

# Development of hybrid rice cultivation in world: a review of breeding and biotechnology

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**ABSTRACT:** Heterosis, or hybrid vigor, refers to the phenomenon that progeny of diverse inbred varieties is superior over both parents on yield, panicle size, number of spikelets per panicle, number of productive tillers, stress tolerance etc. This phenomenon to be a powerful force in the evolution of plants has been exploited extensively in crop production. In fact, the exploitation of heterosis has been the greatest practical achievement of the science of genetics and plant breeding. Rice heterosis was first reported by Jones (1926) who observed that some F1 hybrids had more culms and greater yield than their parents. Between 1962 and 1967, a number of suggestions came from different places of the world for commercial exploitation of heterosis to become a major component of rice improvement programs at national and international level. For example, rice breeders from Japan, China, United States, India, the former Soviet Union and Philippines started their projects to utilize rice heterosis. However, progress had not been sound because of the difficulty for rice to be a strictly self-pollinated crop unlike corn, which made out crossing absolutely essential for hybrid seed production extremely difficult.

**Keywords:** Hybrid rice, rice breeding, QTL mapping

## INTRODUCTION

Rice (*Oryza sativa* L.), belonging to the family Poaceae is widely cultivated in most tropical and subtropical regions of the world (Ezuka and Kaku, 2000). Rice is one of the major food crops of the world especially of the Asian countries like Bangladesh, Pakistan, India, China, Vietnam and Korea More than 90% of the world's rice is produced and consumed in Asia (Virmani, ) and constitutes a staple food for 2.7 billion people worldwide (Salim, 2003). In fact, the exploitation of heterosis has been the greatest practical achievement of the science of genetics and plant breeding (Alam, 2004). Hybrid rice was first developed in China in the 1960s when a mutation in a single rice plant and incorporated into Chinese varieties, mainly by research institutes in Hunan and other South China provinces (Virmani, 1994; F Xie, pers. comm.). (2013). In China, hybrid rice has a yield advantage of 20–30 % over the best available inbred rice cultivars, facilitating a 44.1% increase in production (Cheng, 2007). Hybrid rice accounted for more than 50 % of the total rice cultivation in China, and on average hybrid rice yields 10–20 % more than elite inbred varieties (Chen, 2010). Currently, the development of hybrid rice is primarily based on Three-line (Yuan and Virmani, 1988) and Two-line breeding systems (Yuan, 1994), which were commercially exploited in 1976 and in 1995, respectively. Three-line hybrid rice involves a cytoplasmic male sterile (CMS) line or a line, a maintainer line or B line, and a restorer line or r line. Maintainer lines are crossed with the CMS lines for self-reproduction; the phenotypes and genotypes of maintainer lines are highly similar to CMS lines. Two-line hybrid

rice involves a photo- or thermo sensitive genetic male sterile (PGMS/TGMS) line and a R line (Hu , 2014). Hybrid rice has been used in commercial production for four decades. Currently, there are about 17 million hectares of hybrid rice production in China and another 4 million hectares in other countries, mainly in Bangladesh, India, Indonesia, Myanmar, the Philippines, the US and Vietnam. Heterotic rice hybrids are generally derived from distant parents by geographic origin or different ecotypes (Yuan, 1977; lin and Yuan, 1980). In the earlier stage of hybrid rice development in China, two heterotic groups, that is, early season indica from southern China and mid- or late-season indica from Southeast Asia were identified for three-line hybrid rice based on wild abortive (WA) male sterile cytoplasm (Yuan, 1977). More heterotic groups were studied and identified for three-line hybrids derived from other male sterile cytoplasm and for two-line hybrid rice based on thermo-sensitive genic male sterility (Wang and lu, 2007; lu and Xu, 2010). Different trait may be important to increase the rice grain production. The considered traits may include short plant height, strong culms, moderate tillering, short and erect leaves, large and compact panicles, and early maturation (Paterson , 2005). Tillering in rice is one of the most important agronomic characters for grain production (Smith , 2003). because the tiller number per plant determines the panicle number, a key components of grain yield (Yan , 1998). bacterial blight (BB caused by *Xanthomonas oryzae* pv. *Oryzae* (Xoo) is one of the most destructive bacterial diseases that affect hybrid rice production. The infection of plants at the maximum tillering stage results in a yield reduction of %20 and, in severe cases, as much as 50% (Mew , 1993). To date, at least 38 BB resistance genes conferring host resistance against various races of Xoo have been identified (Bhasin , 2011; Kumar , 2012). Several of these genes have already been incorporated into rice cultivars that are now widely cultivated in many countries (Huang , 1997; Singh , 2001; Sundaram , 2007). The genes Xa4 and Xa21 have been widely used in hybrid rice breeding in China (Zhai 2002).

