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Ownership and responsibility: public property in Creative Commons and rice genomics

Abstract

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Agricultural biotechnology/genomics, more specifically is one of the busiest sites of research and debate at the nexus of science, technology, and policy. The field comprises emergent practices and technologies that produce and use information about plant genomes to improve agricultural production as well as the nutritional value of foods. In particular, intellectual property rights in genes and genome-related information are highly contested in this emerging arena. Intellectual property rights are often represented as binary choices between private and restricted, or public and free. I illustrate how property rights, in practice, can fall along a spectrum of possibilities, from wholly free to completely restricted. The definition of points on this spectrum, moreover, occurs not only (or even) in formal legal or regulatory institutions, but is rather simultaneously defined and defended through scientific practice. This spectrum constitutes a hybrid set of properties that I term public property.

Debates centered on intellectual property rights are also a major focus in the area of copyright, especially among groups attempting to carve out niches for more public availability of information such as music, movies, images and text. Creative Commons is a formalized attempt to develop alternatives to intellectual property laws, working both within and outside the legal system to this end. This study develops the concept of public property through a comparative analysis of intellectual property debates and negotiations in rice genomics and similar practices in Creative Commons. In both cases, public property raises questions about what notions of public and private mean as they get configured through intellectual property debates in technoscience especially in genomics, where such arrangements have received little attention outside the research communities in which they have been developed and where the implications of property configurations will likely impact the entire political economy of rice, from upstream scientific practices to downstream products.

Introduction

Intellectual property questions are at play in multiple domains. Legal debates over the Harvard Oncomouse reach opposing conclusions in different national contexts and raise questions, 1 database rights are granted in the United Kingdom but not the United States, 2 and cultural property becomes a new category in the international arena 3 They are national, transnational, and international debates, run the gamut of intellectual property rights, and question the viability of property claims. Ownership is central: who owns what and under what conditions. Debate usually centers on an all or nothing proposition: either private rights can be claimed (a specific owner, usually one person or a particular entity, is declared) or ownership accrues to the public, becoming a good inheritable by everyone (though who exactly that everyone is remains an open question). Theoretically, at least, private property rights as produced and defined in the legal system sit at one end, and at the other, the public domain (or commons) where there are no owners and no formal protections.

While it is well understood in the field of science studies (and to some extent in anthropology) that such categories are (largely, though not always) purificatory myths (see Latour 1993, Haraway 1997, Coombe 1998) that there is always a spectrum of hybrids that range in the middle of the binary the categories are still argued as realities and they do contain kinds of work for people. Understanding the hybrids, however, helps to raise questions about the implications for those hybrids, and the following question remains: What work does a public/private, individual/communal rhetoric do? (Strathern 2004, 63) I want to take that question and work backwards, showing how the binaries get broken down, both through formal means in a non-profit organization called Creative Commons and via informal means through four efforts to sequence the rice genome. Multiple conceptions of freedom and control in these cases lead to hybrid properties that I term public property. Public property suggests that a range of property formulations exist, calling attention to the fact that legal categories are not particularly stable constructs (Aoki 1998). Instead, information can both be public and private, free and owned and is comprised of property configurations too complex for the simple binary categories of private property or public domain. I will show, through the two cases, how private property and the public domain get configured and translated into new forms of intellectual property that do not reflect notions of property rights that currently dominate legal and legislative discourse.

Following Strathern (2004), I also want to suggest that declarations of ownership are not just (or even) about rights, but also about responsibility; a space is opened in which multiple claims (that is, from many potential owners) can be made. Particularly, ownership claims introduce the possibility for tracing backwards (and eventually forwards) along the chain of connectivities that produced the what for which ownership is concerned, and create the potential for relationships to form across those connectivities regarding the way the what will be used, and for whom. This last bit is critical: there would be no need for property claims were it not for the uses and counterclaims to the something for which intellectual property is desired. Public property, moreover, invites questions about the web of connectivities; it challenges the stability of private property claims and the idea that new knowledge can be completely free and without claims to creation, ownership, innovation, heritage etc.

I first discuss the non-profit organization, Creative Commons (CC), as an entryway into public property. Through a formal institutional configuration CC stabilizes the kinds of hybrid (public) properties that I will illustrate are produced in a less formal way through rice genome science, and it illustrates that these hybrids arise in multiple domains. Third, the CC case helps to situate the stakes in property debates, illustrating the interests involved in property debates and raising questions about what we might call interests in the eventual products of rice genomics. Finally, Creative Commons is beginning to incorporate scientific intellectual property rights in its model, suggesting that the informal public property developments I trace in rice genomics may become formalized to some extent through Creative Commons (or other institutional means like it).

I then introduce the case of rice genome sequencing, arguing that while genomics is typically portrayed as one of the latest attempts at ordering information in the quest for new ways to engineer life, the recent efforts to sequence rice not only illustrate the production of new scientific information, but also the simultaneous constitution of hybrid properties. Classifications that rest on only two possibilities do not help us when the properties in question are not clearly one or the other. The binary does not logically exhaust all the possible solutions (Rose 1986). And, as Stephen Hilgartner (2004) importantly reminds us, we do not have to look to national or international governmental institutions, or non-profit organizations I might add, to see the emergence of property regimes, because properties are constituted alongside the production of new information. Indeed property scholar Carol Rose argues that there are particular types of property, which can be called inherently public property, that are neither individually owned, nor controlled by the state (1986). Rose focuses on landed property waterways and roads but her more relevant point is that some types of property arise and become stabilized through custom instead of through law. In the case of rice genomes, public property suggests that properties are not only hybrids but can be constituted in practice alongside the development of new scientific knowledge.

