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OPEN SOURCE AND COMMONS IN DEVELOPMENT

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Abstract:

This article discusses the interrelation between open source knowledge development and the production of research commons in four development-oriented research networks with an Indian/Dutch composition. The main objective of the article is to describe the planned research activities aimed to understand the functioning of open source and commons from the perspective of local development. The article discusses three hypotheses which will be further investigated in the coming years by the Open Source and Commons Research Group of CTC1, namely:

- The social-technical dynamics in the knowledge development of genomics and other life sciences technologies transform the private-public research setting into more open source and commons oriented research networks
- The open source approach will show a trend towards a blurring of the designer-user dichotomy, as the user will also be challenged to become co-designer, which will create new opportunities and incentives for involving resource-poor client groups and farmers in the process of technology development
- Commons represent a new social condition of knowledge production (to be distinguished from private and public).

By describing the planned research activities the authors aim to stimulate a critical reflection and debate on the social relevance of scientific commons and the opportunities for inclusive technology development that appear to be emerging due to the changes in knowledge production and property regimes.

Key words: Science and technology studies, critical theory, commons, biotechnology

¹ The CTC Study group on Open Source and Commons starts in August 2010 and is composed of .Soutrik Basu, Minthan Bathan Rao, Archana Patnaik, Divyan Rao, Joost Jongerden, Pieter lemmens (from April 2011) and Guido Ruivenkamp. Reactions can be sent to email guido.ruivenkamp@wur.nl

I. Introduction

As early as 1994, it was argued that the relatedness of science and socio-economic context had led to a *new mode of knowledge production* (Gibbons et al. 1994). Rather than a search for fundamental principles determined by scientific interest (referred to as ‘Mode 1’ knowledge production), the twentieth century development of ‘Mode 2’ knowledge production was determined by socio-economic relevance and utility. Characterized by a constant interaction between the fundamental and the practical (Rinia 2007, Nowotny et al. 2003), Mode 2 knowledge production was strongly influenced by private (commercial) interests (Carayol and Thi 2004) and marked by strict protection regimes (Ruivenkamp 1989). Now, however, we see the emergence of another mode of knowledge production, based on a sharing of information (open source) and collective actions (commons), and, in the words of Gibbons et. al., may be referred to as : ‘*Mode 3*’.

The term ‘open source’ refers to free access, here, to scientific information and the ‘source codes’ of technologies, the practical information which enables institutions/persons to participate in and transform common knowledge development. Open source allegedly promotes innovation by making technologies available in easily modified forms, at low or no cost, and under licensing terms *that allow users to make changes to the technology* and to use or distribute the resulting modified versions as they choose. It may, therefore, *erode the distinction between designer and user*, due to the distant, unstable relations – so-called ‘weak ties’ (Hope 2008) – and stimulate an openness to outside linkages within these networks (Hope 2006).

The term ‘commons’ refers to resources belonging equally to or shared equally by any member of a certain community. ‘Commons’ is said to refer to a public interest which is not so much under control of the state but under the control of stakeholders (Hardt and Negri 2004), and thus to a legal regime, to an arrangement whereby the fruits of collective efforts remain under the control of that collective. Recent legal strategies created to protect commons – and thus maintain information as open source – include ‘copyleft’ licensing systems (e.g. GNU General Public and Creative Commons). Commons refers to a system of social relations that *goes beyond public and private* and here signals a metamorphosis in the organization of knowledge production.

Related to the development of Mode 3 knowledge production is the recent emergence of new, ‘open innovation’ business models, based on collaboration, networking and sharing of knowledge (Liard 2001; kaushik 2003; Chesbrough 2003; Reichmann 2003; Bergh and Jong 2006; Rai 2007). In these models the integration of externally developed competences within the company itself is an important aspect in the company’s innovation process. This open approach to technological innovation is increasingly taken up by companies in various sectors. It is also argued that this open innovation model is related to the actual historical context in which the mobility of highly educated labor has increased, a large number of external parties exists that can contribute to innovation, an increased availability of venture capital and a shorter life cycle of products (Bergh and Jong 2006; Chesbrough 2003, Liard 2001). Public and charitable research institutions have also been led to introduce these new models and gain the benefit of quick information exchange. Important landmarks in the field have included the Wellcome Trust / Sanger Institute proposal for open source licensing of genome data from the Human Genome Project (the ‘Bermuda statement’, 1996), and an open

source model for plant germplasm established by the University of Guelph (published on the internet in 1999).

