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Tom Dedeurwaerdere (FRS-FNRS/UCL)

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Design Principles of Successful Genetic-Resource Commons for Food and Agriculture

T. DEDEURWAERDERE¹

¹Research Associate at the National Foundation for Scientific Research, Belgium (F.R.S.-FNRS),
and Professor at the Université catholique de Louvain
Email : tom.dedeurwaerdere@uclouvain.be

ABSTRACT

Recent history shows the benefits of formal arrangements for pooling plant genetic resources on the global scale, such as through the International Treaty on Plant Genetic Resources for Food and Agriculture. New challenges such as global infectious diseases affecting food crops and animals or the impact of climate change on shifts in production practices have lead public and private research entities, farmers and industry to pool genetic resources beyond plant genetic resources only. This paper presents a comparative analysis of such 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, managing use and exchange of global genetic resource as a commons can be a desirable and effective solution to provide essential knowledge assets that contribute to conservation and sustainable use of agricultural biodiversity with major benefits both in developing and industrialized countries.

Keywords: Microbial genetic resources, Plant genetic resources, Animal genetic resources, Access and benefit sharing, Intellectual property.

JEL Classification: Q57.

1. INTRODUCTION

The purpose of this paper is to provide an overview of the development of new theories and case study material in the field of the evolving global commons in genetic resources for food and agriculture. 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 analyzed in a systematic manner with the aim of supporting the development of appropriate institutional and legal frameworks.

This paper shows that, when the research and innovation processes with genetic resources 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 (Reichman, Dedeurwaerdere and Uhler, 2011; Lessig, 2008). 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 paper is structured in the following way. The first section briefly examines the recent literature on 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 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, the final section summarizes some key features of the genetic resource commons that can guide efforts in developing appropriate legal and institutional frameworks.

2. 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). 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 take 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 the innovation process is likely to be extremely low (Simpson, Sedjo and Reid, 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.

3. RESULTS OF CASE STUDIES OF INSTITUTIONAL CHOICES

3.1. Materials and methods

This paper presents a comparative analysis of three such case studies, in the fields of microbial genetic resources, plant genetic resources and animal genetic resources. The methodology of this comparative assessment builds upon the well-established literature on the natural resource commons, by acknowledging that both the biophysical characteristics of the resource, the governance arrangements and the characteristics of the users impact upon the management of the commons (Ostrom, 2005; Agrawal, 2001). Therefore, the discussion of commonalities and differences between the three cases will address the variations along these three dimensions (see also the summary table later in this paper).

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 and the competition from vertical integration and the centralization of the inputs within global companies, among others (Reichman, Dedeurwaerdere and Uhler, 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.

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, Pascual and Dedeurwaerdere 2006; Stromberg, Dedeurwaerdere and Pascual, 2007) 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.

3.2. 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 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.

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 percent of the strains in the WFCC's culture collections that are referenced on Straininfo are unique) (see

<<http://www.straininfo.net>>). 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 of 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, 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.

Some striking features of the results, for the exchanges amongst the formal collections, are the important number of new strains coming directly from in situ settings into the culture collections (37 % from own collecting activities in the field and 27% from research laboratories in academia and hospitals who principally do their own collecting), the dominance of public sector transactions (77% to entities that are largely public) and the importance of reciprocity amongst collections (16% of new material comes from other public culture collections and 9% of existing material goes to other public culture collections).

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 serves 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, Dedeurwaerdere and Uhler, 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 (see StrainInfo at <<http://www.straininfo.net>>). 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 showed an 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, 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 (WFCC, 2010; OECD, 2007). The rise of exclusive contracting poses a real threat to public microbial research.

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.

3.3. 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 (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, 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, Krishna and Pascual, 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, Dedeurwaerdere and Uhler, 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 many of its core features such as its Standard Material Transfer Agreement are still under scrutiny.

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 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 (see <http://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 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 programs 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 program, 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 (SGRP, 2003; CGIAR, 2009).

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.

3.4. Farm animal genetic resources

Three major institutional arrangements are in use for the management and exchange of genetic resources in animal breeding. The first 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 programs that are run by farmer-owned cooperatives and breeder organizations operate in the context of national breeding programs or farmer-driven societies with a regional scope (*ibid.*). 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, the institutional arrangement for commons-based management is not a globally interconnected pool as in the case of plants and microbials 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 (Mäki-Tanila et al., 2008, 21; CGRFA, 2009, 7 and 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, 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 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 in-breeding 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. In this program, 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 program for breed improvement (see www.capgenes.com).

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 program as well as the limited geographic scope of the commons-based improvement programs. The geographical limitations of the this sector remains 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.

4. COMPARATIVE ASSESSMENT OF THE DESIGN FEATURES

As shown in this paper, 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 paper 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 1.

		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 high degree of genetic stability	Relatively well defined breeds
Characteristics of the user groups	Type of users	Mix of public and private	Mostly public sector	Mostly private sector
	Main non-market motivations	Contribution to scientific research ethos Conservation of biodiversity	Food security Contribution to training and research	Animal health Conservation of genetic variety
Features of the Governance arrangements	Governing bodies	Global and regional federations	Secretariat of international treaty	National and local breeding organisations
	Organization of distributed collaboration	Shared resources amongst a distributed network of microbial collections	Shared resources amongst plant breeders, centralized collections for key species	Shared resources amongst farmers of a same breed
	Forms of exchange	Mix of formal and informal	Mainly formal	Mix of formal and informal
Main challenges to the commons-based exchange		Restrictive license policies in high commercial value collections	Broad patents on plant genetic resources	Vertical integration of breeding operations in transnational companies

Table 1. Biophysical, institutional and community characteristics of the genetic resource commons

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 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 that is 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. In this case, the analogy with

the networking of the excess capacity of computing resources in peer-to-peer networks, as analyzed 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 (WFCC, 2010) and the CGIAR policy guidelines that pre-dated the ITPGRFA (SGRP 2003).

5. 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 paper 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.

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