Innovations in genetically modified agricultural technologies in China's public sector

Successes and challenges

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Abstract

Purpose – The purpose of this paper is to assess whether China's public sector can continue to generate advanced genetically modified (GM) technologies that will be competitive in the market.

Design/methodology/approach – The authors investigated all the research teams that have been conducting research projects under the variety development special program. The data collected include detail information on research capacity, research areas, performance, and process of their research projects. Based on the survey data, the authors assessed the innovations and progress of the variety development special program.

Findings – Unlike other countries, most GM products in China are developed by public research institutes. There is rising concern on the ability of China's public sector to continuously generate indigenous GM technology that can compete with multinational companies. The study surveyed 197 research institutes and 487 research teams and found that the GM program in China lacks coordination: researchers do not want to share their research materials with others. Due to the lack of coordination, most of the hundreds of research teams often worked independently in the year 2008-2010. Moreover, the authors found the lack of coordination may be due to the reason that the interests of researchers are not well protected. This paper also provided the recent progress and policy changes of GM program in China, and it found that the efficiency in the later three years improved a lot. In order to establish a competitive national public GM research system, China should continuously consolidate and integrate the upstream, midstream, and downstream activities of the whole GM innovation process. China's public sector may also need to work more closely with both the domestic and international private sectors.

Originality/value – This paper is a comprehensive analysis on the development of transgenic technology in China. The results of this paper can provide evidence for the dynamic adjustment of the policies in the variety development special program and can also provide reference for the future assessment of the variety development special program.

Keywords Innovation, Gene cloning, Gene transformation, Genetically modified technology, Research teams

Paper type Research paper

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1. Introduction

Internationally, the genetically modified (GM) technologies are mainly developed by private sector (e.g. the multinational companies, MNCs) (Huang, Rozelle, Pray, and Wang, 2002; Pray *et al.*, 2002). In each year since the late 1980s, the investment in R&D by MNCs, on average, accounts for about 10 percent of their sale revenues (Alston *et al.*, 1998; Hector *et al.*, 2010). The six major GM MNCs patented 285 GM events of total 359 by 2010 and have dominated global GM crop industry in the world since 1990s (James, 2009). The successes of MNCs in generating GM technology demonstrate the importance of integrating technology innovation chains from upstream to downstream that use the most advanced and patented techniques and genetic materials from both own and other companies (Pray *et al.*, 2002).

Although the largest developers of GM products in the rest of the world are MNCs, in China, most of the development is taking place in hundreds of public research institutes with different administrative jurisdictions (Lin, 1992; Huang, Hu, and Rozelle, 2004; Cohen, 2005). In order to develop its own GM technology, the Chinese government invested substantially in agricultural GM technologies in the 1990s and the early 2000s (Huang, Rozelle, Pray, and Wang, 2002; Pray *et al.*, 2002). The growth rate of investment has even accelerated after China initiated a new National GM variety development special program (GMSP) in 2008 with a total budget of about US$ 3.8 billion in 2008-2020.

While China's public-dominated GM technology development is a unique case, it did generate impressive GM technology in the past (Huang *et al.*, 2008). For example, Bt cotton developed by Chinese scientists has been widely adopted by farmers and recorded a high return on investment (Pray *et al.*, 2001; Huang, Hu, Rozelle, Qiao, and Pray, 2002; Huang, Hu, Van Meijl, and Van Tongeren, 2004; Huang *et al.*, 2008). Benefit from Bt cotton and potential roles of GM technology to boost agricultural productivity and improve the national food security have led China to continue to invest in GM technology. Since 1997, China has approved the commercialization of GM cotton, petunias, tomatoes, sweet peppers, poplar trees and papayas (Huang, Hu, Wang, Keeley, and Zepeda, 2002; James, 2009). In 2009, the Ministry of Agriculture issued production safety certificates for Bt rice and GM phytase maize. There are also several other biotech crops in the pipeline.

