

14 Knowledge commons, intellectual property and the ABS regime

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Introduction

Knowledge about genetic resources accumulates daily. Much of it enters the public domain. The public domain is organized in many different forms, which can be ordered according to the degree of commonality, in other words the freedom to insert information into the systems and the freedom to take and use information from them. The commons character of the public knowledge domain contrasts with various kinds of knowledge privatization. The major instruments of privatization are copyright, trade secret protection, patent/breeders' rights and – a more recent addition – sovereign rights over genetic resources. Privatization means that the producer of knowledge is entitled to control its utilization. According to ruling opinion, this right will reward and stimulate the production of knowledge. Others are concerned, increasingly in recent times, that instead privatization may hinder the progress of research and development.

This chapter will explore, with a focus on knowledge about genetic resources, how the different privatization regimes relate to each other, and how a balance between reasons for a public domain and for privatization can be found. It will start by exploring the characteristics and problems of knowledge commons and proceed to discussing the instruments of and reasons for privatization, with a view to clarifying the specifics of the access to genetic resources and benefit sharing (ABS) regime.

Characteristics and problems of knowledge commons

An advanced knowledge commons consists of a collection of information into which everyone can feed information and from which everyone can take information for unrestricted use.

Knowledge commons are a variant of the 'new commons'. While in the 'old commons', such as common grazing land or fisheries, the resource can be depleted and use is therefore *rivalrous*, in the informatic commons the use is non-rivalrous because utilizing information does not exhaust the information but rather enhances its content (Hess and Ostrom 2007).

This means that the task for the management rules is less difficult than if, for instance, grazing times and intensity on communal land must be allocated and supervised.

While in the old commons, the resource utilized by members (the grazing land or the fish stock) is normally the common *property* of them or the state, this is not necessarily so in the case of knowledge commons. The resource (information) can be private intellectual property if the proprietor feeds it into the common pool on the agreement that it can be used without restriction. However, the pool may require that only information which is not subject to IPRs will be entered into the collection.

Knowledge commons, however, resemble the old commons in respect of the *free-rider problem*. There can be persons who wish to make use of the knowledge but try to avoid feeding their own knowledge into the system. Thus, the possibility of excluding free-riding persons must be ensured. While in the old commons this can be organized by physical exclusion of users, it is more difficult in knowledge commons. It is true that by technically closing data processing media information can be kept secret, but there are many ways to circumvent barriers, and once the information has escaped, it easily spreads around.

A third problem is the possibility of *unequal use* of the communal resource. It frequently arises in the old commons when, for instance, industrial vessels exploit a coastal fishery together with small vessels. This has sometimes been prevented by reserving the coastal area for artisanal fishery or by supporting investment more efficiently (Winter 2009). As for the knowledge commons, the non-rivalry of information use works against such unequal exploitation. There is nonetheless a similar kind of inequity in that the bulk of research on genetic resources is conducted by researchers from developed countries whilst researchers from developing countries often lack the infrastructure and expertise to keep pace. It is, therefore, crucial for knowledge commons to install a mechanism of special support for the developing countries.

Another characterizing dimension is the *geographic scope* of a commons. In the old commons, the resource is normally local, whereas knowledge is geographically unlimited, both by its very nature and by its major carrier, the print and electronic media. In regulatory terms, this means that other than in the old commons, any management rules for the commons will be concerned with many jurisdictions and legal cultures.

The final dimension of comparison is the possibility that parts of the pooled resource (to which the user may have contributed or not) are *appropriated*. This is not problematic in the old commons, because it is part of their rationale that products resulting from the use of the common goods can be sold. For instance, it is part of the institutional setting of common fisheries that the fish caught from a common fish stock can be sold by the individual fisherman. The price is more or less known to and accepted by the pool members, and it is clear to them that with the sales the product leaves the

pool. However, the situation is different with knowledge commons. The genetic resource can remain in the pool even if individual samples are sold or given away. A user may, however, discover that the genetic resource is of extraordinary economic value and seek a permanent monopoly over it by intellectual property protection. The commons must then decide whether to allow this or to require benefit sharing with the pool and/or the provider of the information. This is the question that will be examined in more detail in the remainder of this chapter.

