HIGH-YIELDING TECHNOLOGIES IN CHINA

Qian Qian
China National Rice Research Institute

ABSTRACT
Increasing crop yield is a major challenge for modern agriculture. In China hybrid rice has contributed greatly to the self-sufficiency of food supply. To meet the future demand for rice production, a series of national programs on super-rice breeding, functional genomics and GM breeding have been established in China since 1996. We have cloned some important high yield-related genes, *IPA1* (*Ideal Plant Architecture 1*), *DEP1(dense and erect panicle 1), GIF1(grain-filling 1), Ghd7(grain weight, plant height and heading date)* and *GW2(grain width 2*). The development of new plant type of IPA, has been proposed as a means to enhance rice yield potential over that of existing high-yield varieties. *IPA1*, a semidominant quantitative trait locus, profoundly changes rice plant architecture and substantially enhances rice grain yield. *IPA1* encodes OsSPL14 (SOUAMOSA PROMOTER BINDING PROTEIN-LIKE 14) and is regulated by microRNA (miRNA) OsmiR156 *in vivo*. We demonstrate that a point mutation in *OsSPL14* perturbs OsmiR156-directed regulation of *OsSPL14*, generating an 'ideal' rice plant with a reduced tiller number, increased lodging resistance and enhanced grain yield. So these yield genes have been used in super-rice and GM breeding to improve rice grain yield. Actual yield of a japonica rice variety XS11-ipa1 could increase 10% over its CK XS11.

KEYWORDS: rice, yield, *IPA1* gene, cloning, super-rice breeding

REFERENCES:

1. Jiao Y, Wang Y, Xue D, Wang J, Yan M, Liu G, Dong G, Zeng D, Lu Z, Zhu X, Qian Q, Li J. Regulation of OsSPL14 by OsmiR156 defines ideal plant architecture in rice. Nat Genet. 2010, 42(6):541-544.
2. Huang X.Z., Qian Q., Liu Z.B., Sun H.Y., He S.Y., Luo D., Xia G.M., Chu C.C., Li J.Y., and Fu X.D., Natural variation at the DEP1 locus enhances grain yield in rice, Nature genetics, 2009, 41(4):494-497.
3. Wang Ertao, Jianjun Wang, Xudong Zhu, Wei Hao, Lin Wang, Qun Li, Lixia Zhang, Wei He, Baorong Lu, Hongxuan Lin, Hong Ma, Guian Zhang & Zuhua He. Control of rice grain-filling and yield by a gene with a potential signature of domestication, *Nature Genetics*. 2008, 40:1370-1374.
4. Ashikari M., Sakakibara H., Lin S.Y., Yamamoto T., TTakashi T., Nishimura A., Angeles E.R., Qian Q., Kitano H., and Matsuoka M., Cytokinin Oxidase Regulates Rice Grain Production, Science, 2005, 309: 741-745.
5. Fan C.C., Xing Y.Z., Mao H.L., Lu T.T., Han B., Xu C.G., Li X.H.,and Zhang Q.F., GS3, a major QTL for grain length and weight and minor QTL for grain width and thickness in rice, encodes a putative transmembrane protein, Theoretical and Applied Genetics, 2006, 112(6): 1164-1171

High-yield technologies in China

Qian Qian
钱 前

China National Rice Research Institute (CNRRI)

2011.11 Japan

Food Crisis Always Exist

Rice plays a critical role in food security, improving the rice yield has great meaning

Contents

◆Progress of rice breeding in China

◆Discovery of yield genes in rice

◆Breeding strategies for super hybrid rice

◆Progress of rice breeding in China

◆Discovery of yield genes in rice

◆Breeding strategies for super hybrid rice

Big Question For Big Country

Time: Aug. 24, 1994

Person: Americans, Lester Brown

Question: Who will feed China?

Answer: Chinese

Food production must be further improved

1.1 Three stages in rice breeding

➢ High-yield rice breeding is an eternal theme, getting great achievement in China

Green Revolution ,1950's
（ 2t/ha-4t/ha）

Heterosis, 1970's
(4t/ha-6t/ha）

Super rice research launched in 1996

1.2 Super rice research and ideal-type breeding

➢High-yield breeding has tended to a plateau, since the dwarf and heterosis breeding have taken two breakthroughs. IRRI launched a new strategy of Ideal-type breeding in 1989 and China did the super rice research in 1996. they both achieve some substantive results, but still have a distance away from the break.