However, there is also rising concern regarding the ability of China's public sector to continuously generate innovative GM technology that can compete with the MNCs. Across the world, GM soybean and maize have been commercialized since 1996 (James, 1997). However, in China, except Bt cotton, there is no major GM crops in the farmers' field. Chinese own GM soybean and maize technologies are not expected to be ready for commercialization by late 2010s. Moreover, up to now MNCs have commercialized GM products with many advanced traits against insect, diseases, and herbicide and with multiple/stacked genes (James, 2015). The industry (e.g. MNCs and China's private companies) believes that China will be left far behind the rest of world if the country continues depending primarily on its own public GM technologies (David *et al.*, 2000). Realizing this challenge and market potential for GM technology, several domestic companies, including Da Bei Nong Group and China National Seed Group, two of the top Chinese seed companies, have initiated their own research programs around the year 2009. They have claimed that they can do better than the national GM program in the nearly future and their technology – much better than that developed by the public sector – will be competitive in the field within five years.

The overall goal of this paper is to assess whether China's public sector can continue to generate advanced GM technologies that will be competitive in the market. We try to answer the following question: can China have its own innovative and competitive GM technology solely based on its public sector? Specifically, we have the following three objectives: to assess the institutional framework of R&D in Chinese public GM innovation system; to document the performance of Chinese R&D in GM technology, its competitiveness and innovation capability; and to identify the successes and challenges of Chinese public GM technology program.

To meet the above goal and objectives, the rest of the paper is organized as follows. The next section introduces the data used in this study, which cover all universities and research institutes engaged in the GMSP. We select GMSP because it is by far the largest GM program in China[1]. Section 3 analyzes the performance of China's GM program from 2008 to 2010. Section 4 presents the exchange of research products in the GM program and why researchers do not want to share their research materials. Section 5 describes recent progress and policy changes in the GM program. Section 6 provides conclusions.

2. Data

Data used in this study are from a survey which covers all research teams that have been conducting research projects under GMSP. A research team is defined as a group of scientists within any college or research institute that has conducted a project or sub-project. The data collected include detailed information on research capacity, research areas, performance, and process of their research projects.

To implement the survey, we worked closely with the research management division at each college or research institute as the survey was conducted by post mail. The survey forms were sent to the research management division head in each college or institute. The division head assigned a task force to make sure that the survey form was distributed to all of the research teams that participated in the GMSP and asked each research team leader to fill in the questionnaire. The division head collected all of the research team survey forms and returned them to us. All participants were informed that all information would be used for the research only and that in the final data set their affiliations and names would be eliminated and their survey information could only be identified with the aid of a confidential identifier code. Thus, the response rate was 100 percent. To ensure the quality of data, we made phone calls to the head of research division and research team leaders to clarify the missing information or inconsistence in the data we received.

In total, the surveys covered 505 research teams from 200 biotechnology-related colleges within universities and research institutes that have engaged in the recent GM special program. One college had by far the most research teams at 23[2]. The number of research teams in other colleges ranged from 1 to 21. For this study, we excluded the research teams in the field of microorganism and biosafety appraisal of GM technology[3]. Finally, the data set used in this study includes 197 colleges and 487 research teams. The above two surveys elicited information covering approximately 80 percent of the nation's GM biotechnology research laboratories in 28 provinces or municipalities.

3. Performance and innovation in agricultural GM technology

In contrast with the GM technology innovation process carried out by MNCs, China's GM R&D is conducted by research teams located in hundreds of public universities and research institutes nationwide. In this section, we first describe the GM research activities, and then, we used gene cloning, transformation, and varietal breeding as examples to evaluate the GM technology innovation process in China. Finally, we evaluate the successes and challenges of China's public GM technology innovation.

In public research institutes, one difficulty in evaluating the performance of research teams in R&D of GM technology is to categorize actual research fields of each team in the whole process of GM technology innovation from upstream to midstream and downstream. In the survey, each team leader reported his/her team's one major research field (e.g. gene cloning, gene transformation, or/and varietal breeding) and all research activities conducted in the major field and other fields. Interestingly, we found that many research teams had multiple functions in their works.