Phenomenology of biological knowledge commons

In order to understand better the characteristics and problems of knowledge commons in the realm of genetic resources, some examples of such commons will be presented. Knowledge commons can be pure pools of information, and they can exist side by side with commons of genetic material. Commons of genetic material comprise *ex situ* collections and exchange networks of biological resources (such as botanical gardens and microbial culture collections), exchange networks of individual holders of *ex situ* resources (such as plant and animal breeders), as well as exchange networks of holders of *in situ* resources (such as local seed fairs¹). Most of them are intended to facilitate the exchange of specimen for research and further development.² Often the material collections are combined with information pools related to the material. These are usually also openly accessible.³ However, the bulk of information on biological resources is contained in pools detached from material collections. These pools will form the focus of the remainder of this chapter.

The content of knowledge pools which is of interest in our context can be the following:

- scientific organismic and biological taxonomy (i.e. knowledge about the organism and its life conditions and functions);
- traditional knowledge on organisms and their functions;
- genomics, proteomics and metagenomics (i.e. the knowledge about the genome and the functions of genes and proteins).⁴

In terms of carrier, print media have until recently been the most popular. While the form the author gave to the information is protected by copyright, the information content published in this way has been free for any use. Informal rules of professions ensure that the use of information must be acknowledged by citation of the source. Researchers are motivated to publish their intellectual products by the prestige conveyed by being read and cited. Of course, the material interest of getting a job and being paid is behind this incentive, but it is tied to the immaterial interest because the entrance preconditions for jobs are often related to the scientific standing of the applicant.

Print media are increasingly being complemented and even replaced by electronic media. Many journals and books publish electronic versions of their articles; others appear only in that way. However, much information is not sufficiently original or is too voluminous for publication in article and book format, such as sequenced genomes of organisms or the compilation of already published information. For this purpose, more and more electronic databases have been set up. Databases also contain original information but publication through a journal or book has continued to be more highly esteemed because of quality standards and peer reviewing.

Some examples of databases will be sketched out, most of them public and one private.

Public databases

Scientific knowledge about biological resources

Since biological science emerged, innumerable collections of knowledge about biological resources have developed. Traditionally this has been done in printed form, but for several decades electronic databases have been built up. One example is the Global Biodiversity Information Facility (GBIF). Its mission statement reads that GBIF 'promotes and facilitates the mobilization, access, discovery and use of information about the occurrence of organisms over time and across the planet.'⁵ It is funded by public monies and runs a database on the taxonomy and occurrence of a large and fast increasing number of species. The use of the database is free and unrestricted but subject to the obligation that the database is mentioned as a source in publications. Those who provide data to the database must agree to unrestricted access to the data and ensure that the data are not subject to any intellectual property protection.

Traditional knowledge about biological resources

The most original variants of traditional knowledge (TK) pools are networks and communities of healers, farmers and local populations who generate, exchange and collect knowledge about biological resources.⁶ They are traditionally open for any person contributing and allow use by anyone free of charge or in return for up-front compensation by payment or barter for equivalent TK. In some countries, systematic collections have been built up, first in printed form and more recently in electronic databases. One example of the latter is the Traditional Chinese Medicine Database System, which compiles a large number of pre-existing Chinese medicine databases. Access is possible after registration and against an up-front payment, which is used to cover the cost of maintenance of the system. The user does not have to sign an agreement or disclose the aim of use.⁷

Genomics

GenBank sequence database⁸ is run by the National Center for Biotechnology Information (NCBI) at the National Library of Medicine (NLM), National Institutes of Health (NIH), USA. It is part of the International Nucleotide Sequence Database Collaboration (INSDC), which also includes the DNA Databank of Japan (DDBJ) and the European Molecular Biology Laboratory (EMBL).

GenBank has a collection of annotated sequences of DNA and RNA.⁹ The sequences included in the database stem from more than 100,000 organisms. GenBank entries include a description of the sequence, the scientific name and taxonomy of the source organism and a table of features that identifies coding regions and other sites of biological significance. Protein translations for coding regions are included in the feature table. Bibliographic references are included along with a link to the Medline unique identifier for all published sequences. Sometimes, but not in all entries, the geographic location of the sequenced specimen is also noted.