This move in the direction of Mode 3 knowledge production in biotechnology has been particularly stimulated by the nature of the life sciences themselves, with their information bases and associated technologies which are just too complex and massive for one institution alone to handle and maximize (Louwaarts 2007, Reihman and Uhler 2003). Related to this is the issue of the *relationship* between knowledge development and protection regimes. As genomics has developed over the past two decades and the focus shifted from single genes to the level of genomes (Hughes 2005), practical incentives have been created for companies/institutions to *share the inputs* involved in unveiling and interpreting the vast amounts of information these projects produce (Ruivenkamp 1989; Rausser 2000; Graff 2003; Overwalle 2007; Jongerden & Ruivenkamp 2008). Such sharing is arguably less expensive than closed innovation practice, which is marked by long patenting procedures, fragmented ownership of complementary intellectual assets – e.g. the development of the genetically engineered rice variety Golden Rice with its 70-odd different but overlapping proprietary claims (Kryder et al. 2000; Koo et al. 2003; Chaturvedi 2007) – and the problematic exchange of such assets, which is associated with high transaction costs (Hope 2004). This move towards Mode 3 knowledge production also touches upon the question of affordability of and access to technologies for small-scale farmers in dry areas.

The CTC's research group on open source and commons examines the changing nature of knowledge production and focus on the incentives for research institutions, business and network of civil society organizations to develop a new social organization for knowledge production, i.e. to develop strategies of networking, collaboration and sharing. Particularly, the incentives will be investigated to develop scientific commons, i.e. pools of data and technologies which are shared among or gifted between the collaborating partners. Although the CTC research group is aware that next to this trend towards "Mode 3" knowledge production – the trend of sharing and constructing scientific commons particularly in the upstream, pre-competitive domain – an apparent contradictory reality can be witnessed in increasing the patent protection in downstream product development. Therefore, the CTC's research group will examine the simultaneity of these apparently contradictory trends in the protection of innovations, i.e. an increase in sharing as well as in patenting knowledge or in other words the presence of scientific commons and patented knowledge-intensive products.

This duality in types of protection is reflected in genomics research. The size of genomics projects provides an important incentive to share the costs and energy involved, as well as the sharing of the genomics data in order to interpret the vast amounts of information these projects produce. At the same time, the nature of those data - as a string of nucleotides - allows for the appropriation (and patenting) of interesting bits and pieces for market protection in downstream product development. Traits that are currently difficult to patent because of a lack of knowledge of responsible DNA regions or genes, will in fact be easier to patent once the full genome sequence of the respective crop is available. In other words, companies may consider the expensive and time-consuming sequencing of entire genomes (structural genomics) to be a relatively safe activity to share with others (upstream commons),

but seem to prefer the interpretation of the data and the development of applications (functional genomics) to be in-company (Vroom 2008). The development of upstream scientific commons² may even be subordinated to specific company interests, based on the patented product developments and are therefore referred to as *company scientific commons*. On the other hand the draining and privatization of the common bases of knowledge production through patents may also create obstacles for the further development of that knowledge production and its accessibility to a broad scientific community (Negri, Hardt 2009). It may also lead to the establishment of networks of social-technical activists (Milberry 2008, Deibel 2009) aiming to develop *social scientific commons* (see below). It is clear, anyway, that the knowledge production of research commons can have different social objectives. On one hand it can be an efficient innovation **model for businesses** to maintain their privileged position. On the other hand it can be a **lever for empowering inclusive technology trajectories**. In this article we focus on the question whether research approaches of open source and commons do actually create new opportunities for bottom-up (Bunders 1990) and location-specific, sustainable technology developments (Magnaghi 2005, Puente 2010). In order to develop a thorough understanding of the functioning of open source and commons from the perspective of local, sustainable development we have set up a research program to investigate the interrelation between open source knowledge development and the production of research commons in four development oriented research networks with an Indian/Dutch composition.

II. CTC's research program on open source and commons

The CTC research program examines the changing nature of knowledge production and particularly the incentives to develop scientific commons, i.e. pools of data and technologies which are shared among or gifted between the collaborating partners. However next to this trend of sharing information and constructing scientific commons, an apparent contradictory practice can be witnessed in increasing the patent protection of innovations. To understand these apparently contradictory forms of protection, it has been argued that it is important to take in consideration that some new modes of protection emerge *due to the development of new technologies*, while old modes of protection continue to exist (Louwaars 2007; Reichman and Uhler 2003). For example, private rights in the form of intellectual property rights on knowledge-intensive products and processes (patents) became increasingly important during the emergence of techniques based on modifying and introducing specific genes (biotechnology), but seem to be weakened in the domain of sequencing of entire genomes. Therefore, the CTC's research program also poses the question whether the emergence of research commons is related not only to the rise of new kinds of cooperation between companies and institutes, but also to what extent it is related to the emergence of new technologies (genomics, nanotechnology) (Rajan 2003). A key aspect of our program is the investigation of the ways in which new forms of protection - emerging within the reorganized, collaborative research networks - are mediated through the development of new life science technologies. In other words: the program examines if and how technologies stimulate the development of new modes of protection while continuing old modes.