- Few tiller (no invalid)
- 200-250 grains/panicle
- Strong stem (90-100 cm)
- Dark green, thick and erect leaves
- Strong root activity
- Growth period of 110-130 d
- Harvest index of 0.6
- Yield potential 13-15 t/ha

1.3 Super rice strategy in China

Three-step strategy:

2000: 10.5t /ha

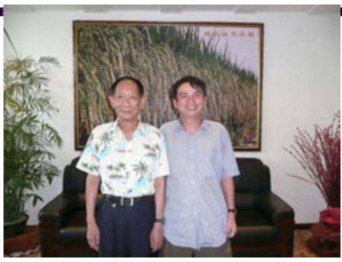
2005: 12t/ha

2015: 13.5t/ha

Theory and application of Super Hybrid Rice Improvement

- Gene discovery
- Molecular breeding
- Breeding by gene design

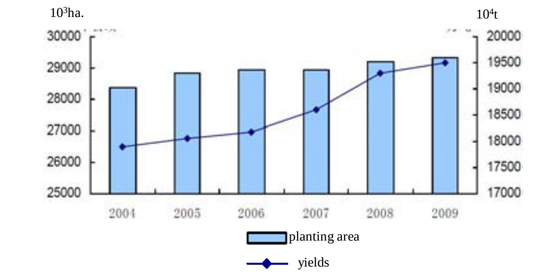
1.3 Super rice achievement in China



Rice average yield over 13.5/667ha in small plot sizes in 2011

1.4 Challenge of rice production and yield in China

◆The variation tendency of rice planting area and yields in China



Future demand for rice production and yield in China

Year	Total output ($\times10^9$ kg)[a]	Increase (%)[b]	Yield (kg/hm^2)	Increase (%)[b]
2010	217.5	19.18	6 885	16.3
2030	247.5	35.62	7 845	32.6

[a]Estimated based on the per capita rice consumption of 150 kg and the rice cropping area of 31.57 × 10^6 hm^2; [b]In comparison with 1995. Chen et al., 2007,JIPB

Rice production demand increased year by year!

Contents

◆Progress of rice breeding in China

◆**Discovery of yield genes in rice**

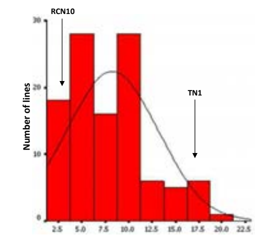
◆Breeding strategies for super hybird rice

2.1 Phenotype of the *ipa1* Mutant

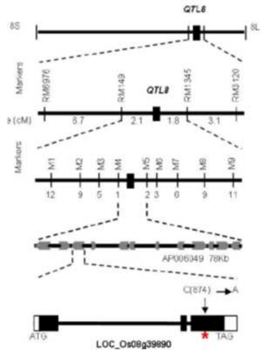
A：phenotype of *ipa1* and TN1; B：panicle of *ipa1;* C： panicle of TN1. Bar, 10cm。

Jiao et al., 2010,N.G.

Fine mapping and high resolution linkage analysis of *IPA1*

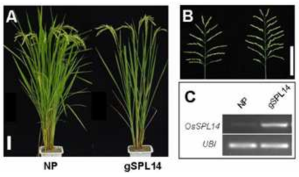


	interval	posit ion	range	LOD	A	H %
qRC No8	RM6976-RM1345	106. 7	98. 7-107. 2	11. 16	-5. 11 83	41. 45

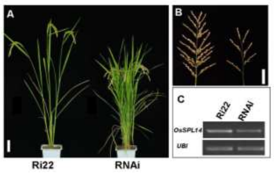


Jiao et al., 2010,N.G.