The most important source for entries into GenBank is scientists. It is the responsibility of submitters to ascertain that they have the right to submit the data. The base does not attach statements to records that restrict access to the data, limit the use of the information in these records, ask for payment of licence fees or prohibit certain types of publications based on these records. Corrections of errors and updates of the records by authors are possible and erroneous records may be removed from the next database release.

Anyone is free to search for and download data. The purpose of use of the data is unrestricted. It is, however, required that GenBank, if used for research, is cited as a source in any publication of research results.

Proteomics

The Universal Protein Knowledge Base (UniProtKB)¹⁰ is operated by the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. It is funded by the US National Institutes of Health (NIH), the European Commission and the Swiss government. It contains a collection of protein sequence data. It is considered to be the world's most comprehensive database on protein information. It has two parts, UniProtKB/Swiss-Prot and UniProtKB/TrEMBL.¹¹ The first strives for a high level of annotation (such as the description of the function of a protein, its domains structure, post-translational modifications, variants, etc.), a minimal level of redundancy and a high level of integration with other databases. The second is a computer-annotated supplement of Swiss-Prot that contains unreviewed protein sequences associated with computationally generated annotation and large-scale functional

characterization. Every UniProtKB/Swiss-Prot entry contains the amino acid sequence, protein name or description, taxonomic data and citation information, and as much annotation as possible.

The source can be animals, plants, microorganisms, viruses etc. The source organism is listed, but not the geographic location of the species or the sample taken for sequencing. More than 99 per cent of the protein sequences provided by UniProtKB are derived from the translation of the coding sequences (CDS) which have been submitted to the public nucleic acid databases, the EMBL-Bank/GenBank/DDBJ databases (INSDC). These CDS are either generated by gene prediction programs or are experimentally proven. A protein identifier ('protein_id') is assigned to the translated CDS and can be found in the original EMBL-Bank/GenBank/DDBJ record and in the relevant UniProtKB entry. All these sequences, as well as the related data submitted by the authors, are automatically integrated into UniProtKB/TrEMBL. The TrEMBL records can be selected for further manual annotation and then integrated into the UniProtKB/Swiss-Prot section.

On the user side, everyone has free access to the databases for unlimited purposes. Even the patenting of a protein and its function is permitted. However, the availability of the information from the database may be regarded as prepublication under patent law.

Meta-databases

The word 'meta' is commonly used to define data about data, in other words an upper level of data about a lower level of data. For instance, data about the methodology of sampling and researching an organism would be metadata of the data about the organism itself. The more first level databases develop, the more important it is to create meta-databases that combine them and provide criteria and tools for targeted searches. This is particularly crucial in microbiology. The microbial genomics data have exponentially grown since the advent of metagenomics, i.e. genomic research that targets not only cultivated samples but also non-cultivable samples taken directly from of the natural environment and representing the huge microbial diversity in the same.¹² A publicly funded database compiling and making data from such research publicly accessible is, for instance, run by the Community Cyberinfrastructure for Advanced Microbial Ecology Research and Analysis (CAMERA).¹³ Another one which is still under construction is StrainInfo. It is publicly funded and publicly accessible (Dawyndt 2011).¹⁴

Commercial databases

BIOBASE¹⁵ is an international bioinformatics company headquartered in Wolfenbüttel, Germany. Its focus is on the generation, maintenance and

licensing of biological databases and their connected software platforms. All BIOBASE databases provide manually curated content. BIOBASE staff collect and structure the required data from peer-reviewed scientific primary publications.

One of the databases operated by BIOBASE is called TRANSFAC®. It compiles published data on eukaryotic transcription factors, their experimentally proven binding sites and regulated genes. Transcription factors are important components of signalling cascades controlling all types of normal cellular processes as well as response to external stimulus, conditions of disease drug treatment, and more. The database contains up-to-date transcription regulation details from the PubMed literature on more than 300 species, with a focus on humans, mice, rats, yeast, worms and plants. It is organized in a one-report-per-protein format.

Access is not free but rather provided after the payment of a fee. The user is not allowed to permit third party access to the database, must keep any proprietary information taken from the database undisclosed, limit access to the database to employees who have agreed in writing to maintain the proprietary information in confidence, and may not transfer any right to any third party without the prior written consent of BIOBASE.