3.1 Research activities conducted by research teams in the public GM sector

Table I presents the profile of research teams in public GM innovation system. Here, the upstream block of research teams is defined as those majorly engaged in gene cloning, the middlestream ones focus mainly on gene transformation, and the downstream ones are those majorly engaged in the development of new varieties. Within the upstream block, we further divided the research teams into three subgroups: engaged only in gene cloning (Clone), engaged in both gene cloning and transformation (Clone+T), and engaged simultaneously in gene cloning, gene transformation, and new varietal development (Clone+T+V). Within the middlestream block, we divided the research teams into four subgroups: engaged only in gene transformation (T), engaged in both gene transformation and gene cloning (T+Clone), engaged simultaneously in gene transformation and new varietal development as well as gene cloning (T+V+Clone), and engaged both in gene transformation and the new variety development (T+V). Within the downstream block, we also divided the research teams into three subgroups: those that are extensively involved in the development of new varieties and minimally in either gene cloning or gene transformation (V+T+Clone) and those that are involved in the development of new variety and gene transformation (V+T). The third category of downstream team does no work in gene cloning or transformation but is purely engaged in the development of new varieties (V).

Table I also tabulates the frequency of research teams by the above-mentioned categories. Of the 487 research teams, 37 percent (182/487) identified themselves as involved in upstream research, 29 percent (142/487) in midstream, and one-third (163/487) in downstream. One interesting result from Table I is that the R&D of GM technology in China's public sector is dominated by gene cloning rather than the development of new varieties. The survey indicates that nearly 50 percent (226/487) (row 2) of the research teams are engaged in gene cloning, even though some of their comparative advantage is either gene transformation or the development of new varieties.

For the 182 teams engaged mainly in gene cloning, more than 30 percent of them (54/182) are also engaged into either midstream or downstream activities of GM technology innovation. This indicates that some of the research teams who are primarily involved in the upstream activities of biotechnology (gene cloning) are extending the R&D to gene transformation or the development of new varieties, suggesting that they may be hesitant to provide cloned gene to the research teams with comparative advantages in the midstream or downstream activities of the innovation.

Of 142 research teams mainly engaged in midstream innovation and 163 research teams mainly engaged in downstream innovation, there were 44 research teams also involved with cloning the genes. Without the availability of cloned gene from external research teams, some research teams in midstream or downstream have to clone gene by themselves in order to fulfill the research goals in gene transformation or obtaining new varieties.

Without the efficient material exchange from upstream to midstream and downstream, of all the 226 research teams engaged in gene cloning, 83 operated their whole innovation processes in-house from the upstream to midstream to downstream areas.

Table I.
The numbers of research teams that engage in gene cloning and obtained cloned genes, 2010

		Upstream research teams conducted research				Midstream research teams conducted research					Downstream research teams conducted research			
	Total	Sum	Clone	Clone+T	Clone+T+V	Sum	T+Clone	T+V+Clone	T	T+V	Sum	V+T+Clone	V+T	V
Total teams	487	182	128	12	42	142	3	11	30	98	163	30	63	70
Engaged in gene cloning	226	182	128	12	42	14	3	11			30	30		
Obtained cloned gene	197	154	102	12	40	13	3	10			30	30		
Plant														
Engaged in gene cloning	188	156	108	12	36	12	2	10			20	20		
Obtained cloned gene	165	133	87	12	34	12	2	10			20	20		
Animal														
Engaged in gene cloning	38	26	20	–	6	2	1	1			10	10		
Obtained cloned gene	32	21	15	–	6	21	1	–			10	10		

Notes: Clone, clone gene; T, gene transformation; V, varietal breeding; the order represents priority of worked. For example, Clone+T+V indicates a team belongs to upstream research (clone gene) but also conducted researches in gene transformation and varietal breeding; V+T represents a team belong to downstream varietal breeding but also conducts middlestream work in gene transformation

Source: Authors' own survey

The results suggest that 37 percent of the research teams (83/226) were fighting among themselves and might not exchange their cloned gene to midstream and downstream research teams.

3.2 The performance of research teams in gene cloning

In this subsection, we use gene cloning as an example to evaluate the performance of China's GM R&D and technology innovation. Table II shows the number of genes cloned and used by different research teams. The results indicate that by August 2010, there were 743 cloned genes available for the next stages of R&D[4]. As mentioned above, some of the teams that major in midstream and downstream cannot obtain the cloned gene from upstream, so they also conducted research in gene cloning. From Table II, we can see that the percentage of the cloned genes being used for transformation in midstream (87.5 percent, 42/48) and downstream (67.5 percent, 81/120) was much higher than that of the upstream (51.7 percent, 297/575). This may be explained by the fact that the researchers in the midstream and downstream areas have very specific, grounded ideas about what kind of gene they actually need. Three quarters of cloned genes were developed by the research teams that are major in gene cloning, and the rest of them are cloned by those majored in midstream and downstream of R&D of GM technology but also engaged in gene cloning.

