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Multi-genotype varieties reduce rice diseases through enhanced genetic diversity and show stability and adaptability in the field

Ping He¹, Cong Wang¹, Neng Zhang¹, Bin Liu¹, Yang Yang¹, Yifan Zhu¹, Xiaofang Li², Xuanli Yu³, Guangyu Han^{1*} and Yun-Yue Wang^{1*}

Abstract

Rice is a crucial food crop worldwide. The genetic diversity in rice germplasm indicates its promising potential utilization in disease and pest control. To explore the relationship between genetic diversity and disease resistance in rice plants, multi-genotype rice varieties developed from multi-parent advanced generation inter-cross (MAGIC) population lines were used here to analyze the correlation between disease occurrence and genetic diversity, as well as for field monitoring of their disease occurrences and yields. We found that genetic diversity and disease resistance of the multi-genotype varieties tested in this study were superior to those of their component lines and mono-genotype varieties, and the incidence of rice blast disease decreased as the genetic diversity of multi-genotype rice varieties increased. We further conducted field trials using these multi-genotype varieties for three years in different rice-planting areas. The results showed that multi-genotype varieties exhibited good disease resistance and high-yielding potential. Thus, proper use of multi-genotype varieties characterized by rich genetic diversity is a promising approach to improve disease resistance of rice plants in agricultural production systems and is of great significance for ensuring food security and achieving sustainable agricultural development.

Keywords: Rice, Multi-genotype variety, Genetic diversity, Disease resistance, Yield

Background

Rice is the staple food for half of the world's population. It is necessary to increase crop production to meet the demands of the growing population (Shin et al. 2020). Stable production of rice is important for food security and sustainable development of agriculture (Renard and Tilman 2019). Over the past five decades, semidwarf varieties and heterosis have been widely utilized in rice production to achieve a marked yield increase (Wing et al. 2018). Moreover, homozygous rice varieties have

replaced heterozygous farmer varieties and natural varieties, resulting in an imbalance of varietal deployment and a decrease in genetic diversity, and subsequently reducing the ability of rice crops to withstand various stresses, including drought, cold and increasing pests and diseases (Li et al. 2014; Huang et al. 2016).

Genetic diversity is an important part of biodiversity and a precondition for sustainable crop production. Previous studies have demonstrated that intercropping increases genetic diversity and disease resistance of crops in planting systems (Trutmann et al. 1993; Han et al. 2016); the use of variety mixture planting increases genetic diversity of rice plants and effectively controls the occurrence of rice blast in the field (Zhu et al. 2000, 2004); the increased crop diversity directly contributes to the stability of crop production and offsets the negative

*Correspondence: hanguangyu9745@163.com; 1371209436@qq.com
¹ State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, Ministry of Education Key Laboratory of Agriculture Biodiversity for Plant Disease Management, College of Plant Protection, Yunnan Agricultural University, Kunming 650201, Yunnan, China
Full list of author information is available at the end of the article



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impact of climate change (Renard and Tilman 2019). Therefore, it is of great significance to restore the diversity of agricultural systems by cultivating rice varieties with rich genetic diversity.

There are also some efforts to solve the aforementioned problems from the perspective of breeding multi-genotype varieties, such as multiline varieties and synthetic varieties. These approaches have significant effects on increasing genetic diversity and enhancing rice resistance (Finckh et al. 2000; Kiær et al. 2009). However, poor performing varieties may be widely deployed, making this a defective breeding strategy. A novel multi-genotype breeding strategy termed as multi-parent advanced generation inter-cross (MAGIC) has been devised in recent years (Cavanagh et al. 2008; Li et al. 2013), by which a large number of genotypes can be created to form basic populations. Then different genotypes, which exhibit similar phenotypes and meet the criteria of high yield, good quality, wide adaptability and strong stress resistance, are matched in proportion to constitute a multi-genotype variety. This breeding approach exploits artificial techniques to develop a polygenic population in which the component lines possess different genotypes, greatly extending the genetic diversity of the population (Additional file 1: Figure S1). This “elite team” inhibits the spread of pathogens and triggers the competition between nonpathogenic and pathogenic microorganisms, effectively controlling diseases through an increase in genetic diversity (Li et al. 2013). In 2012, DuoJiXin-3, a multi-genotype variety developed from MAGIC lines, was approved by Hainan Crop Variety Approval Committee and subsequently underwent commercialization (Xu et al. 2014). This indicates that the value of multi-genotype varieties in agricultural production has begun to be recognized. Undoubtedly, the promotion and application of this new breeding technique will help promote the sustainable development of agriculture.