Knowledge commons and privatization

The public domain character of knowledge pools stands in contrast with different kinds of privatization possibilities and efforts, three of which are crucial: copyrights of text producers, patent/breeders' rights/trade secrets of information producers, and sovereign rights of resource providers.¹⁶ We will discuss them in turn.

Copyright

By providing copyright, states reward those who have created original work. The protection relates to the form of the work, not its substantial idea.¹⁷ In most jurisdictions, the right comes into being by the very creation of the work¹⁸, while in the USA it must be registered, which is facilitated because it is made by mere declaration to the competent authority. The copyright provides the power to exclude anyone from reproducing, adapting, distributing, performing, displaying, communicating and translating a work. Creators of databases are also granted the copyright if the selection or the arrangement of its content is an intellectual creation.¹⁹

Much of the present discussion on databases of genetic resources is concerned with creating commons and defending them against enclosures by copyright holders (Uhlir 2011). The maintenance of commons is possible because the law does not prevent the holder of the copyright from providing a general licence or even from waiving his/her copyright. Such a waiver is proposed by the Creative Commons network. The most far-

reaching version is contained in the declaration called CC0, which reads as follows:

To the greatest extent permitted by, but not in contravention of, applicable law, Affirmer hereby overtly, fully, permanently, irrevocably and unconditionally waives, abandons, and surrenders all of Affirmer's Copyright and Related Rights and associated claims and causes of action, whether now known or unknown (including existing as well as future claims and causes of action), in the Work (i) in all territories worldwide, (ii) for the maximum duration provided by applicable law or treaty (including future time extensions), (iii) in any current or future medium and for any number of copies, and (iv) for any purpose whatsoever, including without limitation commercial, advertising or promotional purposes (the 'Waiver'). Affirmer makes the Waiver for the benefit of each member of the public at large and to the detriment of Affirmer's heirs and successors, fully intending that such Waiver shall not be subject to revocation, rescission, cancellation, termination, or any other legal or equitable action to disrupt the quiet enjoyment of the Work by the public as contemplated by Affirmer's express Statement of Purpose.²⁰

Looking at the reasons why researchers waive their copyrights, it seems that non-monetary considerations such as prestige and the pleasure of enhancing common knowledge are often stronger than monetary incentives, which are difficult to calculate anyway. Sometimes, a monetary reward can even be counterproductive in a collaborative network (Dedeurwaerdere 2010).

Of course, there are limits to the willingness of actors to fully integrate their work into knowledge commons. There are legitimate reasons, for instance if the author makes his/her living out of the production of knowledge. BIOBASE is an example of this. They provide the service of screening published data for genetic transcription factors. It is understandable that they claim copyright in order to be paid by customers. The interest of publishers in having the copyrights transferred and used in order to cover the cost of publishing is also legitimate. Cases in which an author makes use of a freely accessible database and keeps his/her results secret are more problematic. This impoverishes the content of the collection in the long run. The researcher should at least be asked to provide results if the research is publicly funded.²¹ If not, that is if the research aims at commercial products, keeping results secret is understandable, but researchers should then pay fees for data access. In any case, the user of a database should be obliged to make reference to it if his/her research is based on it. This is, for instance, the policy of NIH in relation to the databases run under its auspices (Sheehan 2011: 103).

Patent and breeders' right; trade secrets

While copyright is aimed at enhancing the cultural sphere, patent and breeders' rights are intended to enrich the economic sphere. This is reflected in the requirement (not applicable to copyright) that the information content to be patented must be capable of industrial application. Somewhat similar to the copyright precondition of originality, the information must be an invention and a novelty.²² In contrast to copyright, the content of the information, not its form is patented. The breeders' right, which is an exclusive right on plant varieties, resembles the patent right but is somewhat less demanding in its preconditions. Novelty remains a precondition while industrial applicability is replaced by the more concrete criteria that the variety must be distinct, uniform and stable. Inventiveness is not required. Trade secret protection is also a kind of intellectual property protection. It is akin to the patent and breeders' right, because it is also related to the commercial value of information content and grants the holder an exclusive use right. It is more roughly shaped, however, because the preconditions of protection are less precise and the protective apparatus less sophisticated.