My second case, then, will focus on the development of four rice genomes and explore the public properties that have emerged. My account will track the projects as they

emerge in an international consortium (the International Rice Genome Sequencing Project (IRGSP)), a country (China), two companies (Monsanto and Syngenta), and a publication (Science magazine). Rice genomics is an important case for understanding public property because the debates that occur in this case render visible the dynamics of property debates and new forms of property, and because rice is important from upstream science to downstream agricultural development, throwing up questions of ownership and responsibility across the spectrum of reality and potentiality for the result of rice genome efforts.

Creative Commons

A simple way to illustrate hybrid properties is through an example in the realm of copyright. In 2001, intellectual property lawyer, professor, and activist Lawrence Lessig, along with a group of collaborators at Duke, Harvard, MIT, and Villanova, developed a nonprofit institution called Creative Commons.⁴ Premised both on notions of (at least some) free and open access to informational public goods (that is, goods that could be or are subject to intellectual property rights), and the ability to make ownership claims to creative works through the IP system, Creative Commons works within current copyright law under the slogan some rights reserved (creativecommons.org). To better understand what Creative Commons sets out to do, I want to take it apart: that is, into what is a commons and what is creative about this new effort.

Commons

A commons is generally discussed as the opposite of private property rights, the latter a set of socially instituted and legally defined rights and protections given by a society to an individual or group. Intellectual property rights are based on a legal tradition of granting restricted access to those who make new knowledge; the exclusionary rights are thought to benefit society through a balance between increased incentives to innovate and greater market efficiency. That balance is effected through multiple types of property rights (e.g. copyright and patents) and limits to the amount of time that property rights can be held (e.g. 70 years after the authors death for copyright, and twenty years after an application is granted for patents). The argument is that society benefits from innovations, but innovations will only occur when the investment of labor and capital produce rewards (that is, profit). The concept of private property is sanctioned through a long history of practical and formal recognition in the law including the US Constitution, and legal institutions both national and international. Certainly, though, not every novel thing or thought is subject to intellectual property claims. If private property in the strongest sense means total control, or restricted unless authorized, then the alternative or outside of the intellectual property system (indeed, any property system) is called the public domain or commons,⁵ where nothing is owned [and] all is permitted⁶

These terms, often used synonymously, are poorly defined and contested in legal theory and practice (see **Hess and Ostrom 2003**). Formulations that do exist largely occupy a counter-position to, and are meaningful only when juxtaposed against, private property. Similarly, the public domain and commons refer to whatever is unprotected by intellectual property rights, either as a whole or in a particular context, and is free for all to use (Boyle 2003a). Commons, particularly, is a term popularized by Garrett Hardins 1968 article on the tragedy of the commons. Hardins model is an open pasture where herdsmen compete for grazing space for their cattle. In this case, a commons is a rivalrous resource, meaning that several or many individuals or groups compete for the use of that resource, which is not infinitely renewable. The tragedy occurs because everybody gains from using the resource and nobody has an incentive to restrict his or her use of it, so that the resource is overused and fails to replenish itself. Typical examples include fish stocks in the open ocean or timber forests. Private property rights (or government ownership) are the usual solution to the commons problem, but some commons are not amenable to easy parceling and/or are not beneficially owned by any one individual or group. Elinor Ostrom has suggested that common pool resources can be organized and managed by the likely users, creating public goods instead of negative externalities (**Hess and Ostrom 2003**).

The tragedy of the commons is different in the case of information. The problem of overuse is averted because intellectual products are non-rivalrous: their use by one person does not exclude or otherwise interfere with others use of that same information. Images, music, and text are examples of non-rivalrous goods. However, information is relatively more costly to exclude people from using than more tangible things like fish or timber. The argument typically concludes that in the face of high costs and non-rivalrous goods, property rights are a necessary incentive to promote innovation (see for example Landes and Posner 2003). Others have argued just the opposite: that many informational goods must be freely available and without restrictions because they provide the materials for future innovation (see for example Boyle 2003b and Lessig 2001). Moreover, they say, these goods will still be produced even without the property right. Evidence that information can freely circulate and result in innovative products can be found particularly in the open source software movement⁷ (See Bollier 2002; Vaidhyathan 2001) and to a lesser extent in open-access publication debates.⁸ In both cases incentives to innovation can be extra-economic, where prestige and accreditation are two of the values that may function in this manner (see Strathern 2004, commons and borderlands)

Copyright, which automatically assigns rights, creates an additional dilemma: there is no way for future users of a work to know whether, and to what extent, the copyright holder wishes to lay claim to their rights. While the public domain or commons might be thought of as the counterpart or even predecessor to private property, in current practice public must often be carved out of private.⁹ Essentially, intellectual property laws as they are currently conceived shift the claim to ownership from a state in which new rights must be asserted to one in which the claims are in place at the moment of creation and must be defended against unauthorized appropriation. Ultimately, copyright laws (and other IPRs) seem to shift the terrain of property rights so that control precedes freedom where freedom must be carved out of a realm of control instead of vice versa.