3.3 The research capacity differences between the clone teams and non-clone teams

Table III summarizes the differences between the gene cloning teams and non-clone teams. We divided all samples into university, national, and provincial research institutes. We also use research funding from the GM special program to indicate the funding situation, which is measured as million RMB per person. The proportions of the researchers with PhD Degree are used as a proxy for potential research capacity.

Statistical differences between the gene cloning teams and non-clone teams are conducted by using *t*-test. The results show that, on average, the point estimates for the research teams who cloned gene were higher than those for the counterparts who did not clone gene, except for the research teams in the provincial institutes. *t*-Tests show that significantly statistical differences exist among all the characteristics (column 4).

As the data show, the probability to engage in gene cloning is highest in the research teams from university, followed by those from the national research institute and provincial research institutes. This is expected because the universities and national research institutes have stronger basic research capacity than the provincial institutes. Research teams with higher percentage of researchers with PhD degree and more GM fund are also more likely to swarm into cloning gene. These imply that that in China the institutes with stronger research capacity are more likely to engage in gene cloning.

4. The exchange of research products

4.1 The usage of cloned genes and the source of genes used in gene transformation

Table II also showed that of all the 743 cloned genes, 57 percent of them (420/743) have already been applied for the next stage of R&D. Furthermore, of the 420 cloned genes that have been used in transformation, more than 80 percent (342/420) of them were used solely in-house and 12 percent (52/420) were also shared with other institutes. Only 6 percent (26/420) of the cloned genes were purely used by the researchers outside of the institute. For the 83 teams that operated their whole innovation processes in-house from the upstream to midstream to downstream areas, 80 percent ((137 + 28 + 81)/(153 + 34 + 120), rows 1 and 2) of the cloned genes had already been used in the next stage of R&D. Although the usage of the cloned genes in those teams were much higher than average, the percent of cloned genes that used in-house were also much higher. For those teams, 85 percent of the cloned genes were

Table II. Number of genes cloned and used by different research teams

		Upstream research teams conducted research				Midstream research teams conducted research			Downstream research teams conducted research	
	Total	Sum	Clone	Clone+T	Clone+T+V	Sum	T+Clone	T+V+Clone	Sum	V+T+Clone
Obtained cloned gene	743	575	359	63	153	48	14	34	120	120
Have been used	420	297	100	60	137	42	14	28	81	81
by own institute only	342	249	71	48	130	33	13	20	60	60
by own and other institutes	52	33	16	10	7	8	1	7	11	11
by other institutes only	26	15	13	2	–	1	–	1	10	10
Have not been used	323	278	259	3	16	6	0	6	39	39

Notes: Clone, clone gene; T, gene transformation; V, varietal breeding; the order represents priority of worked. For example, Clone+T+V indicates a team belongs to upstream research (clone gene) but also conducted researches in gene transformation and varietal breeding; V+T represents a team belong to downstream varietal breeding but also conducts middlestream work in gene transformation

Source: Authors' own survey

Table III. Descriptive statistics of the characteristics of research teams worked and not worked in gene cloning, 2010

Indicator	Definition	Total (mean) (1)	Worked in gene cloning (2)	Not worked in gene cloning (3)	*t*-Test (2) vs (3)[a] (4)
University	1 = university; 0 = otherwise	0.51	0.56	0.46	<0.05**
N-institute	1 = national research institute; 0 = otherwise	0.26	0.32	0.21	<0.01***
P-institute	1 = provincial research institute; 0 = otherwise	0.21	0.10	0.30	<0.01***
PhD	The percent of researchers with PhD Degree (%)	43	48	39	<0.01***
GM fund	Annual funding from GM special program, million yuan per person	0.11	0.13	0.09	<0.01***

Notes: [a]*p*-value obtained from *t*-test. **,***Statistically significant at 5 and 1 percent, respectively
Source: Authors' own survey

used in-house and 10 percent were used not only in-house but also by the researchers outside of the institutes, and only 4 percent of the genes were purely used by the researchers outside the institutes. The results suggest that the teams that have established the complete innovation process are less likely to transfer their cloned genes to the outside institutes.