Knowledge commons on genetic resources are constricted both by copyrights and by patent/ breeders' rights/trade secrets. While the intellectual effort of creating the form of the information (i.e. the research article or database) is rewarded by the copyright, the other rights reward the intellectual effort of inventing a new and useful idea. In a sense, the data commons is thus undermined by two sorts of privatization, the privatization of the form and of the content.²³ The challenge from patent/ breeders' rights is, however, more consequential because licence payments are normally higher, and the uses allowed by law more restricted than with copyrights. The reason for this is that usually the industrial application of the idea content yields more income than the publication of idea forms. The higher value of the right content is also reflected in the fact that patent and breeders' rights are granted by law but also individually issued so that the competent authority can check whether the preconditions are met.

There are two major challenges for the knowledge commons from patent/breeders' rights. One is the extension of the right. Patents can be obtained for DNA sequences if their function was discovered. Recent research has revealed that many DNA sequences cross-sect over many species. This means that if one sequence is patented, the right spans very widely. The realm of knowledge commons can thus be severely restricted (Oldham 2005).

The other challenge is free-riding. Users with commercial intentions may draw the benefit of free information from the database but not submit their own R&D results. It is true that the submission of results may not be fitting if they are from applied research and the database only collects

basic research data. But this is not necessarily so. Knowledge commons could well develop in the direction of applied research. For instance, as shown above, most of them already collect data on the transcription of genes into proteins, which could be classified as results from applied research. They may even decide to extend themselves to patentable products like, for instance, genetically modified microorganisms.

The law, of course, does not compel researchers to apply for patenting or breeders' rights. They can decide not to do this. The knowledge commons may provide incentives in that direction. The multilateral system may be taken as an example here. It frees the breeders of varieties taken from the system from paying royalties into the system if they do not exclude others from the use of the new variety.²⁴ A similar incentive could be provided by public databases. They could limit free access to non-commercial research (which may be defined as research aiming at enriching the public domain) and require commercial research to pay a fee or even royalty payments into the system.

Apart from the voluntary decision of breeders not to claim intellectual property, the danger of capture of the public domain can also be reduced by appropriate legal precautions (Rimmer 2008). One is connected with the novelty criterion. A patent or breeders' right is not granted if the information was already public. Thus, for instance, should a researcher download information on the coding of a gene from a public database, this could not be patented because it was already available in the database. Further legal mechanisms should be developed to exclude the sweeping scope of patent rights. This could be done by raising the thresholds for the patent preconditions of inventive step and utility and for the breeders' right precondition of usefulness, as well as by restricting the protective scope of rights so that further R&D remains possible if working within the public domain. As a radical solution, patents could be refused on any natural life form. After all, genes are not invented but discovered.

As an alternative to abstaining from searching property, the producer of the information can also opt for obtaining a patent/ breeders' right and either allow free use of the information (as in the case of the Creative Commons licence of copyright holders) or feed it into an IPR pool he/she forms with other right holders. Realistically, however, there is usually hardly any incentive to do this.²⁵

ABS rights

The right of provider states to control access to genetic resources (GR) and ask for benefit sharing (in short, ABS rights) is a relatively new constraint for material and knowledge commons on GR. Since the Convention on Biological Diversity (CBD) came into force in 1993, and subject to pertinent national legislation, states have sovereign rights to legislate that their GR can only be accessed (and exported, if the case may be) with

prior informed consent of the provider state and according to conditions laid down in a permit or access agreement.²⁶ If they do so this is a form of privatization that adds up to the other forms already presented. I will first clarify the similarities and differences of ABS rights in relation to these other rights and then discuss how the additional challenge can be handled by the knowledge commons.

ABS and the other privatization rights

ABS rights and duties are to be given precise shape by national legislation of provider and user states. The legal relationships created are between the state and individuals as well as between individuals.