Functional analysis of *IPA1*



Confirmation of the *OsSPL14* function by overexpressing *OsSPL14* in Nipponbare

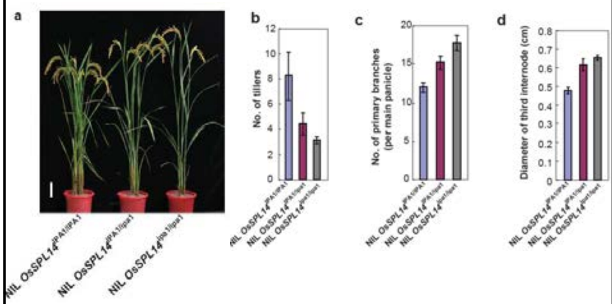


Confirmation of the OsSPL14 function by the down- regulation of OsSPL14 under the Ri22 background

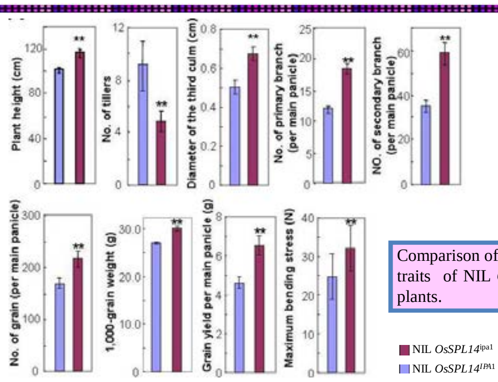
***OsSPL14* is the gene responsible for ideal plant architecture**

Jiao et al., 2010,N.G.

Phenotypic characterization of NIL OsSPL14$^{IPA1/ipa1}$ plants



Potential applications of *IPA1* in rice breeding



Comparison of agricultural traits of NIL *OsSPL14*^{ipa1} plants.

Jiao et al., 2010,N.G.

Potential applications of *IPA1* in rice breeding

- **Yield test in a paddy between XS11 and NILXS11 *OsSPL14*^{ipa1} plants**

Traits	XS11	XS11-*ipa1*
Number of panicles per plot	1972.7±39.1	1079.3±22.2
Number of grains per panicle	91.8±3.2	173.2±7.5
1,000-grain weight (g)	27.5±0.2	29.6±0.5
Theoretical yield per plot (kg)	4.98±0.10	5.53±0.11
Theoretical yield increase over XS11 (%)	-	11.1
Actual yield per plot (kg)	4.44±0.12	4.92±0.14
Actual yield increase over XS11 (%)	-	10.7

Note: The planting density was 19.98 cm × 23.31 cm, with one plant per hill. The area per plot was 6.67 m². Values are means ± s.d.

Jiao et al., 2010,N.G.

2.2 *DEP1* (dense and erect panicle-1)

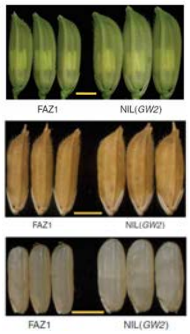
NIL-*dep1* NIL-*DEP1* NIL-*dep1* NIL-*DEP1*

The *DEP1* locus was mapped to chromosome 9. The dominant allele at the *DEP1* locus is a gain-of-function mutation causing truncation of a phosphatidylethanolamine-binding protein-like domain protein. The effect of this allele is to enhance meristematic activity, resulting in a reduced length of the inflorescence internode, an increased number of grains per panicle and grain yield.

Huang *et al., Nat. Genet.* 2009

2.3 *GW2 (grain width and weight 2)*

FAZ1 NIL(*GW2*)



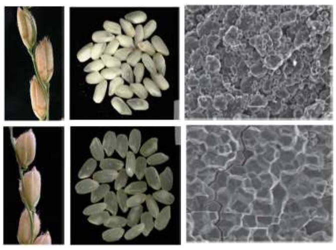
A new QTL that controls rice grain width and weight. Loss of GW2 function increased cell numbers, resulting in a larger (wider) spikelet hull, and it accelerated the grain milk filling rate, resulting in enhanced grain width, weight and yield.

Song et al., 2007, N.G.