From another aspect, Table IV reports that more than 67 percent (656/971) of the genes used in the midstream or downstream were developed solely in-house. Even for those teams who are majorly in midstream, only 43 percent (203/472) of the genes used in their research came from the other institutes. For those who are major in downstream, only 31 percent (81/272) of the genes used in their research came from the other institutes. These results indicate that researchers in the upstream often do not transfer their cloned genes to the midstream or downstream researchers, and the researchers in gene transformation or new variety breeding cannot obtain their expected genes on time, which induced their works on the upstream research.

4.2 Number of genes cloned by upstream, middlestream, and downstream

Regarding the number of genes cloned per research team, it is surprising that the teams in the downstream cloned the most. On average, each team in the downstream cloned four genes (120/30), while those in the upstream cloned 3.2 (575/182) and those in the midstream cloned 3.4 (48/14) (row 1, Table II; row 2, Table I). For the 73 research teams that have established the complete innovation process of R&D and GM technology, the average number of genes cloned by each team was 3.7 (281/83).

Our results also suggest that the number of genes cloned and actually used in transformation was higher in the 73 teams that covered the whole innovation process. The current research system in China seems to encourage the teams not to transfer their creations to others but to establish a complete innovation process within their own small research teams.

The observations are not difficult to understand. Under the public research system and current biotechnology R&D management framework, in order to obtain the desirable cloned gene without suffering from IP conflict, midstream or downstream teams often have to do their own clone gene work because the existing cloned genes are often kept for own use in upstream research team. Meanwhile, the upstream teams tend to expand their research to midstream and downstream works even they are not comparative advanced in gene transformation and new varietal development. Therefore, despite more than 13 thousands researchers working in agricultural biotechnology (Huang *et al.*, 2012), it is difficult to form critical mass in any aspect of GM technology innovation process (upstream, midstream, and downstream).

Table IV. The number and sources of gene used in gene transformation by different research teams by 2010

		Upstream research teams conducted research			Middlestream research teams conducted research					Downstream research teams conducted research		
	Total	Sum	Clone+T	Clone+T+V	Sum	T+Clone	T+V+Clone	T	T+V	Sum	V+T+Clone	V+T
All genes used in gene transformation	971	227	60	167	472	17	40	119	296	272	93	179
The sources of gene												
Own institute	656	200	59	141	269	17	34	60	158	187	70	117
Other domestic institutes	215	20	1	19	130	0	5	36	89	65	18	47
Foreign countries	68	7	0	7	47	0	1	17	29	14	4	10
Do not know	32	0	0	0	26	0	0	6	20	6	1	5

Notes: Clone, clone gene; T, gene transformation; V, varietal breeding; the order represents priority of worked. For example, Clone+T+V indicates a team belongs to upstream research (clone gene) but also conducted researches in gene transformation and varietal breeding; V+T represents a team belong to downstream varietal breeding but also conducts middlestream work in gene transformation

Source: Authors' own survey

4.3 Patents and the sharing of research materials

The above analysis shows that researchers do not want to share their research materials with others: most of the cloned genes were used solely in-house and most of the genes used in the midstream or downstream were developed solely in-house. One reason why researchers do not want to share their research products is that the interests of researchers have not been well protected. This indicates that if interests of researchers are protected by patents, then researchers may have better motivation to share their research products. Table V presents the percent of cloned genes used by own institutes and other institutes. From Table V, we can see that if the cloned genes are protected by patents, the percent of cloned genes that researchers shared with other institutes was 43 percent. However, if the cloned genes are not protected by patents, the percent of cloned genes that researchers shared with other institutes was only 33 percent, which is 10 percent lower than those protected by patents. For the genes protected by patents, the percentage of genes used by "own and other institutes" and "by other institutes only" is 30 and 13 percent, respectively, which is higher than the percentages used by "own and other institutes" and "by other institutes only" for those genes not protected by patents.

To examine the relationship between patents and researchers' research products sharing, we also employed regression analyses to probe the reasons for not sharing research products with others. We use the data in the plant sector[5] and ran a marginal effect probit regression of whether the cloned gene was shared with other institutes against the following: whether the cloned gene was patented; research capacity of the research team, such as the percent of researchers with PhD Degree and per capita funding from GMSP; characteristics of the research team, such as whether it belongs to a national research institute, a college, or a provincial research institute; and the traits of the cloned gene, such as whether the cloned gene was insect resistance, herbicide tolerance, virus resistance, drought tolerance, saline tolerance, high yield, good quality, etc.