The content of these legal relationships is located somewhere between real and intellectual property, with more affinity to the latter. As with any property right, the holder of the genetic potential of organisms (or information about it) is given the power to exclude others from using the resource or information. If compared with other intellectual property rights, ABS rights are more akin to patenting than to copyright, because some content, namely the genetic potential, rather than a form is protected. In both cases – patent/ breeders' rights and ABS rights – the object of the exclusive right is a peculiar mixture of real things (the genetic potential) and information (the knowledge about the real thing).²⁷

However, ABS rights also differ from patent rights in important respects. Other than patent rights (and more similar to copyrights) they arise 'automatically' by international convention and, internally, by national legislative act – in other words, they are not dependent on an administrative decision (provided the national legislator does not decide otherwise). The value for which the asset is protected is not only commercial but also ecological, cultural and scientific. Most importantly, however, while patent rights reward the inventive effort of the right holder, thus reflecting the labour theory of property, ABS rights are provided without any concern for whether an effort was made by the provider state. It suffices that the resource is found *in situ* in the provider state or *ex situ* in a collection. The theoretical background for this is a property theory based on simple possession. Such possession was recognized as a legitimate title by the international community, which is party to the CBD, just as simple possession has long been recognized for minerals, biological resources, etc. In other words, ABS rights are tied to the raw material possessed by a state while patent rights are based on its further development.

The fact that one and the same genetic resource can be subject to two exclusive rights – one for the raw status and one for the 'sophisticated' status of the genetic resource – puts them in conflict with each other. This conflict was intended, as ABS rights were designed to build a counter position of resource states against a one-sided privatization of the resource by developed states. This must be kept in mind in any analysis of knowledge commons.

ABS rights and knowledge commons

As stated above, from the perspective of preserving the knowledge commons, ABS rights are a threat to privatization just as patent rights are. More precisely, the challenge is that provider states may, by controlling access, also determine what kind of research and development activities are allowed. They have good reason to do this because the curtailing of R&D is a promising strategy to master the difficulties of tracking down benefit-generating processes in user states (see Chapter 1). On the other hand, resource states have a fundamental interest in encouraging research and development, and involving themselves in these activities to develop their own capacities. They are thus bound by a dilemma: they will want to support the commons in order to share in the non-monetary benefit of R&D, but they will also want to confine the commons in order to ensure their shares in monetary benefits.

Before discussing how this dilemma can be solved without restricting the commons, however, the extent to which it is true that knowledge of GR is under the command of the ABS regime must be clarified. We must ask whether any information on a genetic resource, be it taxonomic, genomic or functional, is legally under the disposition of the provider state.

The question, under the heading of 'derivatives', was much discussed in the run-up to the Nagoya Protocol. The Protocol itself presents a solution: Article 2 defines derivatives as 'a naturally occurring biochemical compound resulting from the genetic expression or metabolism of biological or genetic resources, even if it does not contain functional units of heredity'. The chemical compounds encoded by the genes are thus included in the scope of applicability of the ABS regime. However, derivatives are made part of the term 'utilization of genetic resources' by Article 2 NP, and not of the term 'genetic resources' itself. This means that the sovereign rights to govern access to GR do not cover chemical compounds. For instance, the provider state cannot claim through its national legislation that, without any specific administrative act or contract, any chemical derived from a GR is subject to its own disposition.

Nevertheless, it is possible for the provider state to achieve this same effect with other methods. Access control can be used not only to fix the conditions of access to GR, but also to determine the conditions of utilization of GR. Thus, the provider state can introduce legislation requiring that conditions will be included in any access permit or access contract that define the allowed utilization and handling of R&D results. If this is implemented in the individual case, the resulting knowledge can only be used as determined by the permit and/or contract. If, for instance, the relevant conditions require that the researcher does not submit the research results to the public domain, or, on the contrary, that he/she may only seek patent protection upon approval by the provider state, he/she must obey these rules.²⁸

An objection to this very far reaching construction of access control is that the provider state's grip on the GR should expire in some way during the often very long and highly branched chain of R&D from initial access up to the final product. Indeed, any other intellectual property regime does accept various kinds of limits. A look at such limits may provide reasonable analogies. While patent and copyrights expire after certain time periods, this is clearly not foreseen in the ABS regime. There is a case for introducing this kind of expiry time in the ABS regime. Likewise, a patent and a breeders' right does not exclude someone using the protected object or information in order to develop a new object or idea.²⁹ If transferred to the ABS regime, it can be argued that if someone uses the information about a gene that 'belongs' to a provider state to construct a different gene, he/she is free of any intervention by the provider state. The situation may be different and an analogy excluded if the genetic potential of an organism is still present in the derived product, such as in the case of breeding or genetic modification. By contrast, if a DNA sequence found in a certain organism can be synthesized, this should not be regarded as removing it from the disposition right of the provider state. Finally, the doctrine of exhaustion of intellectual property rights might provide an analogy. For instance, if a product derived from a GR is sold, the use and resale of the product should be free from the reach of the provider state's right. Details of such delineations should be worked out by pioneering national legislation or guidelines that further specify the Nagoya Protocol.