² The terms 'upstream' and 'downstream' refer to relative positions in an innovation process, with 'upstream' referring to knowledge driven research, and 'downstream' to utility driven research.

Our program does not limit itself to study the relationship between the changed nature of knowledge production and forms of protection mediated through new technologies within the company-oriented research networks. It also examines this relationship within research networks that see themselves as *networks of social-technical activists* aiming to change the social code (Winner 1985) of life science technologies, challenging the dominant power relations (Noble 1987), present in the development of these technologies and striving to bring ethicality and commonality back in the development of life-science technologies (Ruivenkamp 2005). Therefore, the research program also focuses on exploring those experiences of other social actors building a community that jointly creates and maintains knowledge. In the domain of information technology these experiences to open the editing of technologies (software, internet applications) which allows for collective authorship, have already been studied (Sasson, 2006, Deibel 2008; Milberry 2008). The intent is to foster communal development in a virtual space that is jointly owned by all users and for which all users are responsible. In the research network of genomics also open source initiatives have been launched (Hughes 2005) such as the “Biological Innovation for Open Society” (Bios) initiative for the Application of Molecular biology to international Agriculture (CAMBIA) in which it is aimed to “free the tools of genetics” currently locked up in patents so that there might be cropping systems suited to their environment, their societies and their economies (Deibel 2006; O'Neill 2003). The question may be posed what are the implications for such an organization of knowledge production? Some conclude that participating in such projects for knowledge and technology production are characterized by decentralization of authority and horizontal self-organization (Milberry 2008) and open perspectives for a social reconstruction of these technologies. These commons which arise from these types of collaborative research organization may be depicted as *social scientific commons* and as the development of a new public sphere – a sphere of commons - not articulated to commercial interests.

The central question of our research program is:

- **What types of (bio)technological products are emerging through open source approaches and research commons, what is their contribution to local developments and what roles are stakeholders playing in their development?**

Sub-questions are:

1. How do open source and research commons transform the *designer-user* distinction in (bio)technology development? What are the implications for stakeholder involvement and the articulation of their problems in research agendas (i.e. inclusive technology development)?
2. What (new) type of *institutional setting and arrangements* appear in research networks built upon open source and research commons?
3. How do research commons represent a new institutional logic that goes beyond and *transforms the public-private distinction*?
4. Is (bio)technology development - based on open source and research commons - responsive to civil society organizations and does it contribute to *local development*?

The research program is motivated by the concern that open source/commons practices may offer user groups opportunities to include their priorities in the design of new biotechnological products/processes and to contribute to local, self-sustainable developments (Magnaghi 2005). This content of the research program invites a *critical, technographic research methodology*.³ The four PhD research to be launched at August 2010 will all apply and develop further the critical technographic research methodology.

II. 1 The critical technographic research methodology

Technography is akin to ethnography, but with a special focus on technological systems and the social actors involved in those systems. Concretely, the four projects will all adapt the methodological approach of technography described by Steve Woolgar (1999:88) as ‘the social-scientific study of technical settings’, in which, as with the ethnographic method, ‘a main focus is to determine how distinctions – between e.g. technology producer, consumer and user – are created and sustained, as well as determining what effect they have on design and development’. Recent examples of technographic studies include Zannou (2006) and Kassawiki (2008), who describe the approach in terms of an attempt to map the actors, processes and client groups in such a way as to enable analysts to see beyond the technology itself, to the problems technological applications are supposed to solve and the parties and interests that are being mobilized in arriving at solutions (Kassawike 2008:22-23). These general objectives of the technographic approach will be applied to analyze and *deconstruct* the stories of how open source knowledge developments in the four projects have been established and are supposed to respond to stakeholders’ interests (‘legitimizing’ plant breeding activities).

Looking beyond the issue of producing legitimacy for a specific plant breeding research program, the researchers will also elaborate a *critical methodology*, to focus on whether and how opportunities for reconstructing technology development can be realized. This refers to Andrew Feenberg’s *critical social theoretical approach* (1999), a process of *reconstruction* of social configurations involving both the technical means and the societal ends. A core characteristic of the critical social theoretical approach is reflection on the *interwovenness* of technology development with the actual social relations of power and investigation into possible challenges to the social relations from which the technology emerge and a redetermination of the roles of actors such as scientists, breeders, farmers and civil society organizations. This approach is *critical* in the sense that it constantly confronts existing social relations with the needs society is failing to satisfy.

A cornerstone of Feenberg’s approach is the search for developments that announce perspectives for a radical modification in the way technology is developed within society. This implies that the researchers will (also) investigate how the social organization of knowledge-intensive technologies is changing and whether/how this social reorganization of knowledge production is opening perspectives for changes in the (im)material content of the

³ The critical, technographic research methodology invites data collection from a wide range of resources, including case or event studies, participatory observation, interviews, study of policy documents, websites etc. Importantly, the critical method also requires that researchers and stakeholders have confidence in each other: attention will thus also be paid to reciprocal information exchange

technological products and the participation of actors (and their needs) which have previously been neglected in technology development. In other words, researchers will investigate whether/how open source/commons practices (may) become constituent elements for *alternative technology trajectories*.