Creativity in Creative Commons

While the developers of Creative Commons see value in the current IP system, they also persuasively argue that greater flexibility would make the system function better. Creative Commons is a non-profit organization that works within intellectual property laws, but outside legal and legislative institutions, to create a formalized system of public property that complements copyright laws rather than competes with them (see Lessig 2004). CC offers creators a chance to specify how they want others to use and build upon their work, indicating what is free and what is subject to control.

(Graphic taken from the Creative Commons website, viewed 10/24/2004)

The spectrum of rights graphic on the website shows Creative Commons squarely in the middle between full copyright protection and the public domain, but the potential for mixing and matching a creators desire for freedoms and protections is much more flexible in the middle zone. The Creative Commons website explains:

Too often the debate over creative control tends to the extremes. At one pole is a vision of total control a world in which every last use of a work is regulated and in which all rights reserved (and then some) is the norm. At the other end is a vision of anarchy a world in which creators enjoy a wide range of freedom but are left vulnerable to exploitation. Balance, compromise, and moderation once the driving forces of a copyright system that valued innovation and protection equally have become endangered species? Creative Commons is working to revive them. We use private rights to create public goods: creative works set free for certain uses. (<http://creativecommons.org/about/history>)

More specifically, CC provides four formal mechanisms (licenses) for demonstrating to others how a new work can be used: these are attribution, noncommercial, no derivative works, and share alike. A Creative Commons license could include any or all of the specified conditions,¹⁰ which help to make known the explicit wishes of the copyright holder given that intellectual property rights in this area grant protections for reproduction and sale; import and export of a work; the creation of derivative works; public performance or display of the work; and the assignment of these rights to others. Without CC, the copyright holder can exercise any or all of these rights, while others are prohibited from doing so unless they obtain consent from the copyright holder.

The hybrid properties appear in the eleven potential combinations for CC licenses:

	Copyright		Creative Commons licenses				Public Domain
No commercial use (NC)	NC	NC	NC	NC	NC	NC	

No derivative works (ND)		ND	ND	ND			ND				
Attribution (A)		A		A	A	A		A		A	
Share alike (S)					S			S	S	S	

The far right-hand column represents the public domain, where creators retain no rights to their work; on the left is copyright, with all-rights-reserved. Between the two poles, lie the Creative Commons license possibilities: hybrid public property. For example, creators of music, movies, images and text can obtain a license requiring attribution to a work, but not payment and derivative works are allowed. Or they can specify that future uses of their work are subject to non-commercialization and that those who use it must not change it in any way (no derivative works). CC provides the license (for which they are not liable) that tells users in three different ways what combination of rights are both released and withheld by the creator: through a document written for a layperson, one written in legalese, and a machine-readable code that internet search engines (and other applications) can understand. Websites, scholarship, music, film, photography, literature, and courseware are the current focus of the licensing regime.

A science commons, adhering to the same copyright-related principles of some rights reserved, was introduced in early 2005. Science Commons (SC) focuses on three areas of contestation around the public domain and private property issues: publishing of scientific results, material transfer licensing, and databases. In publishing, the debate centers on how to make scholarly work accessible to larger numbers of people while balancing the high costs of publication. Science Commons aims to make copyright negotiation easier in scientific publishing through standardized licenses for individual works and archiving projects.

Material Transfer Agreements (MTAs) are contracts between two parties regarding the use of a tangible research material, usually biological (like genes and model animals), though chemical and even software transfers are effected through MTAs. There are different MTAs that cover exchanges between universities (or other publicly funded research centers), between industry and a university, or between any combination of these and other research configurations (like hospitals). MTAs can range from extremely restrictive (both the original materials and all derivatives from those materials are subject to intellectual property claims from the provider) to fairly relaxed (if patent claims are not in play, a standard agreement typically stipulates that the materials must be used for non-profit or teaching purposes only and cannot be distributed without written consent from the provider). Clearly even in the least restrictive of situations, MTAs have property claims attached to them, and simply sharing materials without such an agreement is risky business for anything that has commercial potential. Science Commons is working to standardize MTAs (though some standardization is already in place, particularly through the National Institute of Health (NIH)), and to expedite the acceptance of MTAs through negotiations with universities, industry, and other research centers. MTAs are already hybrid properties, stipulating the conditions under which, for example, patents will be enforced, sharing is allowed (or not), and who owns what once the materials exchange hands. SC might merely open the possibility for a greater spectrum of property possibilities in this area.

Finally, databases raise a third set of issues for property in scientific knowledge. While protected by copyright if they demonstrate creativity or originality in their arrangement, most databases in scientific information are not protected by intellectual property rights in the United States or under international law, though the United Kingdom initiated a database right in 1998 that covers any database involving substantial financial investment (and thus do not have to meet the creativity requirement).¹¹ The US has considered a similar legal move in recent years. In addition to this encroachment by IP laws, SC also worries that in current practice databases fall into the all-or-nothing domains of secretly held information, or publicly available with no rights reserved by the compiler. However, databases are covered by MTAs, so it seems that their use is less all-or-nothing than SC suggests. As with publications and MTAs, SC focuses on working with identifiable stakeholders to negotiate voluntary standardized agreements with greater flexibility.