Given the fact that, on the whole, the provider states' ABS rights reach rather far, those who advocate the knowledge commons are once again under pressure to offer provider states incentives for waiving their rights. As said before, as to the R&D activities themselves and the R&D results, provider states will normally have self-interest to support communal forms because this gives them the chance to develop their own R&D capacity. Should a provider state prefer to keep the research result to itself, the knowledge commons could take note of that and tighten up access to the commons for this state, for instance by requiring it to pay user fees. This may persuade the provider state to allow R&D results from its GR to be submitted to the commons. However, concerning the privatization of R&D results by patent/breeders' rights, trade secrets and the exclusive bringing to the market of products, the provider state will legitimately wish to introduce effective measures to secure its special share in the resulting monetary benefits.

There are three ways of acceding to this request without fundamentally eroding the knowledge commons (cf. Halewood and Louafi 2012). One is to introduce conditions for the use of data, requiring that any commercial use must first be agreed with the provider state. Concerning submissions of data to databases, the database organisation could be required to ask for disclosure of the country of origin of the sample from which the data were derived. In addition, in order to enable the tracking back and forth of R&D

processes, unique and interchangeable identifiers of genes and tools to connect information would have to be developed (see Chapter 13; Garrity *et al.* 2009). Such tracking information could enhance the effectiveness of the requirement to disclose origin in patent applications or at other commercialization stages (Cabrera Medaglia 2010; Kamau 2009).

A second possibility would be to make database organizations responsible for supervising use and collecting and redistributing shares in monetary benefits. This would mean that not only non-monetary but also monetary benefits are included in the common pool.

However, the first – and even more the second – option would cause high transaction costs, and the databases would be loaded with heavy organizational tasks. Therefore, much speaks in favour of a third solution that has often been rebuffed but may nevertheless prove to be most reasonable and best manageable: the biodiversity charge. Under this scheme, any remuneration for the sales of a product, for a patent or breeders' licence or for the rendering of a service would be subject to the payment of a tax if the value-generating object or activity is based on genetic resources (or TK). Details would, of course, be elaborated, e.g. on the kinds of GR and TK and R&D processes triggering the charge as well as how high it should be. The money would flow into a worldwide fund, possibly managed by the Global Environmental Facility, or into a number of funds concerned with various GR species. Funds would be allocated according to criteria yet to be developed, which would on the one hand aim at supporting the conservation of biodiversity, and on the other hand reward those states who have provided GR that finally enrich the material and knowledge commons. The charge would, however, be detached from the individual provider state, i.e. the state that provided the individual sample or specimen for R&D. Therefore, in the R&D process, the origin of this specimen would not have to be registered where it is not necessary for scientific reasons. Thus, transaction costs could be reduced. At the same time, the concern about 'horizontal' equity would be solved (see Chapter 1). Funds could flow to the most relevant host states of GR rather than to the state that, by chance, was the one in which the GR was accessed. Of course, this alternative to the burdensome monitoring of R&D processes would require the conclusion of a new multilateral agreement and thus the consensus of many states and interest groups.

Notes

- 1 For examples see Chapters 5 and 12.
- 2 See Chapters 10 and 17.
- 3 Recently, collections have been building up more comprehensive information pools. See Chapter 11.
- 4 The functional information is particularly valuable because it allows products to be developed on the basis of the GR. It includes, as Garrity *et al.* (2009: p. 6) state, 'functional or regulatory pathways, structural polymers or biological

functions of an organism that are encoded for by the genetic material, including metabolic products that have some practical applications (e.g., low molecular weight organic acids; anti-microbial agents, such as antibiotics, and other biopharmaceuticals, flavors and fragrances, enzymes for industrial applications)'.⁵

