## **RICE INDUSTRY DEVELOPMENT AND THE CONTRIBUTION OF HYBRID RICE IN CHINA**

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## Content

## > Overview

- > History of hybrid rice in china
- Progress in HR development
- Constraints in HR development
- Reasons for the success of HR
- > Prospect

## **Overview: Rice Production**

## 1) Area & yield



Chinese rice planting area and yield in 2007-2019.

Planting area continues to decrease: 29.69 million ha in 2019, 1.6% decline compare to 2018)
 Average yield: 7.06 t/ha in 2019, highest in Chinese history
 Total output: Stable at 200+ million tons for nine consecutive years

## 2) Import & export



Market prices and rice planting income continues to fall

□ Import continues to decrease: highest at 4.03 million ton in 2017, and decrease due to fall of domestic rice market prices

**Export continues to expand: 2.75 million ton in 2019, 31.5% increase compare to 2018** 

## 3) Problems in rice industry development

#### Cost of rice grain production in the Middle Reaches of the Yangtze River.

Area	Total cost/(Yuan·hm <sup>-2)</sup>		Labor cost /(Yuan·person <sup>-1</sup> d <sup>-1</sup> )		Land rent /(Yuan·hm <sup>-2</sup> )		Urea price/(Yuan·t <sup>-1</sup> )	
	2017	2018	2017	2018	2017	2018	2017	2018
Hunan Province	14101.5	14640	133.2	137.8	4672.5	4740.0	2014	2120
Jiangxi Province	16341.0	16851	128.9	141.6	6906.0	6937.5	1970	2222
Henan Province	13284.0	14154	105.5	117.6	4647.0	4965.0	3808 <sup>1)</sup>	4188 <sup>1)</sup>
Hubei Province	10036.5	10755	134.1	147.5	5379.0	5791.5	1754	1988
the Middle	13441.5	14100	125.4	136.1	5401.5	5608.5	1912 <sup>2)</sup>	2110 <sup>2)</sup>
Reaches of the Yangtze River								

#### Food security is facing severe challenges

+ Production efficiency is low, and farmers' enthusiasm generally declines

- **Relatively small amount of investment**
- 🕈 Unbalanced regional funding
- Weakening of social services in agriculture

## 4) Hybrid Rice Contribution

Basic Chinese situation
population: about 1.4 billion
population rate in the world: 22%
arable land rate in the world: 7%

China became self-sufficient in basic food for the first time in modern history

Tremendous accomplishment in last century, the innovation of HYBRID RICE, made by Prof. Yuan Longping

China is the first country to commercialize hybrid rice

Yearly area: about 17.6 mil. ha, 54% of total rice area

Yield: 7.5t/ha of HR with 20% yield advantage over inbred

Yearly production of HR: about 120 Mil. tons, about 57.5% of the total rice production





## 1. History of hybrid rice in china

## 1) Three-line HR Development

In 1964, Prof. L.P. Yuan initiated HR research in China.

In November 1970, a pollen abortive wild rice (WA) discovered.

In 1972, Prof. Yuan developed the first CMS line: Erjiunan 1A.

In 1974, The first rice hybrid Nanyou No.2 developed by Prof. Yuan.

In 1980, Shanyou 63 developed by Prof. Xie, the largest one of growth area in 1980's



**Completion of the three-line hybrid rice system within 10 years** 

## 2) Two-line HR Development

□ In 1973, the first natural male sterile rice plant discovered by Mr. S.M. Shi. A new way to utilize the heterosis in HR by two-line system with PTGMS.

☐ In 1986, the strategic breeding approach by Prof. Yuan: on the methodology from three-line, two-line to one-line, and on the level of heterosis from inter-varieties, inter-subspecific to distance hybrids.

Bw 1987 to 1995, as the principal scientist, Prof. Yuan developed a comprehensive array of theories of "two-line system hybrid rice"



# The fertility conversion theory and mode of PTSG lines established by Prof. Yuan



The fertility conversion mode of PTSG sterile lines



## The success of two-line hybrid rice research was declared in 1995.





# 2. Progress in HR development

## 1) The stage of rice development



◆ Before 1964 – T.V. stage: about 2 t/ha
◆ 1965 ~ 1976 - SSD stage: ≈about 3.5 t/ha
◆ 1976 to now - HR stage: ≈ 5~6.3 t/ha
The average yield of HR in 1990s:7.5 t/ha

## 2) Development of super HR

## Super rice program launched by MOA of Chinese in 1996 Yield standard of the Super Rice in China

Dhaaa	Hy	Yield			
Phase	First cropping	Second cropping	Single cropping	increase(%)	
1996 level	7.50	8.25	7.50	0	
Phase I	9.75	10.50	9.75	More than 20%	
1996-2000	9.75	10.00	5.15		
Phase II	11 25	12 00	11 25	More than 10%	
2001-2005	11.20	12.00	11.20		
Phase III	1	1	13 50	More than 60%	
2010-2015	1	Ι	13.30		
Phase IV		· · · · · · · · · · · · · · · · · · ·	15.00	Moro than 100%	
2015-2020			15.00		

\* Tons/ha at 2 sites with 6.7 hectares in each site in 2 consecutive years.

## Super HR Program proposed by Prof. Yuan

## Morphological Improvement



## **D** Raising Heterosis Level

The heterosis utilization theory of indicajaponica subspecies proposed by Prof. Yuan



Indica (I) / japonica (JP) / Javanica (JV)

Heterosis in Different kind of Rice Hybrids

![](_page_14_Figure_5.jpeg)

## Super hybrid rice breeding theory and strategy

- > To be the higher plant based on drawf gene
- > To develop the nearer parent from far genetic distance relationship
- Use of dominance combines with super-dominance
- Panicle to be between moderate and large
- Higher ratio of grain to leaf
- Grain plumpness based on well grain filling parents
- > Achieve good grain quality based on Javanica
- > To be well ecological adaptation.

![](_page_15_Picture_9.jpeg)

![](_page_15_Picture_10.jpeg)

## **Utilize the Biotechnology**

I: Utilization of favorable genes from wild rice

![](_page_16_Figure_2.jpeg)

![](_page_16_Picture_3.jpeg)

II. Using Genomic DNA From Barnyard Grass to Create New Source of Rice

## A draft sequence of super hybrid rice parents completed firstly in the world

#### THE RICE GENOME

#### A Draft Sequence of the Rice Genome (*Oryza sativa* L. ssp. *indica*)

Jun Yu,<sup>1,2,3,4\*</sup> Songnian Hu,<sup>1\*</sup> Jun Wang,<sup>1,2,5\*</sup> Gane Ka-Shu Wong, 1,2,4\* Songgang Li, 1,5 Bin Liu, 1 Yajun Deng, 1,6 Li Dai,<sup>1</sup> Yan Zhou,<sup>2,7</sup> Xiuqing Zhang,<sup>1,3</sup> Mengliang Cao,<sup>8</sup> Jing Liu,<sup>2</sup> liandong Sun,<sup>1</sup> Jiabin Tang,<sup>1,3</sup> Yanjiong Chen,<sup>1,6</sup> Xiaobing Huang,<sup>1</sup> Wei Lin,<sup>2</sup> Chen Ye,<sup>1</sup> Wei Tong,<sup>1</sup> Lijuan Cong,<sup>1</sup> Jianing Geng,<sup>1</sup> Yujun Han,<sup>1</sup> Lin Li,<sup>1</sup> Wei Li,<sup>1,9</sup> Guangqiang Hu,<sup>1</sup> Xiangang Huang,<sup>1</sup> Wenjie Li,<sup>1</sup> Jian Li,<sup>1</sup> Zhanwei Liu,<sup>1</sup> Long Li,<sup>1</sup> Jianping Liu,<sup>1</sup> Qiuhui Qi,<sup>1</sup> Jinsong Liu,<sup>1</sup> Li Li,<sup>1</sup> Tao Li,<sup>1</sup> Xuegang Wang,<sup>1</sup> Hong Lu,<sup>1</sup> Tingting Wu,<sup>1</sup> Miao Zhu,<sup>1</sup> Peixiang Ni,<sup>1</sup> Hua Han,<sup>1</sup> Wei Dong,<sup>1,3</sup> Xiaoyu Ren,<sup>1</sup> Xiaoli Feng, 1,3 Peng Cui, 1 Xianran Li, 1 Hao Wang, 1 Xin Xu, 1 Wenxue Zhai,<sup>3</sup> Zhao Xu,<sup>1</sup> Jinsong Zhang,<sup>3</sup> Sijie He,<sup>3</sup> lianguo Zhang,<sup>1</sup> lichen Xu,<sup>3</sup> Kunlin Zhang,<sup>1,5</sup> Xianwu Zheng,<sup>3</sup> Jianhai Dong,<sup>2</sup> Wanyong Zeng,<sup>3</sup> Lin Tao,<sup>2</sup> Jia Ye,<sup>2</sup> Jun Tan,<sup>2</sup> Xide Ren,<sup>1</sup> Xuewei Chen,<sup>3</sup> Jun He,<sup>2</sup> Daofeng Liu,<sup>3</sup> Wei Tian,<sup>2,6</sup> Chaoguang Tian,<sup>1</sup> Hongai Xia,<sup>1</sup> Oiyu Bao,<sup>1</sup> Gang Li,<sup>1</sup> Hui Gao,<sup>1</sup> Ting Cao,<sup>1</sup> Juan Wang,<sup>1</sup> Wenming Zhao,<sup>1</sup> Ping Li,<sup>3</sup> Wei Chen,<sup>1</sup> Xudong Wang,<sup>3</sup> Yong Zhang,<sup>1,5</sup> Jianfei Hu,<sup>1,5</sup> Jing Wang,<sup>1,5</sup> Song Liu,<sup>1</sup> Jian Yang,<sup>1</sup> Guangyu Zhang,<sup>1</sup> Yuqing Xiong,<sup>1</sup> Zhijie Li,<sup>1</sup> Long Mao.<sup>3</sup> Chengshu Zhou.<sup>8</sup> Zhen Zhu.<sup>3</sup> Runsheng Chen.<sup>1,9</sup> Bailin Hao,<sup>2,10</sup> Weimou Zheng,<sup>1,10</sup> Shouyi Chen,<sup>3</sup> Wei Guo,<sup>11</sup> Guojie Li, 12 Siqi Liu, 1,2 Ming Tao, 1,2 Jian Wang, 1,2 Lihuang Zhu, 3+

Longping Yuan,8+ Huanming Yang<sup>1,2,3+</sup>

We have produced a draft sequence of the rice genome for the most widely cultivated subspecies in China, Orga sativa L spp. indica, by whole-genome shotgun sequencing. The genome was 466 megabases in size, with an estimated 46.022 to 55.515 genes. Functional coverage in the assembled sequences was and javanica, two other commonly cultivated subspecies. We have also produced a lowcoverage draft sequence for PA64s. A preliminary assembly and analysis on a subset of this sequence was published in the Chinese Science Bulletin (21). Our discussion will focus largely on the genome landscape of rice, how it differs from that of the other sequenced plant, A. thaliana, and how both plant genomes differ from that of the human. We will show that rice genes exhibit a gradient in GC content, codon usage, and amino acid usage. This compositional gradient reflects a unique phenomenon in the evolutionary history of rice, and perhaps all monocot plants, but not eudicot plants. As a result, about one-half of the predicted rice genes have no obvious homolog in A. thaliana, whereas the other half is almost a replica of the A. thaliana gene set.

The entire rice genome sequence can be downloaded from our Web site at http://btn. genomics.org.cn/rice. Following our announcement of the rice genome sequence at the annual Plant, Animal and Microbe Genomes (PAG X) conference, in San Diego, during the ensuing period from 14 January to 2 March 2002, this sequence was downloaded 556 times, and the BLAST search facilities were used 7008 times by 343 individuals. This sequence has also been deposited at the DNA Data Bank of Japan/European Molecular Biology Laboratory/GenBank under the project accession number AAAA00000000. The version described in this paper is AAAA01000000.

Experimental design. The rice genome project at the Beijing Genomics Institute has been designed in two stages. This is a report

![](_page_17_Picture_9.jpeg)

It promotes the understanding of rice heterosis at the genomics level and molecular breeding applications in HR

# Major breakthroughs were made in molecular mechanism research of rice heterosis in 2009

Using gene chip technology to carry out the super hybrid rice LYP9 and its parent transcriptome studies, identify potential associated with super hybrid rice heterosis functional genes.

"Cell" commented: a new starting line to elucidate the molecular mechanisms of rice heterosis

# <text>

#### A transcriptomic analysis of superhybrid rice LYP9 and its parents

Gang Wei<sup>k,b,1</sup> Yong Tao<sup>5,b,1</sup>, Guochen Liur<sup>6,4</sup>, Chen Chen<sup>6</sup>, Renyuan Luo<sup>6</sup>, Hongai Xia<sup>4</sup>, Olang Gan<sup>3</sup>b, Hajan Zeng<sup>5</sup>, Zhike Lui<sup>4</sup>, Yung Ing Han<sup>5</sup>, Xiaobing Li<sup>4</sup>, Guisheng Song<sup>4</sup>, Hong Li<sup>4</sup>, Xiaojang Peng<sup>4</sup>, Dayong Li<sup>4</sup>, Honglin Xu<sup>4</sup>, Xiaoli Wei<sup>4</sup>, Mengliang Cao<sup>4</sup>, Huafeng Deng<sup>4</sup>, Yeyun Xin<sup>4</sup>, Xiqin Fu<sup>4</sup>, Longping Yuan<sup>4,2</sup>, Jun Yu<sup>4,2</sup>, Zhen Zhu<sup>4,2</sup>, and Lihuang Zhu<sup>4,2</sup>

State Key Laboratory of Plant Genomics and National Center for Plant Gene Research, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing 100101, China: Vorduate School of the Chinese Academy of Sciences, Beijing 100303, China: Key Laboratory of Genomes Sciences and Information, Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing 101300, China: "College of Life Sciences, Hebei Agricultural University, Baoding 07100), China; and "National Hybrid Rice Research and Developmenter Center, Changhat 410125, China:

This contribution is part of the special series of Inaugural Articles by members of the National Academy of Sciences elected in 2006.

Contributed by Longping Yuan, March 13, 2009 (sent for review February 13, 2007)

By using a whole-genome oligonucleotide microarray, designed based on known and predicted infact rise genes, we investigated transcriptome profiles in developing leaves and panicles of suphybrid rise 1799 and its parental cultures 33-17 and A646. We detected 22,266 expressed genes suit of 36.2526 total genes suit stages, fing lowes at hooting, heading, movering, and Hiling stages, and panicles at Hilling stage. Clustering results showed that the F1 hybrid expression profiles resembled those of its parental lines more than that which lise between the Q parental lines. Our di 3226 genes (DG). As we divided DG into those between the parents (DGs) and between the Nitrid and its parents parents (DGs) and between the Nitrid and its parents (DGs). variety, after we sequenced the 2 parental genomes (11, 12). Two-dimensional electrophoresis analysis anong 937-11, Pdo4x, and L7P9 revealed significant numbers of different embryo protein spots, many of which were shown to display mirrored relationships between parents and the first fluid generations isolation of the strain strain strain strain strain strain isolation of the strain strain strain strain strain strain biological processes including nutrient reservoir, response to stores, and metabolism. Among these embryos, most of the storage proteins exhibit overdominance and stress-induced protion deplay additivity (14). We also carried out transcriptione based (15–17) and hybridization-based methods (18). We now

## The authoritative life science publication *Cell* introduce and highly praised in its "*Leading Edge*" column

shows that differentially expressed genes are enriched at known quantitative trait loci (QTLs), suggesting that this list might aid in the discovery of genes that underlie important growth characteristics, such as starch content, grain size, and flowering time. Further analysis reveals that the genes most commonly associated with differential expression in the hybrid include those involved in energy and carbohydrate metabolism. In addition, genes that might regulate epigenetic phenomena, such as methylation and acetylation, are well represented. Although hybrid vigor is undoubtedly very complex, these findings provide a starting point for uncovering its mechanistic basis in one of the world's most important food croos.

G. Wei et al. (2009). Proc. Natl. Acad. Sci. USA. Published online April 16, 2009. 10.1073/pnas.0902340106.

![](_page_18_Picture_14.jpeg)

Gene expression in *LYP9* hybrid rice differs markedly from its parent strains. Image courtesy of L. Zhu.

## **Molecular marker assisted selection (MAS)**

Identified and mapping genes of QTL (yld1.1 and yld2.1) from wild rice (O.r ufipogon) and published in "Nature"; Developed an elite restorer lines and hybrid rice combinations with yield increase of 20%, such as Y liang-you 7

class

PM

6.99

6.90

Allele

effect

1.22

1.14

% of V/64

18.26

17.07

![](_page_19_Figure_2.jpeg)

Nature 384:223-224

### **Favorable genes from barnyard grass transferred and** developed specific parents for super hybrid rice

![](_page_20_Picture_1.jpeg)

![](_page_20_Picture_2.jpeg)

J. Proteome Res., 2007, 6:1354–1363

Journal of Integrative Plant Biology Formerly Acta Botanica Sinica 2005, 47 (12): 1485-1492 http://www.black.well-synergy.com http://www.chineseplantscience.com

1997; Bijoya et al. 1999; Yan et al. 2002) and several

through protoplast fusion (Kisaka et al. 1998; Jelodar

produce hybrids between rice and its distant relatives

We have established a new and simple procedure, termed the "Spike-Stalk Injection Method" (SIM), which

is a modified technique based on the procedure invented

has just undergone moiosis, exogenous DNA is injected

just under the panicle base. After STVI treatment, in the

ranging from 10<sup>-5</sup> to 10<sup>-1</sup> (Zhao et al. 1998). This

method has been used to generate new germplasm

species, such as wild rice, maize, sorghum, Hohinochioa

first generation (D<sub>1</sub>), variants usually occur at a rate

#### DNA Polymorphism Among Yewei B, V20B, and Oryza minuta J. S. Presl. ex C. B. Presl.

Bing-Ran ZHAO<sup>4</sup>, Quan-Hus XING<sup>2</sup>, Hong-Ai XIA<sup>2</sup>, He-Hus YANG<sup>3</sup>, De-Min JIN<sup>2</sup>, Xia LIU<sup>3</sup>, Song-Wen WANG<sup>19</sup>, Bin WANG<sup>2</sup> and Long-Ping YUAN<sup>19</sup> (1. Ching National Ibbrid Rice & & D Center, Charasha 410125, China

2. Justiture of Genetics and Developmental Biology, the Chinese Academy of Sciences, Beijing 100010, China 3. Trantin Agriculture College, Tianjin 300384, China)

Abstract: The new cytoplasmic male sterile (CMS) line Yewei A and its maintainer line Yewei B, with better agronomic characteristics, have been developed from a mutant of V20B (a rice maintainer line) through transformation of genomic DNA of wild rice (Oryza minuta J. S. Presl. ex C. B. Presl.). Analysis of molecular markers. DNA sequences, and Southern blot revealed that high DNA polymorphism exists between the mutant and its recentor, indicating that the special DNA fragment from O, mouta may be integrated into the genome of Yewei B. Therefore, transformation of genomic DNA from distant relatives to the plant of a target receptor may open an avenue for creating a new rice germplasm Key words: DNA sequence, genomic ENA introduction, gemplasm; molecular markers; wild rice.

Rice (Oryza sativa L.) is the most important staple food for human consumption. If ybrid rice has made a intergeneric somatic hybrids have been generated considerable contribution to maintaining basic nutritional levels of the Chinese people during the past 25 years. et al. 1999; Liu et al. 1999). However, it is difficult to Compared with cultivated rice, wild rice possesses higher genetic diversity (Lu 1999; Sun et al. 2002). using these methods. and the yield-enhancing genes from a wild rice species. namely Orvza rulipogon, have been demonstrated to improve rice yield greatly (Xiao et al. 1996). In order to develop new rice cultivars that are expected to have by Pens et al. (1987). When the recipient plant of rice higher yield potential, durable resistance to diseases and insects, and strong tolerance to abiotic stresses, it is into the uppermost internode of a stem, at the position important to enrich the gene reservoir hy creating a new gemplasm (Yuan 1997).

Genes with conditioned resistance to disease and insects, as well as cytoplasmic male sterility, have been transferred from wild species to rice cultivars through through transformation of genomic DNAs of distant protoplast fusion and a variety of hybridization methods in combination with embryo rescue (Brar and Khush erusgalli, and Panicum maximum For example, when

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![](_page_20_Picture_16.jpeg)

barnyard RB207 R207 grass

## C4 rice: get transgenic lines to be used to HR breeding

![](_page_21_Figure_1.jpeg)

Line	Transfrom genes	Compared with CK production increase(%)		
Fengyou299	СК	-		
FengA/09T005	PEPC+PPDK	8.60%		
FengA/09T009	MDH+ME	1.86%		
FengA/09T015	PEPC+PPDKM+D H+ME	3.78%		

![](_page_21_Figure_3.jpeg)

## 3) HR seed production

★ Its difficult to utilize heterosis in rice Dr. J.N.Rutger — Earlirose male-sterile plants averaged 2.4% open-pollinated seed-set From 《Innovative approaches to rice breeding》

The key problem for the HR commercialization
 lower pollen load
 Panicle is not exerted out easily
 Out-crossing rate is very low

## The technology of Hybrid seed production Optimized

![](_page_23_Picture_1.jpeg)

- The average yield in China 274.5kg/ha in 1975
   1.66 t/ha in 1985
   2.25 t/ha in 1990
- Vield on a large scale3~4.5 t/ha in 1990s
- The highest record yield
   7.39 t/ha (0.113 ha) ,Hunan
   China in 1993

![](_page_23_Figure_5.jpeg)

Commercial hybrid rice yield and hybrid rice seed yield in China (1976-2008)

## A new way for hybrid rice seed production: mechanized techniques

![](_page_24_Picture_1.jpeg)

outcrossing rate: 45%

Ratio of R:A 6~8:40~80 hills

Yield of seed production of HR:2.7-3.0t/hm<sup>2</sup>

The pollination, GA spraying and the ration of A:R lines by the unmanned aerial vehicle (UAV)

## 4) Field management of HR

Chinese hybrid rice agronomists developed the systematic methods for high-yielding field management:

"3-ding"Cultivation Technology for Super Hybrid Rice
 Rice Precise and Quantitative Cultivation Technique for
 High Yield

The Improved System of Rice Intensification (MSRI)
 Nitrogen-efficiency and lodging resistance cultivation technique

## 3. Constraints in HR development

The Area of HR at a Standstill for Years (17.6 million ha in 1991)

Lack of japonica hybrid rice with strong heterosis (0.1 mil ha, only 1%-2% in China).

Great yield gap for super hybrid rice (about 5.16 t/ha).

Lack of the breakthrough combinations but HR varieties released yearly with about 400.

Need of the breakthrough for the mechanized technology of HR seed production.

## 4. Main Reasons for the success of HR

- Strong Govt. Leadership: be committed, supportive, well organized to HR R and D.
- High efficient organization and coordination: Leading Group, Consultancy Committee, frequent conferences;
- Resources and techniques: qualified, distributive and shared
- Technology generation and dissemination: R and D cooperation networks, Training, yield trials, on-farm demonstration, study tour and propaganda

## **5. Prospect: HR development in the future** A new idea of super high yield breeding proposed by Prof. L.P. Yuan in 2009

![](_page_28_Figure_1.jpeg)

## New approach for high yield of HR

**Grain yield = Harvest Index X Biomass** 

Nowadays the harvest index (HI) is much higher (above 0.5). Further lifting of rice yield ceiling should rely on increasing biomass because further improvement of HI is quite limited. From view point of morphology,

Further raising rice yield ceiling should rely on increasing biomass.

Increasing plant height is an effective and feasible way to increase biomass

## 1) Develop super hybrid rice to achieve higher yield

![](_page_30_Figure_1.jpeg)

#### From 100 mu to large-scale super high-yield development

![](_page_31_Picture_1.jpeg)

from 2014 to 2016: 12 single-season 100-mu demonstration plots reached 1,000 kg, 4 of the 1,000-mu plots reached 900 kg, and 5 of the 10,000-mu plots reached 800 kg.

Results show that the super hybrid rice can achieve the goal of high yield in large area.

## Chinese rice yield has been greatly improved since the Super Rice Project

![](_page_32_Figure_1.jpeg)

## 2) Development of 3<sup>rd</sup> generation HR

![](_page_33_Figure_1.jpeg)

The genetically engineered male sterile line bred through genetic engineering of ordinary genic male sterile rice not only has the advantages of stable fertility of three-line sterile line and free combination of two-line sterile line, but also overcomes the limitation of combination of three-line sterile lines and the shortcomings of two-line sterile lines and the low reproductive yield. (Yuan Longping, Science Bulletin, 2016)

## Stronger heterosis and higher yield

![](_page_34_Picture_1.jpeg)

Experts including Academician Wan, Xie Hua'an,& Qian Qian measured the Yield with 1046.3 kg/mu(2020.10.21). Yield: 119.8 Kg/d/h Academician Xie Hua'an e again measured the yield of the thirdgeneration hybrid rice to 911.7 kg/mu, and the double-season yield per mu reached 1530.67 kg (2021.11.1).

#### 3) Develop Saline-alkali-tolerant rice to ensure food security

L.P.Yuan : The combination of heterosis and saline-alkali-tolerant gene has great potential

![](_page_35_Picture_2.jpeg)

Academician Yuan proposed to use heterosis to cultivate salinity-tolerant rice, and he has two trump cards

The theoretical yield of Qingdao rice is 620.95kg (2017) Super 1000 yielded 802.9kg per mu in Nantong, Jiangsu (2020)

Academician Yuan specifically proposed that in 5 to 8 years, saline-alkalitolerant rice should strive to develop to 100 million mu, with a yield of more than 300 kg per mu, and achieve the goal of increasing grain output by 30 billion kg per year, which is equivalent to the total annual grain output of Hunan Province, and can feed an additional 100 million people.

# best variety with the package cultivating method can achieve the goal of 30 billion kilograms

![](_page_36_Picture_1.jpeg)

Comprehensive supporting technologies for saline-alkali-tolerant rice: microbial fertilizer adjusts acidity, reduces alkalinity, and dissolves salt to improve soil + plant induces resistance to increase salinity tolerance + highyield cultivation solutions to increase yield

![](_page_37_Picture_0.jpeg)

![](_page_37_Picture_1.jpeg)

For the benefit of the people in the whole world, our Center and I are well prepared to help other countries to develop hybrid rice ----- L.P. Yuan

# Thank you !