To test the robustness of the regression results, we gradually add control variables, from simple to complex, during the regression process. Model (1) only includes the target variables, namely, patented and research capacity of the research team. Certain control variables are added to Model (2), including characteristics of the research team. For Model (3), the traits of cloned genes are added to examine what kinds of genes are more difficult to acquire. Results in Table VI show that all the three models produce similar regression results, and the significance of all variables is robust.

Although patents may create a tragedy of the anticommons and have negative effect on research (Heller and Eisenberg, 1998; Lei *et al.*, 2009), the results in Table VI show that in a weak intellectual property protection environment like China, patents fortified the free flow of the research materials. On average, patent status per se raised the likelihood of sharing research materials by 24 percent, suggesting that if the commercial ties of researchers are well protected, the sharing of research materials could become easier in China. The results in Table VI show that research teams with higher percentage of doctor's degree and more GM fund are more likely to share their research materials with others. These findings imply that research capacity has positive impact on the transfer of research materials. The last column

Table V.
Percent of cloned genes used by own institutes and other institutes

	With patents	Without patents
Used by own institute only	57	67
Used by other institutes	43	33
by own and other institutes	30	23
by other institutes only	13	10

Source: Authors' own survey

Variables	Definition	(1) Shared	(2) Shared	(3) Shared
Patented	1 = the gene was patented; 0 = otherwise	0.24 (0.07)***	0.26 (0.07)***	0.24 (0.07)***
P-doctor	Percent of researchers with PhD Degree	0.002 (0.001)**	0.002 (0.001)**	0.002 (0.001)*
GM fund	Annual funding from GMSP, million yuan per person	0.30 (0.15)*	0.30 (0.15)**	0.30 (0.16)*
N-institute	1 = national research institute; 0 = otherwise		−0.08 (0.10)	−0.11 (0.10)
University	1 = university; 0 = otherwise		−0.01 (0.11)	−0.02 (0.11)
Traits of gene (insect resistance as reference group)				
Herbicide tolerance	1 = herbicide tolerance; 0 = otherwise			−0.13 (0.08)
Virus resistance	1 = virus resistance; 0 = otherwise			−0.07 (0.08)
Drought tolerance	1 = drought tolerance; 0 = otherwise			−0.20 (0.05)***
Saline tolerance	1 = saline tolerance; 0 = otherwise			−0.20 (0.04)***
Other stress tolerance	1 = other stress tolerance; 0 = otherwise			−0.14 (0.06)**
High yield	1 = high yield; 0 = otherwise			−0.23 (0.03)***
Good quality	1 = good quality; 0 = otherwise			−0.09 (0.08)
High yield and good quality	1 = high yield and good quality; 0 = otherwise			−0.23 (0.03)***
Other traits	1 = other traits; 0 = otherwise			−0.12 (0.07)*
Observations		378	378	378

Note: *,**,***Statistically significant at 10, 5 and 1 percent, respectively
Source: Authors' own survey

Table VI. Probit regression for whether the cloned gene was shared with other institutes

of Table VI show that compared with genes traits in insect resistance, the genes traits in stress tolerance (such as drought tolerance, saline tolerance, and other stress tolerance) and high yield (such as high yield and high yield and good quality) are more difficult to acquire.

5. Recent progress and policy changes of GM program in China

Although there are great challenges in the GM program in 2008-2010, the Chinese government also noticed those challenges and changed the policies accordingly. Especially after the year 2014, the Chinese government made great changes in the integration of upstream, middlestream, and downstream activities of the GM program. Some of the GM companies in China are also aiming to buy Syngenta so as to promote the close cooperation of research teams and generate critical mass for product-oriented GM agricultural technologies. Based on the policy adjustment, great progress also has been made in the GM program in China. Table VII presents the number of gene cloned, patents applied, and patents authorized in 2008-2010 and 2011-2015. From Table VII, we can see that, on average, the GM program get 247 cloned gene each year during the period 2008-2010, and the GM

	First 3 years (2008-2010)	Later 5 years (2011-2015)
Gene cloned (number/year)	247	483
Patents applied (number/year)	95	342
Patents authorized (number/year)	29	201

Source: Authors' own survey

Table VII. Comparison of the output between 2008-2010 and 2011-2015 program get 483 cloned gene each year during the period 2011-2015. The number of cloned gene almost doubled in the later five years, which suggests that the efficiency of gene clone of the research teams improved dramatically.

