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# Rapeseed research and production in China



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## ABSTRACT

Rapeseed (*Brassica napus* L.) is the largest oilseed crop in China and accounts for about 20% of world production. For the last 10 years, the production, planting area, and yield of rapeseed have been stable, with improvement of seed quality and especially seed oil content. China is among the leading countries in rapeseed genomic research internationally, having jointly with other countries accomplished the whole genome sequencing of rapeseed and its two parental species, *Brassica oleracea* and *Brassica rapa*. Progress on functional genomics including the identification of QTL governing important agronomic traits such as yield, seed oil content, fertility regulation, disease and insect resistance, abiotic stress, nutrition use efficiency, and pod shattering resistance has been achieved. As a consequence, molecular markers have been developed and used in breeding programs. During 2005–2014, 215 rapeseed varieties were registered nationally, including 210 winter- and 5 spring-type varieties. Mechanization across the whole process of rapeseed production was investigated and operating instructions for all relevant techniques were published. Modern techniques for rapeseed field management such as high-density planting, controlled-release fertilizer, and biocontrol of disease and pests combined with precision tools such as drones have been developed and are being adopted in China. With the application of advanced breeding and production technologies, in the near future, the oil yield and quality of rapeseed varieties will be greatly increased, and more varieties with desirable traits, especially early maturation, high yield, high resistance to biotic and abiotic stress, and suitability for mechanized harvesting will be developed. Application of modern technologies on the mechanized management of rapeseed will greatly increase grower profit.

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## 1. Introduction

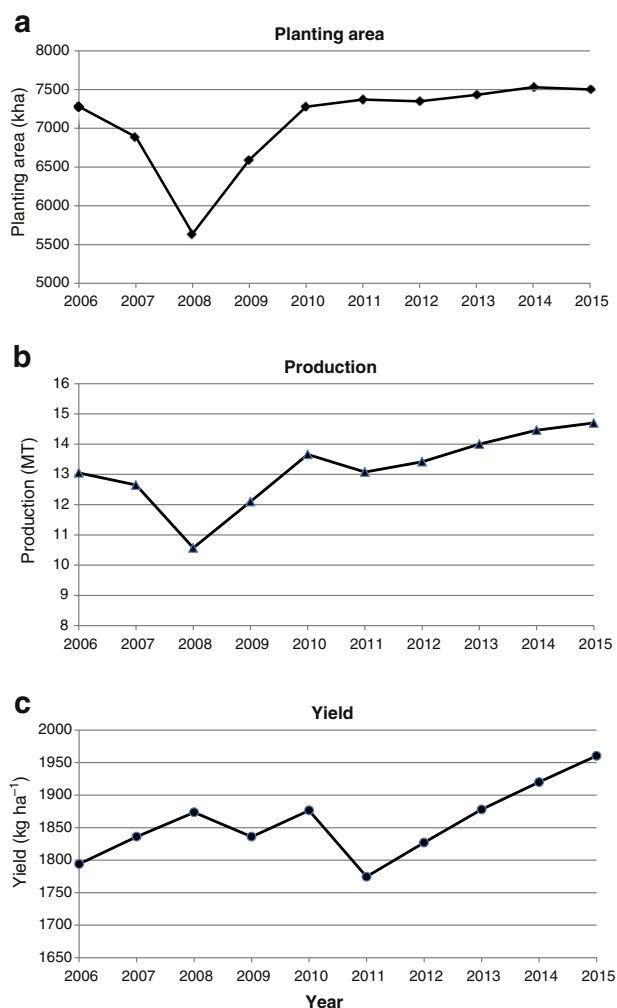
Rapeseed is the most important oil crop and the fourth largest crop in China after rice, maize, and wheat. As the world's largest rapeseed producer, China has ranked first in the world in total rapeseed production since 1980/1981, except for 2011/2012.