### ***Cultivation of the hybrid rice in the world***

hybrid vigor is one of the most important applications of genetics in agriculture (Duvick, 1999). It has not only contributed to food security, but has also established the basis of a billion-dollar agribusiness that has generated significant employment opportunities all over the world (Kloppenburg, 2005). Since the release of hybrid rice in China during the 1970s, the cultivated area has increased consistently (Peng ,1999). In this country, hybrid varieties could obtain about 30 % grain yield advantage over inbred (pure-line) varieties. In the first 20 years of cultivation, hybrid rice was cropped on about 50 % of the national rice surface, and helped China to increase rice yield from 5.0 t/ha of conventional rice to 6.6 t/ha, reaching consistently 7.5 t/ha in the Sichuan province (Yuan, 2003). Hybrid rice has now become a commercial success in several Asian countries, such as Vietnam, India, the Philippines, Bangladesh, and an estimated 6 million ha of extra production area would be required if hybrid rice had not been developed (Tu , 2000). In the last few decades, USA, Brazil, and other southern American countries have also begun the commercial production of hybrid rice. Several researchers improved hybrid rice resistance through the addition of resistance genes to many diseases, both with normal breeding and genetic engineering (Song ,1995; Zhu , 2000).

### ***Super hybrid rice***

In , a super high-yielding rice program was initiated by the Chinese Ministry of Agriculture with the aim of achieving very high yields (ca. 10 tonnes ha<sup>-1</sup> in the majority of Chinese rice-growing areas, and up to 12 tonnes ha<sup>-1</sup> in large field trials). Super hybrid rice involves heterosis achieved through hybridization between indica and japonica rice (intersubspecific) as well as pyramiding of heterosis genes for different rice ecotypes and the incorporation of useful genes (including genes for anti-herbivore resistance) from near and distant relatives (Cheng , 1998, 2007; Wu, 2009). Some of these new-generation hybrids (i.e., Liangyoupeijiu and Liangyou 293) have demonstrated high yields in field trials (Zhang , 2009), however, apart from some studies promoting the incorporation or pyramiding of herbivore-resistant genes (Zhang, 2007; Wu, 2009) little attention has been given to issues of herbivore resistance, and there are few published studies (but see Xu , 2007). that examine susceptibility to herbivores of the super hybrids compared to either 'ordinary' hybrids or conventional varieties.

### ***Effects of elevated ozone and carbon dioxide on the grain quality of hybrid rice***

Concomitant with the increase of the CO<sub>2</sub> concentration, the ground-level ozone concentration (O<sub>3</sub>) has also risen rapidly, especially in regions with high population density and vibrant economic growth (Chan and Yao, 2008; Engardt, 2008; Wang , 2009, 2011b). Rice (*Oryza sativa*L.) is the main staple food which presently provides 20% or more of the daily food energy to half the world's population (Timmer , 2010), and the demand for high quality rice will continue to rise in the near future because most of the riceconsuming countries are still experiencing a population growth and a shrink of cropland (Bruinsma, 2009). In view of the socio-economic importance of rice

under the scenario of global environmental change, much research has been conducted to assess the impacts of rising CO<sub>2</sub> or O<sub>3</sub>, separately, on rice production, but almost none have evaluated the two factors in combination (A in sworth, 2008). To our knowledge, there is no publication on rice quality response to the combined elevation of CO<sub>2</sub> and O<sub>3</sub> up to date. The effects of single gas enrichment of CO<sub>2</sub> (Lievering , 2004; Lee , 2013; Taub , 2008; Yang , 2007) or O<sub>3</sub> (Frei , 2012; Wang , 2012) on rice quality have been inconsistent except changes in protein and nitrogen concentrations. Wang (2014) concluded that the O<sub>3</sub> concentration projected for the coming few decades will have more substantial effects on grain quality of Chinese hybrid rice than the projected high CO<sub>2</sub> concentration alone, and the combination of two gases caused fewer significant changes in grain quality than individual gas treatments.