III. Investigating the knowledge production of open source and commons

The CTC's research group on open source and commons investigates the interrelation between open source knowledge development and the production of research commons in **four** development-oriented research networks with an Indian/Dutch composition. The main objective of the program is to develop a thorough understanding of the functioning of open source and commons from the perspective of local development. This study of these networks is based on three hypotheses:

- The social-technical dynamics in the knowledge development of genomics and other life sciences technologies *transform* the private-public research setting into more open source and commons oriented research networks
- The open source approach will show a trend towards a *blurring* of the designer-user dichotomy, as the user will also be challenged to become co-designer, which will create new opportunities and incentives for involving farmers in the process of technology development
- Commons represent a *new social condition* of knowledge production (to be distinguished from private and public).

Aiming to understand the open source and commons paradigm in technology development, the program applies a *critically-based, technographic research methodology – technographic* in the sense that it aims to map, analyze and deconstruct open source and commons activities; and *critical* in the sense that it considers relations of power and indicates opportunities for institutional rearrangements to strengthen an inclusive technology development. This involves an empirical analysis of technology development and actors involved, and a quest to create institutional space in which village communities and farmer's and women's self-help groups can become co-innovators.

Four strongly interrelated projects are established to examine assumptions, considerations and interests in the development of open source and research commons for *location specific developments*, focusing on:

1. The local application of (global) *open source vectors and markers* in Indian breeding research institutions,
2. The translation of the *open source genomic information* of the Arabidopsis network into crop- and location-specific breeding programs,
3. The development and use of ICRISAT *archives* as a knowledge commons for stakeholders,
4. The use (and abuse) of a *common pool of upstream breeding services* – delivered by the General Challenge Program - in downstream location-specific breeding programs in which research institutes are working with civil society organizations.

The four projects will be carried out in collaboration with research groups in various Indian research institutions (particularly in the state of Andhra Pradesh and Haryana) and with a variety of civil society organizations (inter)national and local. Projects 1 and 3 focus on the Indian side of the research networks, while Projects 2 and 4 also investigate the Dutch partners of the Indian-Dutch research networks.

IV. Description of Research Projects

“It is not so much about getting access to old patented technology – it is about forging collaboration to develop better, more powerful tools with a “protected commons” to get different problem solvers to the table” (Richard Jefferson: Cambia/IRRI Open source alliance December 2005).

IV.1. Project 1: The local application of open source vectors and markers in Indian breeding research institutions, developing bacterial-blight tolerant rice and millet varieties

The first project investigates the use of open source markers (from international research networks such as BIOS/Cambia) for the development of new lines of rice and millet by Indian plant breeding research institutions, working together with civil society organizations.

Cambia promotes BIOS (Biological Innovation for Open Source) as a means to create open access to capabilities for innovation. Cambia’s open source approach to foster decentralized, cooperative innovation in the application of biological technologies for development is claimed to have received a strong impetus from an agreement made with IRRI (International Rice Research Institute) to establish a joint venture. The aim of this venture is to advance the BIOS initiative, galvanizing agricultural research focused on poverty alleviation and hunger reduction (OS Alliance Cambia-IRRI, 7 Dec. 2005). Various Indian agricultural universities and research institutions have successfully employed open source sequence tagged site (STS) markers and have been able to create *resistance to the widespread disease of bacterial blight* in very popular rice and millet varieties. Some of these lines are in the final stage of field evaluation, while some millet varieties have already been disseminated to farmers, who have in turn disseminated the seeds to different villages (Shailaja Hittalman, personal communication).

In this project the CTC’s research group will study Indian universities’ use of Cambia’s first explicit ‘open source biotechnology toolkit’ (Nature 2005). Made freely available under BIOS licenses, this ‘toolkit’ includes the technology Transbacter, in which the technique of plant gene transfer by *Agrobacterium* – covered by hundreds of patents – is bypassed (symbiotic bacteria being used to add beneficial genes to rice and other plants, such as millet and Indian mustard). Usage of this first open source biotechnology toolkit will be mapped and deconstructed using a critical technographic research methodology.

The **research issues** of this project are:

1. What types of open source products/markers are used?; What kind of open source (re-arrangements are created and how do Indian institutions benefit from and contribute to these open source knowledge systems? (e.g. How do the research institutions participate in the open source licensing of the markers?);
2. Do (and how) open source knowledge development transform the designer-user distinction and create opportunities for an inclusive technology development?;
3. How are open source and improved crosses and combinations of bacterial-blight resistant rice and millet lines be developed?;
4. Do (and how) these improved crosses and lines, developed through open source markers, remain open source products for breeders?
5. How these improved lines can be made more accessible to resource poor client groups and how farmers are able to benefit from the open source knowledge production and participate in the continuing innovation of open source markers development.