From Table VII, we can see that the number of patents applied in the later five years is three times as larger as those in the first three years. The number of patents authorized in the period 2011-2015 is almost seven times as larger as those in the first three years. The larger number of patents applied and authorized in the later five years also suggests the improvement of the efficiency of GM program in China. The percent of patents applied in the first three years is 38 percent (95/247), and those in the later five years is 71 percent (342/483). The increase in the percentage of patents applied suggests that the awareness of researchers' intellectual property rights protection has enhanced. The percent of patents authorized in the later five years is 59 percent (201/342), which is almost two times as larger as those in the first three years (31 percent), suggesting that the quality of research materials also improved in the later five years.

Besides the progress mentioned above, the GM program also obtained 137 genes with important application value, such as ten new insecticidal Bt genes are now used in the rice and maize, which significantly improve the insecticidal effect. The research of genomics and gene clone of rice in China is now internationally advanced. There were 16 papers in this field published on Science, Nature or Cell in the year 2014-2015 and 69 percent of them were published by the Chinese scientists. The China National Seed company also has invested RMB5 billion (equivalent to US$ 769 million) to set up the GM variety development research center, and Da Bei Nong had also invested more than US$ 276 million in the research of GM technologies. Although the successes in the GM program are impressive, until now, except Bt cotton, there are still no other major GM crops approved for commercialization. The delay of GM crops' commercialization may hinder the private sectors' investment on the research and development of GM technologies in the future.

6. Conclusion

This study shows that in the national GM special program, by far the largest agricultural R&D program in China, more than 500 research teams have been working with aims of creating innovated GM new varieties to improve China's agricultural productivity and national food security. Research outputs generated by individual research teams are impressive. Numerous genes have been cloned by upstream teams, as well as by midstream and downstream teams. Many cloned genes have also been used for transformation and varietal development. Especially in the recent five years, the efficiency of GM program has improved dramatically. Although we have not examined the final products (new varieties) generated from China's GM R&D and its innovation system, we expect there will be emerging GM varieties, regardless of quality, from the hundreds of research teams engaged in China's agricultural biotechnology industry.

However, our analyses also suggest that China's public sector-led GM technology program is facing great challenges. Unlike the GM programs of the MNCs, China's public-led GM program lacks efficient coordination. No oriented and integrated (upstream, midstream, and downstream) innovation process for the production of agricultural varieties has yet been formulated. The R&D of GM technology in China's public sector is dominated by gene cloning, and most of the institutes with stronger research capacity are swarming into gene cloning rather than new variety breeding. Due to the lack of commercial tie arrangement, the researchers in upstream are hesitant to transfer their research materials and tools to the researchers in midstream or downstream, in turn, it will constraint the R&D in the midstream or downstream and make people who work on the midstream or downstream waste the capital and time to do repeat early-stage or risky research. To have a strong national public GM technology, better institutional arrangement should be made to promote the close cooperation of teams in the public sector with those in private sector, both domestically and internationally. Otherwise, China's public-led GM technology could be much far behind the GM technology in the rest of world in the future.

Notes

1. The program covers five major crops (rice, wheat, maize, soybean and cotton) and three major livestock (swine, cattle and sheep). This program aims to generate new GM varieties of above five crops and three kinds of livestock. Research projects under the program range from the upstream (e.g. gene cloning and gene transformation techniques) to the middlestream (e.g. gene transformation) and the downstream (e.g. breeding and varietal development) of the whole GM technology generation process.
2. We did not uncover the name of the university here, because in the data collection process, we have an agreement with all the universities and institutes that their university will be given a ID code in the data set and their names will be confidential after cleaning the data set even within the research group.
3. There are 6 and 12 research teams in the field of microorganism and security appraisal, respectively. We exclude the former one because the sample size is too small and the later one does not refer to gene cloning, gene transformation and new variety breeding.
4. The cloned genes included in our survey are those whose traits (e.g. insect resistance and disease resistance) have been well acknowledged by the researcher by the year 2010.
5. We exclude the genes in the field of animals because the sample size is too small.

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