The developers of Creative Commons and Science Commons recognize that social systems can be tools that, in addition to the law, produce desired ends (Kelty 2004). Both projects (CC and SC) rely on private voluntary agreements with the holders and users of property rights, and enforcement comes as much from social norms as from legal coercion. While this culture-as-tool approach serves a functional goal of expanding a narrow realm of property conceptualization and practice, the dynamic and situated character of these systems is not captured (Kelty 2004). CC and SC open up the possibility of multifarious property possibilities, but cannot show the iterative nature of hybrid properties as they occur in practice simultaneous, not linear process (and indeed this would not be the goal).

In fact, most critical accounts of intellectual property begin at the end, so to speak, arguing that the rule regimes are either too restrictive, not restrictive enough, dealing with the wrong problems, not targeted at the right people, or some combination of the above (see for example Bollier 2002; Barton and Berger 2001; Rai and Eisenberg 2001; Boyle 1996; Buttel and Belsky 1987). The hard question for these analysts is deciding what can be apportioned to intellectual property rights and what should be part of the public domain or commons (Boyle 2003b). In rice genomics, the cultural norms of science conflict with the terms of intellectual property laws as suggested by the SC model, but these competing ideals generate reorderings of both systems: scientific (and other) norms get mixed together with those of IPR to produce a simultaneous development of new knowledge and hybrid properties.

Rice genomes

I wish to admit to - own up to - a growing uneasiness with the tendency to reduce questions about access to information to simple dichotomies of private and public, commodity or commons. Such characterization too easily fits within dominant ideologies and reproduces the myopias of free market imaginaries. More significantly, this characterization ignores the way "information" is actually generated and used in the world: in social contexts in which it has meaning, value, and significance - affect as well as effect. (Coombe, 1996)

Creative Commons (and Science Commons to a lesser extent) illustrates how formally established hybrid public property mediates and facilitates the production of new knowledge and the social worlds that both create and use that knowledge. One might suspect that this is not the only arena in which public property arises, and indeed exactly that is happening around the development of rice genomes. I now turn to the latter story (picking up where Science Commons has left off) as a direct route into understanding how new technoscience imaginations shape the way property and notions of public and private are constructed and deployed. I show that property rights for biotechnology are emerging, not only in formal, top-down modes like patent suits, regulatory frameworks, multilateral treaties and trade agreements, (or in places like Creative Commons and Science Commons) but also at diverse sites in the everyday practices of genomic research. Using the theoretical lens of co-production (see Jasanoff 2004; Reardon 2001; and Jasanoff et al. 2001 [1995]), I aim to treat the development of knowledge and social orders as an interactive and simultaneous process that reifies neither the natural nor the social as ontologically or institutionally prior. Compared with Creative Commons, the hybrids are subtler and more complicated, and they introduce further questions about the way ownership is made known and thus opened to contestation among those who locate themselves as stakeholders.

I argue that what relationships form in the making of rice genomes and public properties creates a tracing backwards and forwards through rice as we know it and will come to know it: as scientific (genetic and genomic) information, as a model cereal, as a major food staple, as a cultural icon, and so forth. Tracing public property raises these questions about ownership and relationships, access to scientific information and responsibility for where that information travels, and the very social connections what Rosemary Coombe (1996) suggests are meaning, value, and significance along the chain of knowledge production.

Four different sequencing efforts for rice were initiated by early 2000, two of which were publicly funded while two others were based in private firms. To date all four groups have produced drafts of the rice genome and one of the public projects has produced complete sequences for three of the twelve chromosomes found in rice. Along with the rapidly growing genomic data, property rights are accumulating and being redefined in the work of genomics researchers. As I have previously suggested, debates over private property and the public domain/commons are critically important not only in the area of copyright, but also with regard to patents and trade secrets, and the fate of databases and access to scientific information (especially through licenses) particularly in genome research (See Hilgartner 2004; Rai and Eisenberg 2003; Haraway 1997; and Boyle 1996). In what follows, I will show how public property is informally constituted in the journal Science, two privately funded biotech companies (Monsanto and Syngenta), a country (China), and an international research consortium (the International Rice Genome Sequencing Project).

Publication: Science magazine

In April of 2002, Science published two rice genome drafts.¹² In the pages of the magazine, in newspapers and other print media, and on the websites of the participants in rice genome research, these drafts were applauded as the most exciting efforts since the human genome projects announced only two years earlier. The rice projects were described as the solution to food security concerns in the Third World and the key to mapping more commercially valuable but more genetically complex cereal grains. The publication was also surrounded by controversy. Even before the rice genome publication was officially announced, a group of twenty concerned scientists, including two Nobel laureates, wrote a letter to the editors at Science voicing dissatisfaction with the journals decision to allow a private company to publish its results without conforming to the traditional norms of scientific practice. Based on belief in the long-standing norms of scientific knowledge production, stipulating that new knowledge should be openly available to advance discovery and innovation, they argued that publication should constitute free and unrestricted access to the data used to produce the published article. Science, and other journals like it, long adhered to policies requiring the deposit of genomic data in GenBank or a similar databank as a corollary to publication. The letter emphasized that allowing Syngenta to publish its research without this additional step was a very serious threat¹³ to genomics research and a potential threat to the genomes prospects for humanitarian aid, suggesting that the involvement of market interests in the production and dissemination of scientific information was encroaching on highly cherished (if slightly utopian) ideals of scientific practice.