The **core objective** of this project is to envisage how *open source markers* in Indian breeding institutions are used for local self-sustainable developments. In view of the position of this project in the total research program, it should particularly deliver insight into *how open source knowledge development transforms the designer-user distinction* (subquestion1) and *whether technology development based on open source is responsive to civil society organizations and contributes to local development* (subquestion 4). The project is set up with various partners, including scientific supervisors (promoters), participating research institutions and external resource persons, which may further be extended during the execution of the research project.

In Appendix 1 some additional information is presented about the provisional CTC's research plans to investigate the open source development of bacterial-blight tolerant rice and millet variety lines in Indian research institutions.

IV.2. Project 2: The use of open source genes from the Arabidopsis network into location and crop specific breeding programs

This project investigates the establishment of open source arrangements on the Dutch side of a research network of the modelplant Arabidopsis. A case-study will be made of the *institutional arrangements* between the Dutch participants of the global Arabidopsis network and their Indian partners to facilitate Indian researchers' use of open source drought tolerant traits – found in this network – in their rice and Indian mustard lines.

Drought is generally considered the most widespread abiotic stress experienced by crop plants and is becoming an increasingly severe problem in many regions of the world, particularly in India where the gradual decline in rainfall and increased aridity have created additional problems for both modern farmers cultivating new rice varieties as well as for peasants cultivating Indian mustard lines. Genome sequencing recently opened the possibility of finding candidate genes for complex traits (quantitative trait loci, QTLs) such as drought in the genome of crop species such as rice and Arabidopsis. Still there is a long way to go to adapt these open source knowledge systems for the breeding of varieties attuned to the needs of local groups of farmers.

Various open source arrangements have been established and may be used to facilitate this research on developing drought tolerant crops. In India Genetwister Company, a daughter firm of Genetwister Netherlands, is interested to investigate whether and in which ways the tagged genes for drought tolerance found in Arabidopsis can be applied in the breeding program for drought tolerant rice and drought tolerant Indian mustard.

Apart from open source genes accessible from the Arabidopsis network, the General Challenge Program (GCP) of the Consultative Group on International Agricultural Development (CGIAR) offers services for developing drought tolerant lines attuned to location-specific eco-conditions, which will be dealt with in research project 4

Employing a critical technographic research methodology, the project will map how the open source genomic information of the Arabidopsis network is translated into crop-specific research priorities of Haryana based research institutions and search for concrete opportunities for how progressive farmers and self-help groups can steer the selection of the research priorities within these institutions and connect them with local self-sustainable developments. This project aims to understand:

- Which open source approaches are applied to find specific traits,

- What new crop varieties have been developed with open source Arabidopsis markers, and how open source drought tolerant traits have been incorporated in rice and Indian mustard line breeding programs in India,
- What kinds of international relations are developed between Dutch and Indian research institutions in the course of knowledge production of plant genomics research tools (e.g. which divisions in labor, how the institutions contribute to/benefit from the open source system),
- Whether/how the crops thus developed with these open source markers remain research commons.

The **core objective** of this project is to understand what kind of open source *institutional arrangements* are (and may be) created to utilize and apply locally the open source drought-tolerant genes from the Arabidopsis network. In view of the position of this project in the total research program this project aims to deliver insight into *what (new) type of institutional setting and arrangements appear in research networks built upon open source* (subquestion 2) and *whether the open source approach is responsive to civil society organizations* (subquestion 4) and *transforms the designer-user distinction in the development of drought tolerant rice and Indian mustard lines* (subquestion 1)

IV. 3. Project 3: The development and use ICRISAT archives as a pool of knowledge commons

The third project investigates the establishment of a *knowledge common* and the co-creation of the knowledge common by open-source. A case-study will be made of the open access to scientific information as organized by the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) through electronic repositories. The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) – alongside FAO's international information program for the agricultural sciences and technology (AGRIS) – has set up an *open archive system* in India, to enable concerned user groups, civil society organizations and individuals to use scientific information freely, paving the way for greater scientific literacy and potential involvement of stakeholders in the further development of science and technology.

This ICRISAT initiative aims to enable research institutions and researchers to develop open source scientific approaches in life science technologies in India. In the project ICRISAT's (already established specific) forms of cooperation with regional institutions for disclosing the electronic repositories for their specific research priorities will be investigated.

Through a critical technographic research methodology the project *will map these alliances* between regional institutions and ICRISAT, and investigate whether/how the specific forms of cooperation imply a *new dynamism* in open source knowledge production. It will also investigate whether/how these regional institutions make use of the free, accessible information sources, how abuse of the open source information source occurs, and whether/how such abuse might be prevented without endangering the whole open source practice.