There has been a steady trend of increase in total production, planting area, and yield of rapeseed in China for the last ten years (Fig. 1). Conventional rapeseed crop management is very expensive, labor-intensive, and inefficient owing to its low level of mechanization. A shortage of labor in rural areas and a lack of arable land available for commercial rapeseed cultivation have

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**Fig. 1 – Rapeseed production in China over the last 10 years. (a) Planting area in kilohectares (kha); (b) production in metric tons (MT); (c) yield (kg ha<sup>-1</sup>). Data from USDA (<http://apps.fas.usda.gov/psdonline/>).**

put further pressure on farmers to adopt modern tools for mechanized farming. With the enhancement of research and extension of mechanization, the rapeseed industry has begun a transition from manual to mechanized farming. During the past three years, with the development of machines for seeding and harvesting, precision technologies for planting density adjustment, weed management, and controlled-release fertilizers, the planting area, total production, and yield per unit area of rapeseed has significantly improved. According to USDA data (<http://apps.fas.usda.gov/psdonline/>), rapeseed production in 2014/2015 in China reached 14.7 million tones.

In the last ten years, the quality of Chinese rapeseed has also been improved by advanced breeding and production technologies. Conventional rapeseed oil with high erucic acid has been changed to low-erucic acid oil with high nutritional value, and rapeseed meal with a low glucosinolate content has become a high-quality protein feed source instead of fertilizer. Data from the Center for Quality Supervision and

Inspection of Oil and Products of the Chinese Ministry of Agriculture shows that rapeseed collected from areas covered by the National Rapeseed Modern Industry Technology System in 2015 had the highest average oil content (43.79%) and the lowest erucic acid content (4.00%) in history. The oil contents of the current varieties Zhongshuang 11 and Qinzayou 4 have exceeded 49% and 50%, respectively.

## 2. Rapeseed functional genomics and marker-assisted breeding

### 2.1. Brassica genomics and functional gene identification

Rapeseed genome sequencing research in China is recognized worldwide. In collaboration with international partners, China has completed the whole-genome sequencing of rapeseed and its parental species *Brassica oleracea* and *Brassica rapa*. Annotation was performed for 44,940 genes in *B. oleracea*, 41,174 in *B. rapa*, and more than 100,000 in *Brassica napus* [1–3]. Comparative genome analyses of the sequence assemblies have shown evolutionary patterns and genome duplications (72×) from the basal flowering plant species *Amborella* and thrice-duplicated genes from its parental species, *B. oleracea* and *B. rapa*. An international consortium involving Chinese researchers and the Illumina Company ([www.illumina.com/](http://www.illumina.com/)) has developed a high-density 60K Infinium SNP array of rapeseed. This resource has been used worldwide, including the first report on QTL mapping for seed fiber content in rapeseed [4].

Functional genomics, as a supporting technology for molecular breeding, has become the focus of rapeseed research over the last ten years in China. Great progress has been made in China in the identification of functional genes for important traits such as yield, seed oil content, fertility regulation, disease and insect resistance, abiotic stress, nutrient-use efficiency, and pod shattering resistance (Table 1). In 2015, genes regulating both seed weight (*BnaA.ARF18.a*) and seed number per pod (*BnaC9.SMG7b*) were identified in China [5,6]. Rapeseed orthologs of *Arabidopsis* genes such as *SHB1* (*short hypocotyl under blue1*) and *HAIKU2* were shown to affect seed weight [7]. The transcription factors *LEC1* (*leafy cotyledon 1*) and *WRI1* (*wrinkled1*) were revealed to be involved in regulation of glycolysis and ultimately promote oil accumulation in seed [8,9]. Maternal organs including pod wall and seed coat were shown to affect seed oil content strongly in rapeseed [10,11]. Cytoplasmic effects were also shown to affect oil accumulation [12]. Two other genes, *GRF2* (*growth-regulating factor 2-like*, regulating photosynthesis and cell size) and *ORF188* (*open reading frame 188*, associated with cytoplasmic effects), were found to participate in a regulatory pathway involved in oil content [13,14]. Three genes for genic male sterility and restoration including *BnMs1* (*male sterility 1*), *BnMs2*, and *BnaC.Tic40* (*translocon at the inner membrane of chloroplasts with 40 kDa*) were cloned [15–17], deepening understanding of the mechanisms of male sterility. Genes associated with flower color (*BnaC3.ccd4*, *carotenoid cleavage dioxygenase 4*) [18], vitamin E biosynthesis (*hydroxyphenylpyruvate dioxygenase*, *HPPDase*) [19], and drought resistance (*sddt*) (unpublished data) have been identified recently. All these achievements of Chinese researchers have laid the foundation for rapeseed functional genomic research.

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