The introductory editorial to the April 5th edition answered to these charges. Mirroring a similar controversy at Science with the human genome publication by Celera Genomics, editor Donald Kennedy justified the decision with the following reasoning:

Science normally requires that nucleotide sequence data reported in its papers be deposited in GenBank. On rare occasions, however, we make an exception and allow the data to reside elsewhere as long as public access is ensured. We did that with the historic publication of the human genome sequence by Celera, copies of which are still freely available with the sole restriction that it cannot be redistributed.

Effectively, Kennedy adjudicated the construction of (at least) a two-tiered property regime for genomic information. Weighing the arguments on both sides (compromising community standards and access to proprietary information versus making an exception that serves the public good), and reasoning that accessibility to the data is different from the place in which it is deposited, Kennedy determined that an exception, like that made for the human genome, was acceptable in this case. However, availability of data in this case means an agreement allowing the company to provide access to its information through its own website¹⁴ or via CD-ROM instead of placing the data in GenBank, as would normally accompany such a publication.¹⁵ While publication releases information about research results, it is generally accepted that results and descriptions of the process are not sufficient to reproduce results in most genomics work. Let me offer an analogy to clarify this important distinction: the difference between publication and depositing the information in a database is like producing a telephone directory for which an analysis (the publication) tells the reader how many instances of each last name were found and what regions of the city they tend to live in, but does not provide any of the specific names, telephone numbers, addresses, etc. (the genomic data itself). Thus, by not placing the information in a database, Syngenta effectively held onto the most important part of information transfer for public use.

Also, while publication released the trade secret protection on Syngentas procedures and other sequencing information, it did not prevent the company from withholding the genomic data itself or the annotations (which provide critical information about the usefulness of particular genes or gene sequences). The scientists who wrote the letter of concern to Science worry that access to (and control over) information is at stake; public property is not just about who has rights as defined through intellectual property categories (e.g. patents and trade secrets), but also how rights to access are defined across multiple users and in the face of changing institutional circumstances where an increasing amount of basic research becoming proprietary.¹⁶

Though Syngenta eventually agreed to wider release of its data, that is, allowing the International Rice Genome Sequencing Project (IRGSP) to have complete access, the information must still be kept confidential.¹⁷ So, while no reach-through agreements are required,¹⁸ the sequence data are only available for non-commercial (academic) research purposes, and access is still limited.¹⁹ Moreover, patents on individual genes are still possible a major restriction on information that Kennedy says is in the public domain. Finally, it is important to point out that this public information is never fully unrestricted or free. Science is a market-driven enterprise as well as an academic one. It costs money to obtain the magazine or access its online issues, and scientists do not have access to this magazine in all parts of the world (especially those the journal most seeks to benefit).

The publication followed five years of mapping and sequencing efforts by four different groups, two publicly and two privately funded. While the Science publications render these projects and the property debates surrounding them public for the first time, this was simply the culmination of long-standing and ongoing negotiations over the property rights that would emerge with the new scientific information. From the time an international consortium of scientists began the first mapping effort in 1997, soon followed by the private biotechnology firm Monsanto in 1998, new conceptions of property rights arose alongside the generation of genomic data. Debates over this information have and continue to occur at multiple levels of social organization within scientific practice, at the national level and in international arenas.

Biotechnology Companies: Monsanto and Syngenta

Two different companies produced drafts of the genome using two different techniques, constituting two different genomes, and different but similar public properties. Monsanto, a biotechnology corporation based in the United States, began its sequencing effort in 1998, funding Leroy Hoods research team at the University of Washington to produce a draft sequence using a traditional approach of contiguous mapping in clone libraries. This technique relies on mapping the genome from end to end and expects to meet a very stringent error rate. Their efforts identified approximately 95% of the genes, but the map they produced did not contain enough information to count as a complete sequence.²⁰ Their draft, which announced in 2000, was not published and the data were not placed in a public database, though negotiations with IRGSP led to an agreement to provide the public consortium with Monsantos data to facilitate the consortiums efforts.

Syngenta also began its sequencing project in the late 1990s. Though the firm is based in Switzerland, the genome project was run out of the Torrey Mesa Research Institute (TMRI) in Southern California, and in collaboration with Myriad Genetics Inc, a US-based biopharmaceutical company, and the Clemson University Genomics Institute (CUGI) (which is funded by Novartis, a subsidiary of Syngenta). Syngenta used a new sequencing method, the so-called whole genome shotgun strategy. This technique breaks the genome into small DNA segments and sequences those pieces many times over to reduce gaps and errors, and then realigns the now-sequenced fragments in order using automated supercomputers. A draft was completed in early 2001, identifying 99% of the genes at 99.8% accuracy.²¹

Both companies present themselves as market-driven enterprises, but also as benevolent stewards of the public interest (see Greffe and Linsky 1995). Monsantos homepage asks the viewer to imagine a world in which small-scale farms in Africa produce abundant cotton, young Asian children do not go blind from Vitamin-A deficiency, and a host of environmental problems like soil erosion, energy consumption, and pesticide use find innovative solutions.²² Similarly, Syngenta provides an overview of its dedication to social responsibility through sustainable agriculture, stakeholder engagement, and product stewardship, among other commitments.²³ The two websites present visions of abundance in the face of scarcity, and aid for those in need.