The project aims to understand:

- a) If/how this ICRISAT initiative enables concerned user groups, civil society organizations and individuals to use scientific information freely,
- b) Whether this ICRISAT initiative is paving the way for greater involvement of stakeholders in the further development of science and technology,

- c) Whether the open archives enable policy makers to be better informed about fundamental research activities and more able to anticipate to their impacts on society.

The **core objective** of this project is to examine the functioning of the open source archives in order to understand whether a new institutional logic emerges that goes beyond the public-private distinction and gives civil society organizations new opportunities to become involved in science and technology developments. In view of the position of this project in the total research program, this project investigates *whether open access to scientific information facilitates and increases the participation of civil society organizations in the development of life science technologies* (subquestion 4); and *whether a common pool of knowledge transforms the public-private distinction* (subquestion 3) and *leads to a new type of research network* (question 2). The project will be undertaken with ICRISAT, and various Indian partners such as RIS, the consortium of Indian Farmers Associations, the Sri Aurobindo Institute of Rural Development (SAIRD) and Krishi Vigyan Kendra (KVK)/ICAR Hyderabad.

IV.4. Project 4: The use (and abuse) of a common pool of plant breeding services delivered through the Generation Challenge Program (GCP)

The fourth project investigates the establishment of a *common pool of services* and its location-specific uses. A case-study will be made of whether/how the services for developing drought-tolerant lines – such as the Genotyping Support Service (Vroom 2009) – delivered through the General Challenge Program (GCP) to Indian breeding institutions are attuned to location specific eco- and social conditions.

The General Challenge Program (GCP) of the Consultative Group on International Agricultural Development (CGIAR), headed in Wageningen, has set up a pool of upstream genomics knowledge, capacity and research tools to allow different types of downstream research partners to develop their own research programs, depending on local needs. Indeed, the GCP has introduced an institutional novelty to challenge “in between and above” the various agricultural centres four key issues⁴, among which drought-tolerance. The aim of that drought tolerant program is “tapping into crop diversity to improve drought tolerance” by delivering several services, such as the Genotyping Support Service (Vroom 2009). This Generation Challenge Program is committed to the use of comparative genomics, marker assisted breeding and genotyping technologies to empower plant breeding for resource poor farmers. The underlying rationale is that these kinds of modern genetic technologies are increasingly being used in plant breeding in developed countries and provide powerful ways of advancing plant breeding, but are difficult to access and use by breeders in developing countries (Ribaut et al. 2008), cited by Vroom 2009). So far investments in genomic maps of agricultural crops have mainly been limited to a few model crops – as Arabidopsis - or crops of commercial interest to developed countries, while many crops of significance for developing world agriculture have remained “orphan crops” in terms of research investments

⁴ Indeed, the current four Challenge Programs focus on “tapping into crop diversity to improve drought tolerance (Generation Challenge Program, GCP), nutritional quality (Harvest Plus), managing food production and water scarcity (Water & Food) and reviving agriculture in Sub Saharan Africa (Sub Saharan Africa CP).

(Naylor et al. 2005). Moreover intellectual property restrictions on newly developed technology and biological material often restricts the use of these innovations for agricultural development in the South (Atkinson et al. 2003; Louwaarts 2007).

In other words through the GCP the CGIAR's have set up an institutional novelty to provide a *common pool of genomics knowledge, capacity and research tools* to allow national research institutions to develop their own lines and find solutions for their location-specific problems.

Through a critical technographic research methodology, this project will map how the common pool of upstream breeding services is used (or even abused) in downstream location specific breeding programs of national research institutes and whether (or not) and how (and why not) these institutes are working together with civil society organizations (CSOs).

The project aims to understand:

- a) How Indian research institutions take advantage of the General Challenge Program's services,
- b) Which genotyping facilities and services are used,
- c) How the drought tolerant lines evolve from the open source knowledge approaches,
- d) How Indian research institutions develop a strategy of research commons.

The **core objective** of this project is to understand how the common pool of services enhances the opportunities for civil society organizations to become co-innovators of science and technology developments. In view of its position in the whole research program, this project will also deliver insight into whether the availability of a common pool of genomics information and genotyping facilities *transforms the public-private distinction within the research networks* (subquestion3), and *whether it does create opportunities for civil society organizations and farmer groups to include their interests and developmental perspectives in the design of location-specific products and crop varieties* (subquestion4).

This project will be carried out with the General Challenge Program participants in Indian Agricultural State University of Andhra Pradesh and with KVK's and the women self help group Rural Development Society (RDS), in Andhra Pradesh.