2.4 *GIF1 (grain incomplete filling 1)*

Mutant

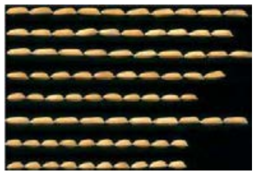
Wild-type



- Grain-filling is an important trait that contributes greatly to grain weight. The rice *GIF1* gene that encodes a cell-wall invertase required for carbon partitioning during early grain-filling
- Fine mapping with introgression lines revealed that the wild rice *GIF1* is responsible for grain weight reduction

Wang et al., 2008,N.G.

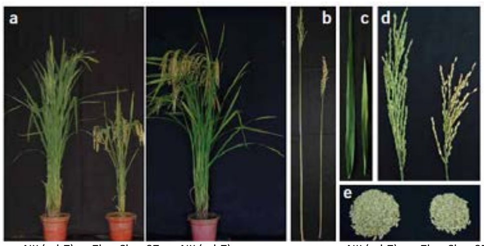
2.5 *GS3*（*Grain size 3*）



- The major QTL for grain length and weight and minor QTL for grain width and thickness in rice
- GS3 has at least four different alleles according to the coding sequence:
  GS3-1 (Zhenshan 97), GS3-2 (Nipponbare), GS3-3,(Minghui 63), GS3-4 (Chuan 7)

Fan et al., 2006, TAG; Mao et al., 2010, PNAS

2.6 *Ghd7* (*grains per panicle, plant height ,heading date*)



NIL(mh7) ZhenShan97 NIL(mh7) NIL(mh7) ZhenShan97

Ghd7 **has played crucial roles for increasing productivity and adaptability of rice globally.**

Xue et al., 2008, N.G.

Contents

◆Progress of rice breeding in China

◆Discovery of yield genes in rice

◆**Breeding strategies for super hybird rice**

3.1 Application of yield genes in rice breeding

Cultivars: Shengnong265, *DEP1* contained

***DEP1* has widely applied in Japonica plant-type breeding in Northern China**

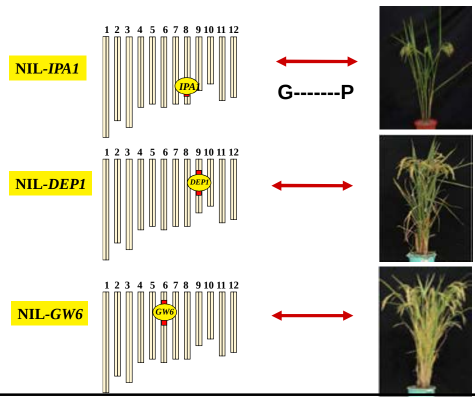
● Application of *IPA1* gene

Breeding nursery

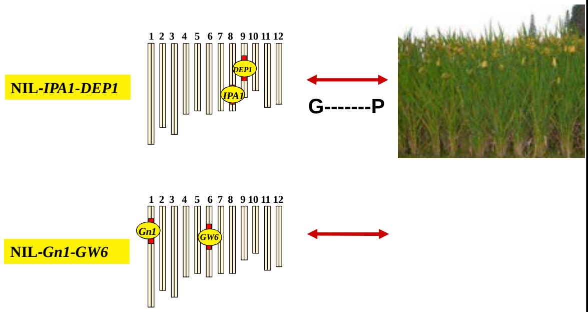
New breeding lines contains *IPA1* CK

***IPA1* as a key gene in rice ideal plant type**

◆Production analysis of single yield gene



◆ Production analysis of TWO yield genes



Construction of Genotype/Phenotype data pool

GP data pool

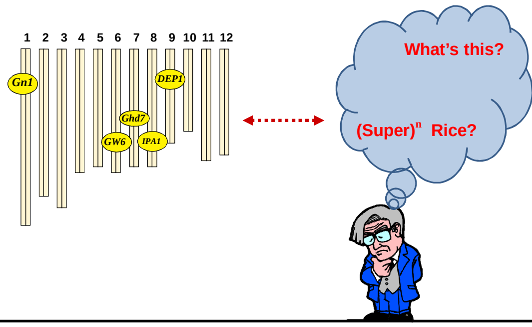
■ Design target genotypes using 9311 of *DEP1*、*Gn1*、*MOC1*、*gwp9*