In this paper, we focused on disease severities of rice multi-genotype varieties derived from MAGIC lines and their component lines in plot experiments. The genetic

diversity of these rice varieties/lines was detected using SSR markers. The relationship between disease occurrence and genetic diversity was analyzed to explore whether the richness of gene diversity is associated with disease resistance of multi-genotype varieties. The adaptability of these multi-genotype varieties was then investigated in different rice-producing areas of Yunnan Province for three years. This study is of great significance for further elaboration of the effect of genetic diversity on improving crop resistance and yield, as well as for the promotion and application of multi-genotype varieties in various rice-producing regions.

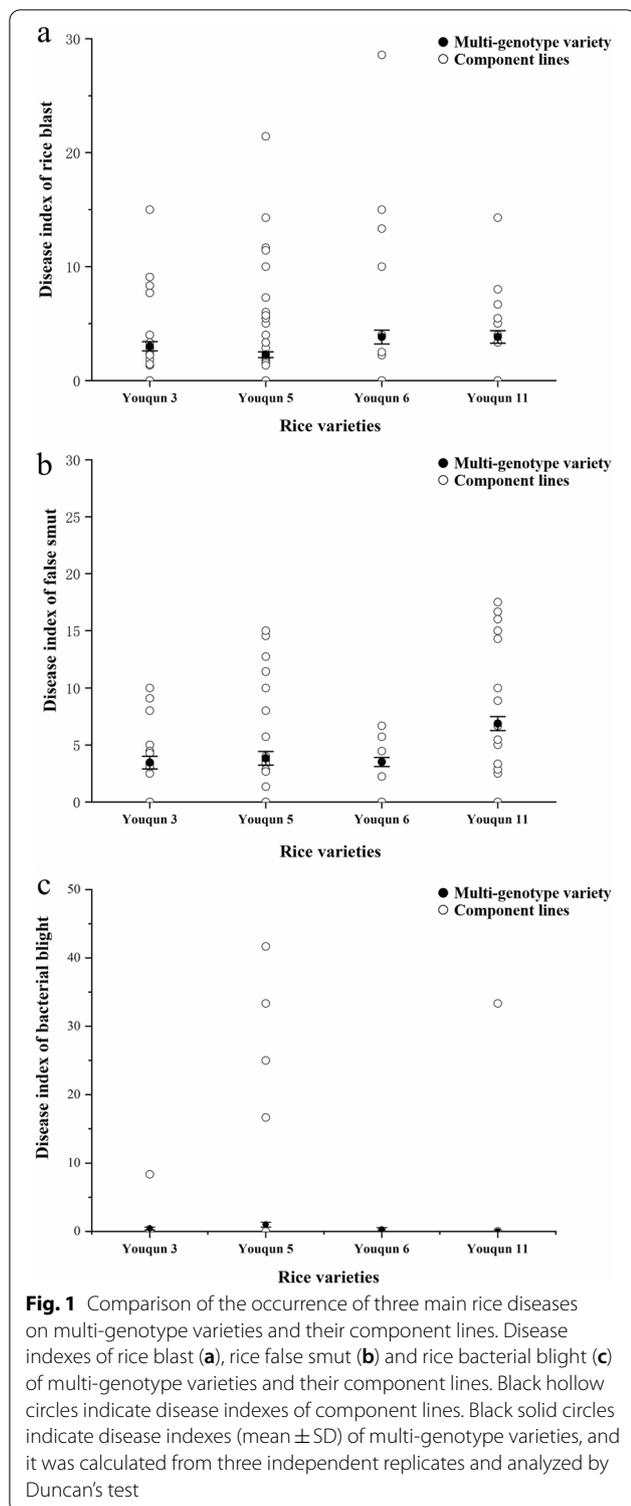
Results

Multi-genotype rice varieties have better disease resistance than their mono-genotype component lines

Multi-genotype varieties derived from MAGIC population lines consist of several component lines that have different genotypes. Here, four multi-genotype varieties (YQ-3, YQ-5, YQ-6 and YQ-11) and their component lines (Table 1) were assessed for the resistance to rice blast, false smut and bacterial blight diseases via plot experiments. The results showed that these multi-genotype varieties had mild disease occurrence ($DI < 10$), while their component lines exhibited a much larger variation in disease index (Fig. 1). Specifically, for rice blast, the disease index of these four multi-genotype varieties ranged from 2.27 to 3.83, while their component lines had a larger scope, and the disease index of the YQ-6' component lines ranged from 0 to 28.57 (Fig. 1a, Additional file 1: Figure S2a and Additional file 2: Table S1). For rice false smut, there were also great differences between multi-genotype varieties and their component lines in disease index; it was 3.83 for YQ-5, and 1.11–7.45 for its component lines (Fig. 1b, Additional file 1: Figure S2b and Additional file 2: Table S1). There was almost no occurrence of bacterial blight in the tested multi-genotype varieties, whereas the disease index of YQ-5' component lines reached 41.67 (Fig. 1c, Additional file 1: Figure S2c and Additional file 2: Table S1).

Table 1 Multi-genotype varieties and planting regions for field experiments in different years

Years	Multi-genotype varieties	MAGIC component lines	Planting regions
2014	YQ3	3-1, 3-2, 3-3, 3-4, 3-5	Dehong, Yunnan
	YQ5	5-1, 5-2, 5-3, 5-4, 5-5, 5-6, 5-7	
	YQ6	6-1, 6-2, 6-3, 6-4, 6-5	
	YQ11	11-1, 11-2, 11-3, 11-4, 11-5	
2015	YQ6, NBN	/	Dehong/Wenshan/Honghe/Chuxiong, Yunan
2016	GY1, GD18	/	Dehong/Wenshan/Qujing/Chuxiong, Yunan
2017	DJX6, NBN, YQ1	/	Dehong/Wenshan/Honghe/Chuxiong, Yunan



In addition, the agronomic traits of multi-genotype varieties, including yield, thousand-grain weight, seed-setting rate, panicle length and plant height, were not significantly different from those of the high-yielding hybrid

rice variety YiXiangYou2115 (control variety, CK). The yields of YQ-3, YQ-6 and YQ-11 were lower than that of YiXiangYou2115 but were not significantly different. The seed-setting rates of YQ-3, YQ-5 and YQ-6 also showed no significant difference from that of the control variety (Additional file 2: Table S2). In summary, we demonstrated that multi-genotype varieties have good rice blast resistance in the field, and they are better than their component lines.

Multi-genotype rice varieties have a richer genetic diversity compared with their component lines

In addition to investigating the disease resistance of multi-genotype varieties, we also detected their genetic diversity using molecular methods. A total of 29 SSR alleles were selected for the detection of genetic diversity in four multi-genotype varieties (YQ-3, YQ-5, YQ-6 and YQ-11) and their component lines. Among them, 24 SSR primer pairs amplified clear and repeatable bands. The molecular weight of these bands ranged from 100 to 500 bp (Additional file 1: Figure S3). The results showed that abundant polymorphic bands were amplified in multi-genotype varieties. In general, the genetic diversity of multi-genotype varieties was significantly higher than those of their component lines and YiXiangYou2115 (control variety). The Shannon index of multi-genotype varieties (0.096) was significantly higher than those of their component lines (0.042) and the control variety (0.011). The Nei's (0.052) and expected heterozygosity (0.053) of multi-genotype varieties were higher than those of the component lines ($H=0.025$, $H_e=0.027$, $P>0.05$) and significantly higher than that of the control variety ($H=0.007$, $H_e=0.007$, $P<0.05$). The average apparent heterozygosity was not significantly different among the multi-genotype varieties (1.072), their component lines (0.992) and the control variety (1.010) (Fig. 2 and Additional file 2: Table S3). Therefore, we confirmed that multi-genotype varieties are genetically more diverse than other rice varieties we tested.