V. Final remarks about the launching of the research program

As emphasized above the main objective of the research program is to study the potentials of open source and commons approaches in knowledge production for democratizing inclusive life science technologies developments. In view of this objective we also find it logic that this research program itself is also characterized by an open source knowledge approach. Therefore we present our provisional research plans, ask for comments and are looking for transforming our critical-science journal on Tailoring Biotechnologies (www.ctc.wur.nl) into an open source journal in which the provisional results of the four research projects will be published and hopefully added by comments from various angles.

We hope that the presentation of our research program on this conference will become the start for an open source debate on the objectives of the research program and a further elaboration of the main hypotheses of the CTC's research program on open source and commons.

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Appendix 1: Additional information about research project 1: Open source vectors and markers for developing bacterial-blight tolerant rice and millet varieties

The first of the four research PhD projects examines the scope of open source markers for the development of bacterial-blight tolerant rice and millet variety lines within Indian research institutions.

Bacterial blight is a widespread disease in rice growing areas, caused by *Xanthomonas oryzae* pv. *Oryzae*, leading to widespread yield losses. The incorporation of host plant resistance through conventional breeding has made important contribution to reduce the use of pesticides. However the pest often overcomes the resistant pathogen gene and plant breeders must continually adding and changing genes just to maintain the same level of resistance. Breeding effort spent in “maintenance” is a potential loss of gains in other traits. A more sustainable system can be developed by deploying more than one resistance gene at the same time. The challenge is to find the right combination of genes and put them into varieties most suitable for local production. When two or more genes are incorporated into the variety it is called “gene pyramiding.” Up to four genes for bacterial resistance have been pyramided in rice, and there is evidence that collectively they are more effective than would be ascribed to their additive effects. Because each gene may mask the presence of another gene, it is difficult to pyramid more than two genes by conventional breeding and selection; but it can be done with molecular markers.

A *marker* is a “genetic tag” that identifies a particular location within a plant’s DNA sequences. Markers have been extensively used to pinpoint those chromosomal regions important for the trait under investigation (Van Heusden 2009). Marker-aided selection (MAS) is the application of molecular landmarks -usually DNA markers near target genes- to assist the accumulation of desirable genes in plant varieties.

In the Journal “Nature” in February 2005 CAMBIA published the first explicit *open source biotechnology toolkit*, including the technology “TransBacter” in which the technique of plant gene transfer by *Agrobacterium* covered by hundreds of patents, was bypassed using other symbiotic bacteria to add beneficial genes to rice and other plants. This and other technologies have been made freely available under BiOS licenses⁵. Indeed the open source biotechnology development was further strengthened by the announcement of CAMBIA and IRRI (International Rice Research Institute) to establish a joint venture to advance the Bios-Initiative that will galvanize agricultural research focused on poverty alleviation and hunger reduction (OS Alliance Cambia-IRRI, 7 Dec 2005).

⁵ The BiOS Initiative – Biological Innovation for Open Society – is often called Open Source Biotechnology

Over the past several years, scientists at the International Rice Research Institute (IRRI) and its national partners in the Asian Rice Biotechnology Network (ARBN) have applied DNA marker technology to address the *bacterial blight problem*, using open source approaches. First, DNA markers are used to tag nearly all the bacterial blight resistance genes in available genetic stocks. Second, DNA markers are used to describe the composition of pathogen populations unique to each region. This parallel analysis of the host and the pathogen has enabled scientists to determine the right combination of genes to use in each locality

Concerning the genetic stocks so far 25 resistance genes have been identified (Kinoshita, T. in Rice genetic news 1995,12:9-153), of which in Asia a number of resistance genes (Xa4, xa5, Xa7, Xa13, Xa21), all with molecular tags, have been introduced in various combinations into locally adapted varieties. Still the right combination of pathogen genes in each locality needs further research. Indeed, in the past the introduction of the Xa4 gene resulted in the development of many bacterial blight-resistant varieties which have played a vital role in sustaining the rice yields in India and in many other countries. However, large-scale and long-term cultivation of varieties carrying Xa4 resulted in a significant shift of the dominant bacterial blight pathogens. Rice varieties with only Xa4 gene have become susceptible to the bacterial blight diseases not only in India but also in Indonesia, China and the Philippines (Babu et al 2004). One way to delay such a breakdown in bacterial blight resistance is pyramid⁶ multiple resistance genes into rice varieties.