But a quick look below the homepage shows the drive behind the vision: research is focused predominantly on corn and soybeans and their products are targeted toward these crops. There are no commercial rice products and no ongoing rice genome research projects. The message is clear: Though rice itself is not a major biotech investment for Monsanto or Syngenta, its basic genetic structure is similar to other, more profitable cereals like corn, wheat, and maize.²⁴ As in many scientific research efforts, potential profitability and funding go hand in hand. One Science article outlines the nearly twenty years of independently-initiated projects to map the rice genome in China, Japan, and the United States and the lack of interest in these endeavors until the early 1990s when researchers began to realize that rice could facilitate knowledge about the more valuable cereals.²⁵ This ambiguous position between profit-making enterprise and philanthropic organization permeates the process of sequencing rice and the manner in which the resulting information is held and used. The tensions between conceptions of private property and the public domain are nowhere more challenging than in the production of genomes at Syngenta and Monsanto.

Making public property transformed private information in at least two ways: through data sharing agreements and through Syngentas publication in Science as I have already discussed. When Monsanto announced the completion of its genome map in 1998, it did not publish its findings or place any of its information in a publicly available

database. What it did do was agree to share its information with IRGSP to facilitate the public effort. This decision released the trade secret status of the information and at the time was a largely unprecedented collaboration between a private company and public research effort.²⁶ A similar agreement was reached between Syngenta and the IRGSP in 2002 after the private company announced its own genomic sequencing achievement. Trade secret release might be analogized to placing information in the public domain,²⁷ but at the time of the Science publication, a spokesperson for Syngenta suggested something altogether different:

Our data is publicly available. To the IRGSP or any other investigators around the world. It's just not in the public domain. Think of it like a book or a movie. It's available to you, you can get the book, you can watch the movie; but it isn't in the public domain, you've got to go pay for it. Somebody owns it, and provides access to it. But we're not charging people for access to it for non-commercial uses. So to academics and so forth it's available without charge. But what we require is that if a commercial invention is made from the collaboration, that Syngenta has an option to consider a license for it.²⁸

Publication and data sharing agreements may make the information visible to others, but whether or not that means it resides in the public domain remains unclear and access in this case is contingent: commercial interests are subject to a different rule regime from purely academic research. Neither publication nor data sharing agreements limit either company's ability to take out patents on particular genes or gene sequences of interest (i.e. for potential commercial value). In genomic research intellectual property protection takes the form of trade secrets and patents. Trade secret laws protect commercially valuable knowledge so long as that knowledge remains a secret. Trade secret status is both more and less protective and restrictive than patents: it is more restrictive if the information is kept completely confidential, but if the information becomes available either legally or because it was easy to guess, it is no longer a secret and thus no longer protected. Both companies released their trademark claims through publication (for Syngenta) and through data sharing agreements with the international consortium.

Patents allocate exclusionary protections (monopoly power) to a group or individual creator to prevent others from using their inventions without authorization for twenty years. This includes sale, distribution, and use without license or some other agreement. In exchange, the inventor must release information that would allow others to replicate their creation. To obtain patent rights, the invention must meet three requirements: novelty (has someone already done this?); non-obviousness (would someone who is skilled in the area see this as an obvious step in the process of innovation?); and utility in the United States (is it useful?) or industrial applicability in the United Kingdom.

Patent protections, for which an application must be made and granted, do not function in quite the same way as I suggested in copyright, for which a commons in the latter must be carved out of automatic private rights. However, one might argue that trade secrets function as the automatic claim, the information subject to secrecy and made available to the public through patents, the latter guarding the innovative (and financial) interests of the creative party. Creating public knowledge requires information release and can be maintained through agreements not to take out patents or through proactive patenting by parties that do not intend to enforce those patents (though it is also important to make clear to those interested in using genome data that the patents will not be enforced).

Ultimately, what may seem public (like databases and publications) can still be kept private through patents, licensing agreements, and trade secrets (to a lesser extent). Property rights have advanced into realms that were unimaginable even fifteen years ago (see Boyle 2003; Rai and Eisenberg 2003; Hayden 2003; Mackenzie, Keating and Cambrosio 1990). Patents can be issued for the gene itself, plants transformed with the gene, and for the seed and progeny of the patented plants.²⁹ The distinction between nature and innovation has shifted many times, notably through the US Plant Patent Act of 1930, authorized patenting for asexually reproduced plants, and the Plant Variety Protection Act of 1970, which extended protection on sexually reproduced plant varieties. The landmark case of *Diamond v. Chakrabarty* in 1980 granted patent protection to anything under the sun that is made by man, including biological organisms, traits, and genes.³⁰ John Doll, former director of biotechnology for the US Patent and Trademark Office, explains that while patents may be sought for genes that are isolated and purified from the chromosome, they may not extend to anything as it exists in nature (2001). An article in *Science* puts it in a slightly different way: Genes themselves cannot be patented, only the uses to which the information can be put.³¹ The line is fine indeed. Doll estimates that since 1980, more than 20,000 patents have been granted for genes or gene sequences and that another 25,000 are waiting in the queue.³²

While no genome in its entirety has been patented, as of 2004 the US Department of Energy cites the number of genome-related patents filed at more than 3 million. Monsanto and Syngenta are two of the top three agriculturally related patent-holders worldwide, and 74 percent of agriculture patents are held by private companies⁴⁰ percent of which are concentrated in just five companies.³³ With the passage of the Bayh-Dole Act, research conducted at universities and other federally funded institutions has also become patentable. Holding enough key patents on specific genes might amount to ownership of the entire genome if the portfolio of patents includes enough of the most important genes.