#### ***Using line of hybrid rice for discovery of DNA polymorphisms***

The advent of next-generation sequencing (nGS) technologies has aided the discovery of genome-wide Dna variation. nGS enables identification of markers such as single-nucleotide polymorphisms (SnPs) and insertion and deletions (InDels) in a rapid, efficient, relatively low cost, and high-throughput manner (Bentley, 2006; Davey , 2011; Gao , 2012). The availability of the complete and or draft genome sequences (Yu , 2002; Goff , 2002). Matsumoto ( 2005) of rice opened the door for whole genome re-sequencing, which has subsequently enabled the discovery of SnPs and InDels at the genome-wide scale within both germplasm diversity collections and breeding lines of rice (Varshney , 2009; Huang , 2009) Very recently, a series of parental lines of Three-line hybrid rice have been re-sequenced and analyzed. (li , 2012) re-sequenced three important representative restorer lines (Ir24, MH63, and SH527) and identified numerous SnPs, InDels, and structural variations (SVs). These results showed higher than expected genetic variation among restorer lines. Hu (2014) identified Dna polymorphisms at the genome-wide scale and uncovered the high level of genetic diversity between V20B (*Oryza sativa* L. ssp. indica). and 93-11 (*Oryza sativa* l. ssp. indica). they proved that next-generation sequencing technologies can be powerful tools to study genome-wide Dna polymorphisms, to query genetic diversity, and to enable molecular improvement efforts with Three-line hybrid rice Further, their results also indicated that 93-11 could be used as core germplasm for the improvement of wild-abortive CMS lines and the maintainer lines.

#### ***Dominance and epistasis are the main contributors to heterosis***

Recently, a novel informative design termed "immortalized F<sub>2</sub> population" (IF<sub>2</sub>) was first developed for heterosis research in rice (Hua , 2002), and maize (Tang , 2010). Chromosome segment substitution lines (CSSLs) are near isogenic lines, they do not have such a limitation, and have been used for heterosis in tomato, Arabidopsis, and rice (Semel , 2006; Wang , 2012), in the self-fertile rice, dominance or dominance and epistasis is believed to play an important role for yield related traits (Xiao ,1995; Yu ,1997; Li , 2008), Some studies in rice (Li , 2001; Zhou , 2012), supported the over dominance hypothesis. Few studies in rice ( Li , 2008; Hua , 2003), and maize (Tang , 2010), compromised the role of dominance, over dominance and epistasis in heterosis.

#### ***Application of a simplified marker-assisted backcross technique***

bacterial blight (BB) caused by *Xanthomonas oryzae* pv. *Oryzae* (Xoo) is one of the most destructive bacterial diseases that affect hybrid rice production. (Mew ,1993).The marker-assisted backcross breeding (MABB) technique is usually used to improve disease resistance while preserving identical backgrounds by repeatedly crossing to a recurrent parent (Chevalet and Mulsant, 1992). Although background selection is very useful for rapid recovery of the recurrent parent genome, its use in breeding programs is constrained by the limitation of detecting polymorphisms with markers such as simple sequence repeats (SSRs), its cost, and the need for timely execution (Singh , 2012).(2014 5) Zhijuan (2014) with using this technique introgressed bacterial blight resistance gene Xa2311 into HN189 and improved restorer lines, HBH145 (with one generation of backcrossing) and HBH146 (with two generations of backcrossing), were obtained that had a significant bacterial blight resistance advantage over HN189. They displayed using of the marker-assisted backcross breeding technique with one generation of backcrossing and without background selection in rice breeding programs shortened the breeding period of the rice.

### **Genetic Diversity of Hybrid Rice Germplasm Measured by Molecular Markers**

Since 1990's, several types of molecular markers are being increasingly utilized for investigating germplasm diversity and genetic relationships (Hamrick and Godt, 1997; Westman and Kresovich, 1997; Melchinger, 1999). Among these DNA markers, simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) markers are currently widely employed for rice genetic diversity analysis (Chen , 1997; Garris , 2005; McNally , 2009; Chen , 2011). In rice, the overall genetic diversity of representative samples of the global rice germplasm has been well investigated (Yu , 2003; Garris , 2005; Caicedo , 2007). Duan (2002) observed a low genetic diversity among 35 restorer lines genotyped with 25 SSR markers, which indicated a vulnerable genetic background and a limited utilization in rice heterosis breeding. He (2012) indicate that both of the SSR and SNP markers have distinguishable power to detect polymorphism and are appropriate for genetic diversity analysis among tropical hybrid rice parents. A subset of 60 SSR markers were also chosen by the Core Hunter with 368 alleles, and the cluster analysis based on the total and subset of SSR markers highly corresponded at  $r = 0.91$ , they suggested that fewer SSR markers can be used to classify and evaluate genetic diversity among parental lines.

### **Conclusion**

In summary, hybrid rice is still a major source of elite rice cultivars. However, hybrid rice production is rather time-consuming and the limited available genetic resources leave little room for the continued improvement of rice. With the completion of rice genome sequence, scientists are better equipped to unravel rice gene functions on a genome-wide scale, providing breeders with abundant genetic resources for continued generation of elite rice varieties to maintain a sustainable food supply. The immediate goal is to breed varieties with a further improved yield potential, enhanced stress resistance and good grain quality by using molecular and genomic information to break the rice yield plateau in the future.

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