The International Rice Research Institute (IRRI), Philippines and Punjab Agricultural University have successfully employed molecular-assisted selection (MAS) to pyramid genes for bacterial blight. All possible combinations of the four resistance genes viz Xa4, Xa5, Xa13 and Xa21 were pyramided using *sequence tagged site (STS) markers*, **developed in the public domain**. By applying these markers the Centre for Cellular Molecular Biology (CCMB), Directorate of Rice Research and Acharya N.G. Ranga Agricultural University have put three genes – Xa5, Xa13, Xa21 in the popular rice variety, called *Samba Masuri*, through back cross method. Alongside the activities of these three Hyderabad-based research institutions, also in New Delhi researchers of the Indian Agricultural Research Institute (IARI) have used Xa13 and Xa 21 genes to improve the Pusa Basmati Rice Variety creating resistance to bacterial blight. Some lines are in the final stage of field evaluation before release to farmers. The Asian Rice Biotechnology Network (ARBN) is promoting *sharing of these elite lines and gene pyramids* from different countries amongst other countries in Asia so that the useful MAS products can be rapidly disseminated through collaborative field testing across the region.

This project will investigate *how Indian institutions benefit from and contribute to these and other open source initiatives* and *how the room of manoeuvre for open source MAS can be broadened* in an environment in which also intellectual property rights are claimed and a complete sequencing of the rice genome has been established by the Rice Genome Research Program of Tsukuba Japan.

⁶ When two or more genes are incorporated into the variety it is called “gene pyramiding”. Up to four genes for bacterial resistance have been pyramided in rice, and there is evidence .. Because each gene masks the presence of another gene, it is difficult to pyramid more than two genes by conventional breeding and selection, but it can be done with molecular markers.

Next to the open source knowledge development on rice - as a main crop for Indian industrialized farming systems – there is also open source knowledge development of millet - as an important crop for **Indian peasantry**. Indeed, the University of Agricultural Sciences in Bangalore (prof. Shailaja Hittalmani's group) has been working through molecular-assisted selection (MAS) for improvement of RAGI, a millet crop that is extensively grown in rain-fed areas of South India⁷. In collaboration with the University of Wisconsin, USA (Dr. Sally Leong), the University of Georgia, USA (Dr. Katrien Devos) and the University of Agricultural Sciences of Bangalore, India (Dr. Shailaja Hittalmani) blast-resistant (and drought tolerant) varieties have been developed and disseminated to hundreds of farmers through farm demonstrations and trial on farmer fields in the dry region of Karnataka.

The seeds were disseminated by farmers themselves from village to village, while in the last four years multilocation trials of the lines have been conducted by the millet coordinator of that program. From the trials conducted in five farmers' field, representing different agro climatic conditions, three promising genotypes ML 31, ML 322, ML 365 were selected as the most preferred genotypes based on grain yield, fodder yield, fodder quality, cooking quality and nutrition parameters, while ML181 was found to be superior in grain and straw yield under water limited conditions (S. Hittalmani, progress report). 95 new SSR markers were developed and the SSR primers *were shared*. Moreover, a preliminary map was developed and comparative analysis with other cereals is reported, while also a co-linearity between finger millet and rice was reported.⁸ Primers, ESTs and other sequences have *deposited in Gen Bank* and articles presenting results on map development, evaluation for blast disease and participatory evaluation have been submitted for publication.

In view of the above-mentioned open source activities it is possible to focus the research on answering the following main and sub-questions:

- **What open source (STS) marker development takes place and how these markers can be integrated in Indian agricultural research for an inclusive technology approach?**

Sub questions are:

- How do the participating research institutions in India *get access* to knowledge developments about STS markers in public domain?
- How do the participating research institutions *contribute to* the development of public STS markers?
- How are open source markers *integrated* in Indian agricultural research on rice and millet breeding?
- Do public STS markers facilitate a *diversification* of plant breeding programs and an *attuning* of plant breeding research to location specific potentialities for development?

The research will start with:

⁷ Ragi is prescribed for diabetics as it contains low calories high fiber and protein content and is particularly cultivated in peasant production systems

⁸ Six finger millet homeologous groups correspond to a single rice chromosome and three to two rice chromosomes.

- A general analysis of open-source databases, such as the Patent Lens of Biological Innovation for Open Society (BiOS) and other organizations such as PIPRA (Public Intellectual Property Resource for Agriculture) which are promoting open access to biological innovations targeted to agricultural improvement, especially for crops important to the developing world. For example, the Patent Lens is a comprehensive database which is intended as a virtual broker for the development of new tools, such as marker assisted breeding and the development of true hybrids of crop species, that would allow farmers to use hybrid seeds year after year (and combine the positive traits of hybrids and open pollinated varieties).
- An analysis of open source initiatives in rice and millet and which research institutions benefit from the open source knowledge approach and how they contribute to it.
- An investigation of the evolution of open source in respectively in the rice and millet research networks, reflecting on whether and how new lines – developed through open source markers and genes – can remain in the domain of commons.

The research objectives are:

- To deliver insight in how open source markers and genes are developed and used by Indian research institutions;
- how the open source knowledge approach can be strengthened and whether the open source knowledge development facilitates an integration of users perspectives in the technology development; and
- whether the developed rice and millet varieties have (can) become research commons and do create opportunities for civil society organizations to realize an inclusive technology development.