- 5 <http://www.gbif.org>, viewed 28 January 2013. For further details, see Chapter 13.
- 6 See the case studies in Chapters 2, 3, 4 and 5.
- 7 See Chapter 8.
- 8 The following description is compiled from the GenBank website, <http://www.ncbi.nlm.nih.gov/genbank>, viewed 28 January 2013.
- 9 Deoxyribonucleic acid (DNA) is a macromolecule carrying the information for the development and functioning of an organism. Ribonucleic acid (RNA) is a macromolecule that helps to translate DNA information into the synthesis of proteins.
- 10 The following description is compiled from the UniProt/KB website, <http://www.uniprot.org/help/uniprotkb>, viewed 28 January 2013.
- 11 TrEMBL means Translated EMBL Nucleotide Sequence Data Library. EMBL is the European Molecular Biology Laboratory.
- 12 The term was introduced by Handelsman *et al.* (1998); cf Wikipedia article on Metagenomics.
- 13 <http://camera.calit2.net>, viewed 28 January 2013. See Sun *et al.* 2011.
- 14 <http://www.straininfo.net>, viewed 28 January 2013.
- 15 The following description is based on the BIOBASE website, <http://www.biobase-international.com>, viewed 28 January 2013.
- 16 Geographical indications could be considered as a fourth (see Correa (2010) for a recent report on this discussion) but will be excluded from further analysis.
- 17 Article 2, WIPO Copyright Treaty states: 'Copyright protection extends to expressions and not to ideas, procedures, methods of operation or mathematical concepts as such.'
- 18 Article 5 (2) Berne Convention for the Protection of Literary and Artistic Works: 'The enjoyment and the exercise of these rights shall not be subject to any formality.'
- 19 See Article 5 WIPO Copyright Treaty: 'Compilations of data or other material, in any form, which by reason of the selection or arrangement of their contents constitute intellectual creations, are protected as such. This protection does not extend to the data or the material itself and is without prejudice to any copyright subsisting in the data or material contained in the compilation.'
- 20 <http://creativecommons.org/publicdomain/zero/1.0/legalcode>, viewed 28 January 2013. It is controversial if the law in all states allows such a waiver. For these cases Creative Commons proposes to add to the waiver a declaration by which the right holder provides a general licence to any user.
- 21 Since the 1990s a counter-tendency has emerged. Universities ask for non-disclosure in order to allow for patenting the research result. There is a longer-standing practice of governments keeping results secret for political reasons.
- 22 Article 27.1, Agreement on Trade-Related Aspects of Intellectual Property Rights (TRIPS Agreement).
- 23 It should be kept in mind that the information content of the public domain as such is not shrinking as a result of patent rights because they require the right holder to disclose the information. In that respect, patenting is better than keeping information as a trade secret (Dinwoodie and Dreyfuss 2006: 198). However, the usability of the information is severely restricted. As free

utilization is one of the intentions of many commons, this is, of course, a challenge for them.

24 See Chapter 17.

25 See Chapter 9.

26 Encouraged by the International Treaty on Plant Genetic Resources for Food and Agriculture, Article 9, states can also introduce protection of local landraces by establishing *sui generis* farmers' rights. See Chiarolla, Louafi and Schloen (2013: 93, 110).

27 Sometimes the distinction between the real thing and the information about it is not accepted. See, for instance, the definition of genetic resources by Garrity *et al.* (2009: p. 14) which reads: 'Genetic resources are essentially "packets of informational goods" that are presented as biological material (e.g., an entire specimen, a leaf, skin, etc.) and include DNA and RNA molecules as well as gene or protein sequences.' In my view, this definition does not lead to a clear understanding. I believe that the reality of a DNA string with all its potentialities must still be distinguished from the information representing this reality. In other words: the perfect description of a gene in silico does not bring the gene to life.

28 It is true, however, that the provider state when designing conditions is not allowed to exaggerate; it must respect its obligation under Article 15.2 CBD also to 'endeavour to create conditions to facilitate access to genetic resources for environmentally sound uses'. What that means exactly is still open for discussion.

29 Traditionally, non-commercial users could claim to freely use the patented information or object for scientific purposes. But this defence has recently been curbed by court jurisprudence on the grounds that universities nowadays also aim to secure intellectual property (Dinwoodie and Dreyfuss 2006: pp. 204, 206).

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