Table 2 Design target genotypes using 9311

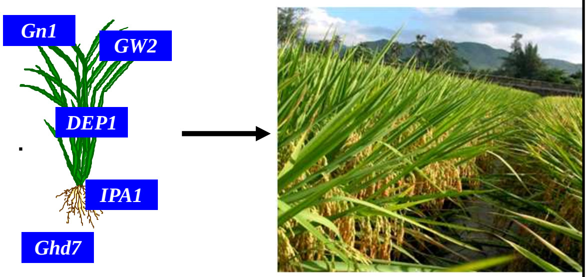
	FM/*MOC1*	FM/*Gn1*	FM/*DEP1*	FM/*gwp9*	FM/*gw6*	Yield (T/ha)
Min. Tillers		1	1	1	1	8.2
Max. Grain No.	1		1	1	1	11.2
Max. panicle dense	1	1		1	1	12.6
Max. grain weight/plant	1	1	1		1	11.9
Max. grain weight	1	1	1	1		10.6
Breeding by design						13.0
CSSL1			1	1	1	10.5
CSSL2	1	1		1		13.6
CSSL3	1			1	1	13.9

(9311- *DEP1*、*Gn1*、*MOC1*、*gwp9*; IR64- *DEP1*、*Gn1*、*MOC1*、*gwp9*)

◆ Production effect analysis of polygenic combination



● Application of multi-genes



Pyramid Breeding and application of high-yield lines

Model of Super Rice in the Future

Green Revolution (CK)
Taken in 1996

Super rice M1 in Yuannan in 2011

Super rice M2 in Hangzhou in 2011

3.2 Mid-type restorer of *indica/japonica* is more beneficial to increase yield in super hybrid rice

Development of medium type restore lines in subspecies differentiation

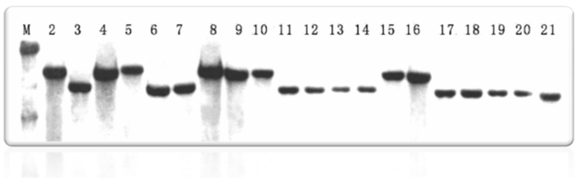
- **Medium type restorer lines in subspecies differentiation has become more and more applied in the hybrid rice breeding programs in China**
- **In the indica rice growing regions of China the breeders adopted the methodology of introgressing japonica blood into an indica rice background to develop *indicalinous* germplasms**
- **In the japonica rice growing regions introgressing indica blood into japonica rice background to develop *japonicalinous* germplasms**

Identified some indica-japonica markers related to morphological index

Indica-japonica markers and their locations

Chromosome	RFLP marker（28）	SSR marker（21）
1	RG101, RG345, RG462, RG472	RM23, RM259
2	RG171, RG256, RG322	RM29, RM250
3	RG482, RG96	RM16, RM251
4	RG214, RG620	RM226
5	RG207, RG474	RM13
6	RG64, RZ828	RM217
7	RG351, RG511	RM18, RM234, RM248
8	RG978, RZ562	RM25
9	RG553, RG570, RG667	RM245, RM205
10	RG752, RZ811	RM258, RM228
11	RG167	RM202
12	RG81, RG543, RG958	RM4, RM20, RM247

Using marker RG345 to check DH of indica/japonica

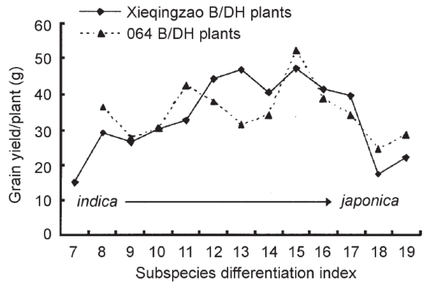


Note:
Marker: λ/HindⅢ; 2:Teqing; 3,02428; 4-5 and 8-10, *Indica* cultivars; 6-7, *Japonica* cultivars; 11-21,Lines of DH population

Coefficient between markers and morphological index

Canonical variable	canonical correlation coefficient R	χ^2 value χ^2	Degree of freedom DF	significant level P
1	0.8744	399.02	162	<0.001
2	0.7255	249.02	130	<0.001
3	0.6629	171.83	100	<0.001
4	0.5909	112.81	72	0.002
5	0.5727	69.58	46	0.014
6	0.5180	30.31	22	0.111
7	0.0002	-1.8E-06	0	1

Relationship between subspecies differentiation index of the paternal parents and grain yield per plant of their F1 hybrids



Chen et al., 2007,JIPB

Improvement strategy for mid-type restorers

- To breed mid-type restorer using multi-backcross between indica and japonica.
- Morph-index: 12-16，japonica marker index: 0.3-0.6.
- Successfully gained restorers: Zhonghui8006 and Zhonghui111, their marker index: 0.25 and 0.39.