A National Genome: BGI

In early 2000 the Beijing Genomics Institute (BGI), a publicly funded research group in China, also began sequencing rice using the same shotgun sequencing method as Syngenta. BGI's sequence was produced very rapidly in only two years and while identifying only 92% of the genes, the sequence accuracy is approximately 99.9% for more than 90% of the sequence produced thus far.³⁴

BGI was also interested in expanding the kind of data available by sequencing a different rice variety. Other sequencing efforts, those initiated by Monsanto, Syngenta and the IRGSP focused on the Nipponbare cultivar (*japonica* subspecies) while BGI chose to sequence *indica*, which is the subspecies consumed by most people in the world, including the Chinese (one source placing production of *indica* at 80% relative to other varieties (see Smith and Dilday 2003)). While both *indica* and *japonica* varieties are believed to have originated in China, *indica*, with long-grains that do not stick together when cooked (Latham 1998), is preferred by most rice-consuming nations. Explaining the decision, an introductory statement on the BGI website tells us that the other sequencing projects used the subspecies *japonica* (Nipponbare) as target materials even though *indica* is dominantly planted in Asia and other regions in the world, and has provided the unique hybrid rice strain that has greatly contributed to solving the food supply problem in China [my emphasis].³⁵ Commenting on why BGI chose to sequence *indica* instead of *japonica*, the director of the program said: there was a feeling that China should sequence its own rice [my emphasis].³⁶ Thus a genome map that is distinctly Chinese, but also Asian is bound up in the way BGI represents itself. Moreover, BGI's success counts in a different way:

China is the almost the only developing country in the genomics race, and the only one to make its mark. It has all the usual disadvantages, lack of finance, of supporting technologies and scientists. Whereas the United States and Japan have about 70 researchers and engineers per 10,000 population, China has only six. Despite that, she has come out well ahead of the west.³⁷

The project positions China as an underdog developing country against well-funded and well-trained developed country projects. At the same time that it places the US and Japan in the developed country category, BGI also situates itself as a pointedly non-Western effort.

Nationalism and catching-up in science are foregrounded in China's rice genome project. This identity is reflected in BGI's genomic practices, rules and norms. On their website, BGI explains that they initiated their sequencing project to accelerate and broaden the scope of genome research with a commitment to placing all of its sequencing information in the public domain and to eschewing patents generally.³⁸ In addition to publishing their results in *Science*, BGI implemented a data-sharing program with the DNA Databank of Japan (DDBJ),³⁹ the database of the European Molecular Biology Organization (EMBO), and the US National Institute of Health (NIH)-led GenBank.⁴⁰ BGI also made its genome information available to the public on their website via its own online database.⁴¹ On a spectrum of availability, BGI's genome project is perhaps the closest set of public properties to the public domain: trade secret was released and patents are frowned upon; the results were published in myriad forums, making the information accessible to a range of potential users; the materials and other information underlying the publication were placed in an assortment of databases; a new kind of information was made available (that of the *indica* variety); and BGI is committed to sharing its results to the widest extent possible.

An International Genome: IRGSP

The International Rice Genome Research Project (IRGSP), a consortium of scientists dedicated solely to sequencing the rice genome, began the first mapping initiative in 1997.⁴² Representing a (rather) new form of collaborative effort, IRGSP is comprised of scientists from publicly-funded universities and research institutes in ten different

countries: Japan, the United States, Brazil, China, France, India, Korea, Taiwan, Thailand, and the United Kingdom. United by a genome, the research groups participating in the consortium portray themselves as a global research body dedicated to a global object—rice. Simultaneously, national identities are mapped into the genomic imagination; the globally produced genome is also chromosomally country-specific. For example, Taiwanese researchers are sequencing chromosome four, while another team in France is working on chromosome twelve; the national interests in genome research across the ten participating countries are likely very different as well.

From its inception, the collaborative group has been committed to completing the rice genome instead of only producing a draft.⁴³ Using a traditional approach of contiguous mapping in clone libraries (similar to Monsanto's method), research groups in each of the ten different countries agreed to sequence particular chromosome segments.⁴⁴ Following the Bermuda Principles concerning human genomic data and intellectual property,⁴⁵ the IRGSP seeks 99.9% accuracy in its genomic map, which means no more than one error in every 10,000 base pairs sequenced, despite the slow and costly process.⁴⁶

An international consortium working on an international genome, the IRGSP calls for international access to its genome data. From its earliest inception, the IRGSP decided that its mapping endeavor would benefit from full disclosure to anybody and everybody who wanted access. Again following the Bermuda Principles, IRGSP concluded that all genome sequencing data should be freely available and in the public domain to encourage research and ensure societal benefit.⁴⁷ Consortium participants must agree to share materials, including libraries, and to the timely release to public databases of physical mapping information and annotated DNA sequences.⁴⁸ In an article on the IRGSP website, Tajuki Sasaki, who heads the Japanese team in the IRGSP stresses that individualistic, competitive efforts to map the rice genome waste both effort and precious resources.⁴⁹ Thus, in line with the scientists who opposed the controversial publication of Syngenta's sequencing data, and counter to popular reasoning for private property rights, he suggests that public (unrestricted) access is important and necessary for scientific flourishing. Identification in the consortium rests on collaboration and timely placement in public repositories. New mapping results are shared with the entire network of participating laboratories through their own data-banking system, which is not publicly available outside the consortium, and then with scientists, writ large, through placement in DDBJ, EMBO, and GenBank.

Constructing its own database, with its own rules and protocols, the IRGSP (like BGI) instituted a new method for collecting, storing, and sharing genomic data. Anyone with Internet access can also download the sequence data via any of the three public databases (DDBJ, EMBO, or GenBank) though there is no guarantee that the data can be used without restriction because individual genes and gene sequences may be patented.⁵⁰ The IRGSP's requirement that consortium data be deposited in a publicly accessible genome bank was an attempt to situate information among a set of actors with a set of rules and practices that defined the boundaries of genomic property (Hilgartner 2004; see also Jasanoff 2004). This public property benefits a public that includes participating scientists, other interested researchers, and anyone who has the ability to access the Internet (and has the money and knowledge to utilize it).

Interestingly, however, multiple notions of public are at play in the IRGSP project. First, public is often conflated or used interchangeably with free, or unrestrictive. For example, while IRGSP members release their data to public databases, the IRGSP's own database is not accessible outside the consortium. Moreover, it is unclear whether consortium members have taken patents on individual genes. A newsletter dating back to the inception of the consortium on the IRGSP website notes that while withholding sequence information for patenting is incompatible with the rules of the consortium, there is no rule that says patents could not be obtained downstream of data generation and release.⁵¹ Additionally, any information in the three public databases (e.g. GenBank) may be patented as well. So, while the information can be used for research purposes, there is always the possibility that the information is subject to intellectual property rights (it is the users responsibility to figure out whether the information is subject to a patent). The slippage is not unimportant. It indicates both a multivalent and shifting conception of what can or should be public, and a lack of legal definition to stabilize the terrain. Thus, a public consortium of scientists, determined to build a publicly accessible repository for the rice genome, defined a boundary around what should not be considered proprietary and to whom.

So, while discussions of public span a fairly wide range of possibilities, patents on genes and related procedures still seem fair game both for the private biotech companies as well as the publicly funded efforts like IRGSP (the latter again made possible in the US through the Bayh-Dole Act⁵²). Moreover, Western notions of private property (American notions, in particular) have traveled to the international level where similar private property rights are granted through treaties such as the TRIPS⁵³ agreement as well as bilateral and regional trade agreements.⁵⁴

Whereas many have argued that the genome map should be in the public domain, genes can still be patented. In a sense, companies, consortiums and countries have negotiated and defined an upper limit of patentability for genetic information: maps are for everyone but individual genes that may be isolated from the map are potentially patentable and thus commodifiable far cry from free or unrestrictive. Lawrence Lessig, writing about the internet, eloquently argues that while the information contained therein is described as free, the code that delivers that information is based on an architecture of control that will close off access to new thought and free expression (2001). I argue that the same can be said for genomes, where access is granted freely at the genome level, but control is exercised at the level of the gene.

	Private Property	Monsanto	Syngenta	IRGSP	BGI	Public Domain (Commons)
Trade secret	Upheld	Released	Released	No	No	No
Patents	Yes	Yes, with multi-level enforcement	Yes, with multi-level enforcement	Possibly	No	No
Database release	No	Not through public databases: accessible on company websites	Not through public databases: accessible on company websites	Yes, but also has a private database	Yes	Yes
Sharing	No	Yes with IRGSP, but commercial use not allowed	Yes with IRGSP, but commercial use not allowed	Yes, but unclear re. annotations	Yes, but unclear re. annotations	Yes, including annotations
Publication	No	No	Yes, in Science	Yes, online	Yes, in Science and online	Yes, in journals and online

[Public property in rice genomics: The rows, defined along the far left-hand column, illustrate property choices. The far right-hand (shaded) column represents a theoretical public domain (or commons), while the left-hand (shaded) column represents full or strong private property rights. In the middle lie public properties as they were negotiated by the four rice genome sequencing projects.]

Conclusion

National interests (and nationalism), corporate social responsibility, scientific norms, and profitability among other things impact the way new genome research becomes public property. Creative Commons illustrates that categorical distinctions between private property and the public domain (or commons) provide a structure for argument and in some cases become codified in law, but it is these other values that create tensions around what happens to new scientific knowledge. Rice genomes, and the properties negotiated to attend them, link the scientists who make and use the new information for basic research to scientists involved in breeding and studying rice and other cereals. Private companies and scientific publications also insert their obligations—defining and defending how and where they will deploy rice genomes (and to whose benefit). Negotiation over how that information travels produces linkages among the participants that trace notions of responsibility: of affect as well as effect. Public property becomes an important space in which these multitudinous values and interests come together, specifying hybrid practices that will inform the way we understand all of these values as they are constantly reworked, and creating new meanings for genomes and for rice.