects (Benkler, 2006, p. 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 which is open to new users and contributors to the system, under a standardized non-exclusive contracts. 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 the material is exchanged under a formal viral license, because of the major threat of exclusion from key research resources through 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.

4.4. Farm animal genetic resources

Three major institutional arrangements are in use for the management and exchange of genetic resources in animal breeding. The first has been 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 through technological means. As a result, in areas where hybrid breeding is a well developed technological option – mainly poultry and pigs – an exclusive-access regime has developed within a centralized and large-scale breeding industry (CGRFA, 2009).

Most livestock breeding is, however, based on experimental breeding within a pool of animals which are managed in an open commons. On the one hand, when animals are exchanged between livestock keepers, the assumption is normally 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 (CGRFA, 2009). On the other hand, sustainable breeding requires a high level of coordination and has to adjust to local consumption patterns and available feed resources. Therefore, the majority of experimental breeding programs that are run by farmer-owned co-operatives and breeder organizations operate in the context of national breeding programs or farmer-driven societies with a regional scope (CGRFA, 2009). Such programs 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, this institutional arrangement for commons-based management is not a globally interconnected pool

as in the case of plants and microbials, but can be better characterized as a global network of exchange amongst limited (national or regional) commons.

Commons-based experimental breeding is, however, increasingly coming under pressure from international companies that are taking over farmer-owned cooperative schemes, especially cattle-breeding schemes (Mäki-Tanila et al., 2008). This has led to the development of a third institutional regime, based on the operations of centralized commercial-breeding companies, with high expectations of quick profits and a unilateral focus on productive traits. This centralization of 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 (Mäki-Tanila et al., 2008, p. 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 causing 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 (Mäki-Tanila et al., 2008, p. 24).

Non-market values play an important role in the organization of the traditional commons-based production sector in animal breeding, described above, although these values have to be combined with the productivity constraints of the private farms that are breeding the animals (Mäki-Tanila et al., 2008, p. 21; CGRFA, 2009, p. 7; p. 20). Animal breeding is part of national food security, and cooperative breeding programs 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. That explains why most schemes are developing common guidelines for quality management and sustainable breeding. They are also actively promoting these guidelines amongst 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 state approved, comply with a set of quality-management standards, and undertake conservation-breeding programs.

The modular organization of the experimental breeding program has been developed as a solution to deal with the specific problems of animal breeding, such as the need to limit inbreeding and to maintain a sufficiently diverse breeding base for disease management. The goat improvement program developed in France by Capgènes aptly illustrates this modular organization (www.capgenes.com). In this program, a yearly selection of the 1000 best-performing animals is made from a pool of 170,000 goats on 800 farms. From this 1000, 40 male goats are selected after a lengthy process of quality checking and off-breeding. These males then turn serve as the starting point for the following year's artificial insemination program for breed improvement.

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 are the reliance on private actors (rather than

public collections) whose resources are pooled in a collective breeding program, and the limited geographic scope of the commons-based improvement programs. The latter remains true in spite of 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 weak. However, the recent introduction of new business practices may lead to a rapid change in this situation.

5. Discussion

The hypothesis of this paper is that the design principles established for the digital-information commons are also relevant to our understanding of the practices for sharing within the global genetic-resource commons. The main similarities shown by our comparative case-study 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.

This analysis has also shown some important differences between the genetic-resource and digital-knowledge commons. One is the costs of the collections: the costs of creating genetic-resource collections are very substantial because 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 to access the network (Benkler, 2006). In the field of microbial and plant-genetic resources, part of this capacity problem is addressed through the global networking of distributed collections. Examples of this are the breeding programs 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 contributed to collective breeding-improvement programs is to a certain extent excess capacity, as local farm breeding would continue in the absence of the collective breeding program. Here the analogy with the networking of the excess capacity of computing resources in peer-to-peer networks, as analyzed by Benkler (2006, p. 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. This can be done either through formal legal rules which modify the behavioral incentive structures for the participants, or through informal means which act directly on the development of social and intrinsic motivations. An example of 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 regulating the setting up 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 international FAO treaty.

6. Conclusion

There has been a dramatic increase in interest in commons in the last 10 to 15 years, from traditional commons managing the use of exhaustible natural resources by fixed numbers of people within natural borders, to global information commons, dealing 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 paper shows that networking pools of genetic resources in a global commons potentially is 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. 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 are combined into new compounds or screened to find organisms with new properties.

In the current legal environment, the range of obstacles to the full realization of the new opportunities offered by global networking of genetic resources presents a formidable challenge (Reichman et al., 2009). This shows the need for appropriate organizational forms, legal arrangements and social practices, which 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 paper, 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 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.

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