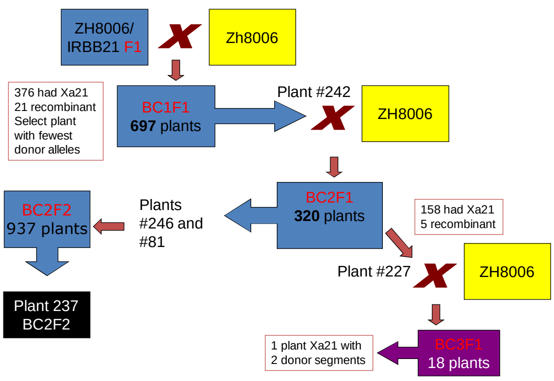
Excellent restorer Zhonghui8006

ZH8006

Xa4+xa5+xa13+Xa21

- New variety protection NA001233E
- Variety certification：
  Guodao1（Zhong9A/Zhonghui8006）
  Guodao3（Zhong8A/Zhonghui8006）
  II-you8006（II-32A/Zhonghui8006）
  Guodao6（Neixiang2A/Zhonghui8006）
  Tianyou6（TianfengA/Zhonghui8006）

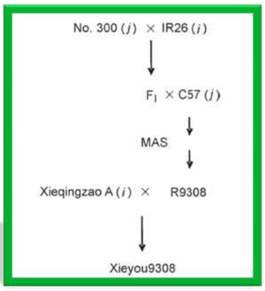
Selection for ZH8006+*Xa21*



Super rice restorer with multi-genes

Restorer	Heading date/d	Spikelet /panicle	setting percentage/%	1000-grains weight/g	Genes
Zhonghui8006	90	176	84	27	*Xa4+xa5+xa13+Xa21*
Zhonghui111	87	178	87	27	*xa5+Xa21+Pi25*
Zhonghui8015	90	154	89	31	*Pi25+Xa21*
Zhonghui161	92	163	88	26	*Pib+Pita+Xa4+xa13+wx*
Zhongzu14	130	138	77.1	21	*xa5+ Pi25 +Bph15*
Zhongjia A	66	97	0	24	*xa5+Xa23*
Zhongjin 2A	76	103	0	25	*Pi1 ＋Pi2 ＋Pi33*
Zhongjiazao17	85	125	90	27	*xa5+Pi25*
Zhonghui333	90	145	87	26	*Xa4 + Xa21*

Medium type restorer line R9308 and its super hybrid Xieyou 9308



Field performance of Xieyou 9308 with harmonious plant type, in Xinchang, Zhejiang Province, China

25% japonica genetic components in R9308
12.5% japonica genetic components in Xieyou 9308

Conclusion

- **Great success on rice production was achieved via semi-dwarf breeding, Heterosis utilization and super rice project.**
- **A series of rice germplasm and yield genes, *IPA1*, *DEP1*, have been discovered and cloned.**
- **New breeding strategies, including breeding by gene design, pyramiding breeding and mid-type restorer selection, has been used in super hybrid rice breeding**

Acknowledgement:

Chinese National Rice Research Institute:
Prof. Shihua Cheng,
Prof. Longbiao Guo,
Prof. Dali Zeng,
Prof. Liyong Cao
Prof. Guanghang Zhang,
Jiang Hu, Zhengyu Gao et al.

Chinese Academy of Sciences, Institute of Genetics and Developmental Biology:
Prof. Jiayang Li
Prof. Xiangdong Fu

Nagoya University:
Prof. M.Masutoka
Prof. M.Ashikari

Grants: