

The Situation and Challenge of Breeding Major Crops in Northeast China and Advance in Breeding Molecular Rice with Complex Quantitative Traits

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Abstract

China is an agricultural country. Rice, maize and soybean are major crops for national economy and people's livelihood. These three crops are also the pillar industry in northeast China, especially in Heilongjiang province.

1. The situation and challenge of breeding the three major crops in northeast China

Compared with other major soybean production countries, such as USA, Brazil and Argentina, China's soybean production reached highest total yield of 17.2 Mt in 2003 and drop to 14.02 Mt with yield per unit of 1.802 t/ha in 2017, accounting for about 11.8% yield of USA. Heilongjiang is an advantageous industrial area of soybean production, but recently soybean production has been much affected by industrial policy and comparative profit. At present, China has shifted from export country since 1996 into an import country owing to larger quantity of requirement. In 2017, major sources of China soybean import were Brazil (53.31%) and USA (34.39%), and other countries such as Argentina (6.89%, Uruguay (2.69%), and Canada (2.14%). In the soybean breeding history of China, Zhonghuang 13 is quite noteworthy. It won the First Prize of National Sc-Tech Progress and reached 6.7 Mha area up to 2017, holding the record of the largest soybean planting area in China (Fig. 1). The biggest challenges of soybean breeding in China are improving yield per unit and decreasing production cost.

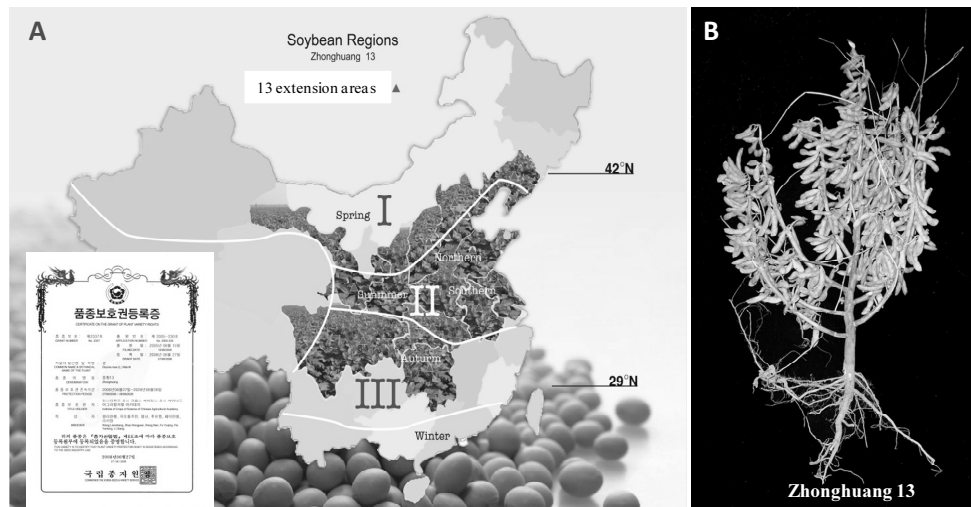


Fig. 1 Extension areas of Zhonghuang 13 (A) and its plant (B)

China has almost same maize production area (39 M ha) as USA but with much low yield per unit (396.51 vs. 730.69 kg/0.067ha). Maize was mainly used for feeding animals (59%), industrial consumption (31%), and human food (9%) in China (2016-2017). Heilongjiang plays an important role in maize production in China with planting area of 6.44 million ha, ranking the first in China and accounting for 14.2% of the total maize area of China. In 2017, maize planting area in Heilongjiang dropped by 0.71 million M ha to 40 million ha due to adjustment of industrial policy through reducing non-dominant planting regions of the third, fourth, and fifth temperate zone. Maize production ability is far behind home demand, with an estimation of 20 Mt annual shortfall in 2020. Three varieties including late maturing Jingke 968 (Fig. 2), medium maturing Xianyu 335 and early maturing Demeiya 1 occupied areas of 1.31, 0.90 and 0.53 million ha respectively in northeast China. Early-maturing, density-tolerance, ideal plant type, stress tolerance, quick dehydration, high and stable yield, suitable for mechanized harvesting will be breeding directions in future.

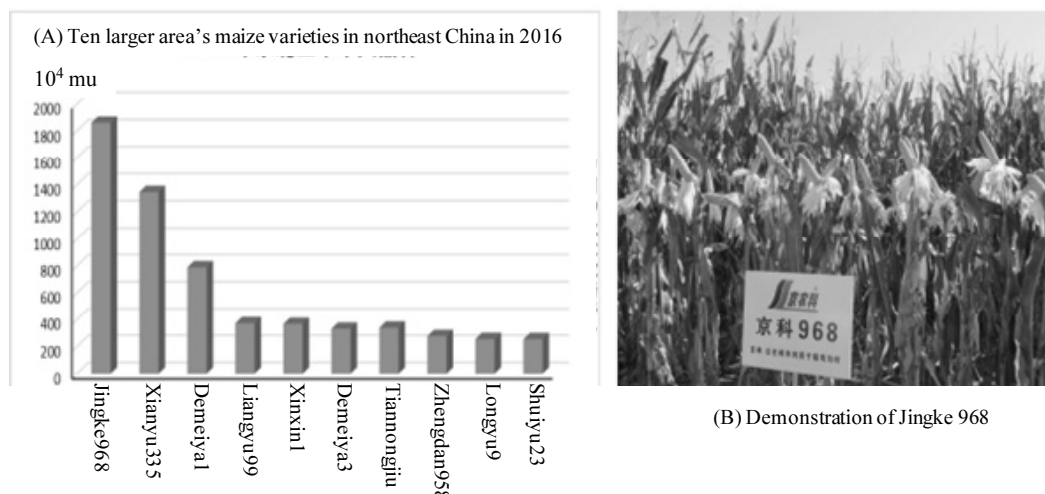


Fig. 2 Ten maize varieties in northeast China (A) and demonstration of Jingke 968 (B)

Heilongjiang is the most important commodity grain base in China, being more than 70 million mu with an average yield of 468.2 kg in 2017, accounting for 50% of japonica plant area of China. Around 90% varieties reach high quality rice II (national standard), 98% rice were used for food and 75% for export. Recently rice breeders overcame the key bottlenecks (low yield and susceptible to blast and cold stress) for rice breeding in cold zone by integrating seedling vigor of indica into early japonica rice (one-V) and improving resistance to blast, cold stress and lodging (three-R). Meanwhile, selection techniques including improving plant height, grain number per panicle, and grain weight (three-I) suitably, and decreasing panicle number (one-D) as well as good eating, good appearance and good milling qualities (three-G) suitably were applied. A batch of super rice varieties such as Longgeng 31, Longgeng 25, Longgeng 21, and Longgeng 39 has been bred with high and stable yield, covering 70% suitable area in Helongjiang. Among them, Longgeng 31 occupied 16.923 million mu in 2013, which made a new record of the extension area of single variety annually, thus breaking the Japanese variety's (Kongyu 131) dominance in Heilongjiang. Nowadays, more and more breeding organizations or private enterprises jump to Heilongjiang for rice breeding under attraction of industrial profit.

Table 1. Performance of Longgeng 31 in yield, grain quality and disease and cold resistance

Yield test	Regional yield test		Production test		Two years super rice test (kg/Mu)	
	Yield per unit (kg/Mu)	Yield gain (%)	Yield per unit (kg/Mu)	Yield gain (%)		
	544.4	5.7	609.3	12.6	758.5	746.4
Grain quality	Season	Brown rice (%)	Head rice (%)	Chalkiness degree (%)	Percentage of Chalky Grain (%)	Amylose content (%)
	2009-2010	81.2	71.7	0.1	1	17.2
Disease and cold resistance	Cultivars	Leaf blast (grade)	Panicle blast (grade)	Unfilled grain percentage (%)		
	Longgeng 31	3.7	3	12.5		
	Kongyu 131/CK	6.3	8.3	17.5		

2. Advance in molecular rice breeding in complex quantitative traits

Although more and more functional genes have been cloned, unlike our expectation, their applications in rice improvement have been slow. The most important reasons include the lack of favorable alleles (genes) and incomplete understanding of the genetic control over complicated traits in rice. Germplasms hold a large of genetic variation for improving agricultural crops. Recently, we finished re-sequencing of 3010 diverse accessions of Asian cultivated rice (Nature 2018) and released two sets

of databases of SNP genotype and pan genome. Based on SNP genotypic data, QTL mapping for many important agronomic traits, such as appearance and milling grain quality, vascular bundle related traits (Fig. 3), and black-streaked dwarf virus, was conducted by GWAS analysis, and some candidate genes for important loci have been inferred by gene-based association analysis and bioinformatics. After validation, candidate genes will be used for trait improvement by MAS.

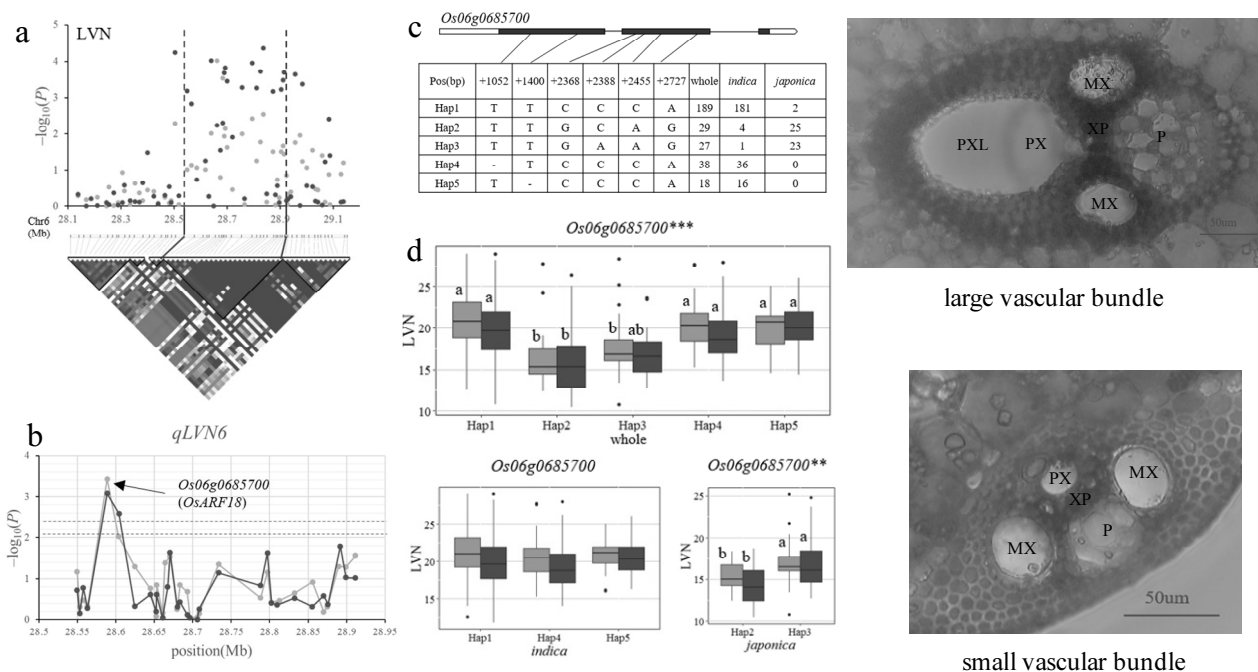


Fig. 3: Gene-based association analysis and haplotype analysis of targeted genes related to *qLVN6*. (a) Local Manhattan plot (top) and LD block (bottom) surrounding the peak on chromosome 6. Dashed lines indicate the candidate region for the peak. (b) Gene-based association analysis of targeted genes related to *qLVN6*. Each point is a gene indicated by one SNP having largest $-\log_{10}(P)$ value. Dash line show the threshold to determine significant SNP. (c) Exon-intron structure of *Os06g0685700* and DNA polymorphism in that gene. (d) Boxplots for LVN based on the haplotypes (Hap) for *Os06g0685700* in the whole, *indica* and *japonica* populations. The ** and *** suggest significance of ANOVA at $P < 0.01$ and $P < 0.001$, respectively. The letter on histogram (a, and b) indicate multiple comparisons result at the significant level 0.05. Green and red colors indicate in 2015 and 2016, respectively.

Most breeding traits such as yield, quality, abiotic and biotic stress tolerance, and fertilizer use efficiency, are genetically complicated. Separation of mapping population derived from bi-parents from breeding population has defects in favorable allele mining and direct use of favorable allele in breeding program due to background effect on QTL expression. So in the past decade, we have been dedicated to the integration of QTL mapping with QTL-based breeding by developing trait-specific introgression lines (ILs) in elite background. Using eight BC1 populations derived from a widely adaptable recipient and eight donors plus three rounds of phenotypic selection, we developed 496 ILs with significantly higher yield under drought, salt and/or non-stress conditions (Fig. 4). Based on high throughput SNP data of trait-specific ILs, QTL affecting the target traits (selected traits such as drought and salt tolerance) and non-target traits (other non-selected traits such as disease resistance, nitrogen use efficiency) were identified using segregation distortion approach and GWAS respectively. Based on distribution of favorable alleles and phenotypic performance of trait-specific ILs, designed QTL pyramiding (DQP) was conducted to improve drought tolerance and nitrogen use efficiency by accumulating different favorable alleles from different donors. Our results demonstrate that trait-specific ILs could effectively connect QTL mapping and QTL pyramiding breeding. In addition, designed QTL pyramiding (DQP) using ILs could be more effective in molecular rice breeding for complex quantitative traits.

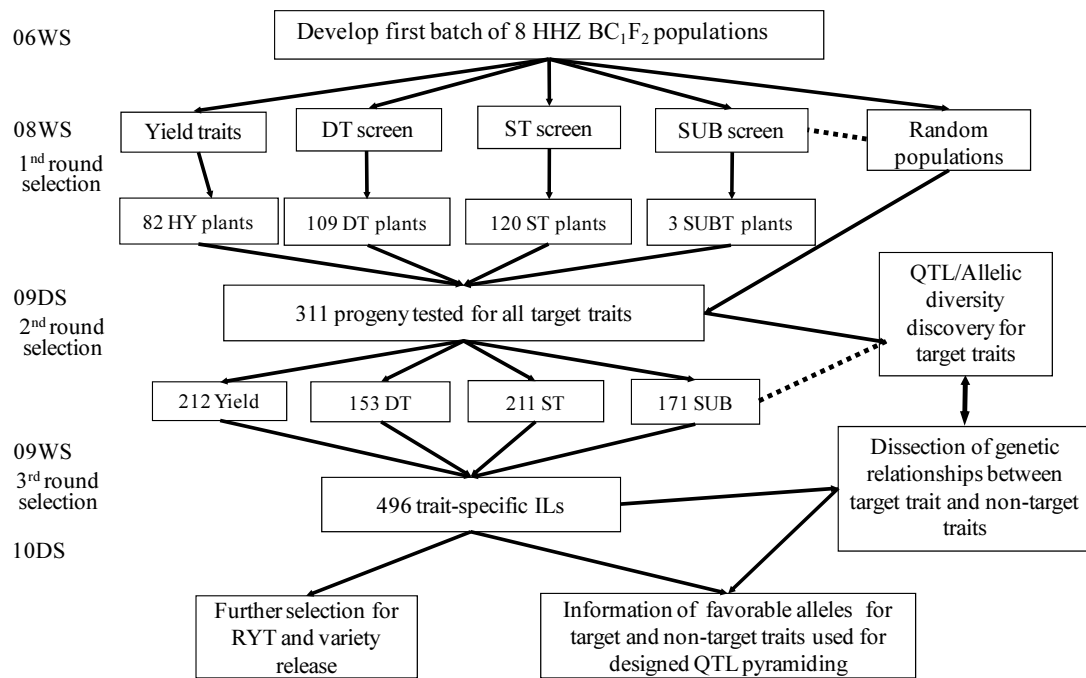


Fig. 4 The introgression breeding procedure

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