The occurrence of rice blast disease is much suppressed with the increase of genetic diversity in multi-genotype varieties

To elucidate whether there is a relationship between genetic diversity and disease resistance in multi-genotype varieties, the correlation between genetic diversity and the occurrence of rice blast disease was analyzed in our study. The results showed that with the increase in genetic diversity, the disease index of rice plants gradually decreased, showing a weak correlation (Fig. 3a; $y = -10.49x + 3.59$, $R = 0.21$, $P = 0.248$). Stability is the key factor for disease control, thus the variation of disease index measured by dispersion degree (standard error, SE)

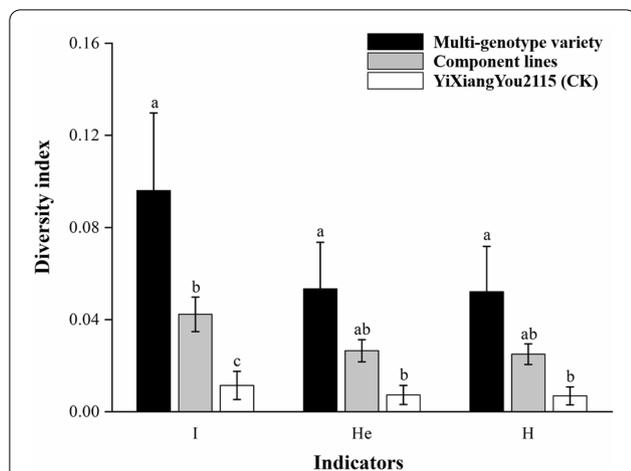


Fig. 2 Genetic diversity of multi-genotype varieties and their component lines detected by SSR makers. I, Shannon index; He, expected heterozygosity; H, Nei's diversity index. Bars represent standard error and different letters above bars indicate significant differences at $P < 0.05$ based on Duncan's test ($n = 3$)

is used to assess the stability of disease occurrence. We found that the variation range of rice blast disease was significantly decreased with increasing genetic diversity and showed a strong correlation (Fig. 3b; $y = -21.62x + 1.81$, $R = 0.61$, $P = 0.021$). This indicated that the high genetic diversity in multi-genotype varieties could not directly reduce the occurrence of disease in crops (weak correlation). However, the higher the multi-genotype varieties have in their genetic diversity, the more greatly the degree of variation in disease occurrence decreases, suggesting that the occurrence of disease tends to be stable. The results demonstrate that the richness of genetic diversity is negatively related with disease severity in multi-genotype varieties.

Multi-genotype varieties have stable and adaptable disease resistance in the field

After establishing a preliminary understanding of the genetic diversity in multi-genotype varieties and its potential impact on improving disease resistance and yield, to further investigate ecological responses of multi-genotype varieties in the field, we selected 6 multi-genotype varieties (DJX6, GD18, GY1, YQ1, YQ6, NBN) and a local high-yielding and disease-resistant variety HongYou-7 (HY7, control variety) for field resistance screening experiments in four different rice-producing regions of Yunnan Province during 2015–2017.

For rice blast, a mild disease occurrence ($DI \leq 5$) was observed on HY7 (CK) and most multi-genotype varieties that we tested; a moderate occurrence was on YQ1 in Dehong ($DI = 9.80$) and DJX6 in Wenshan ($DI = 8.33$) in 2017; a severe incidence ($DI = 48.66$) was only observed

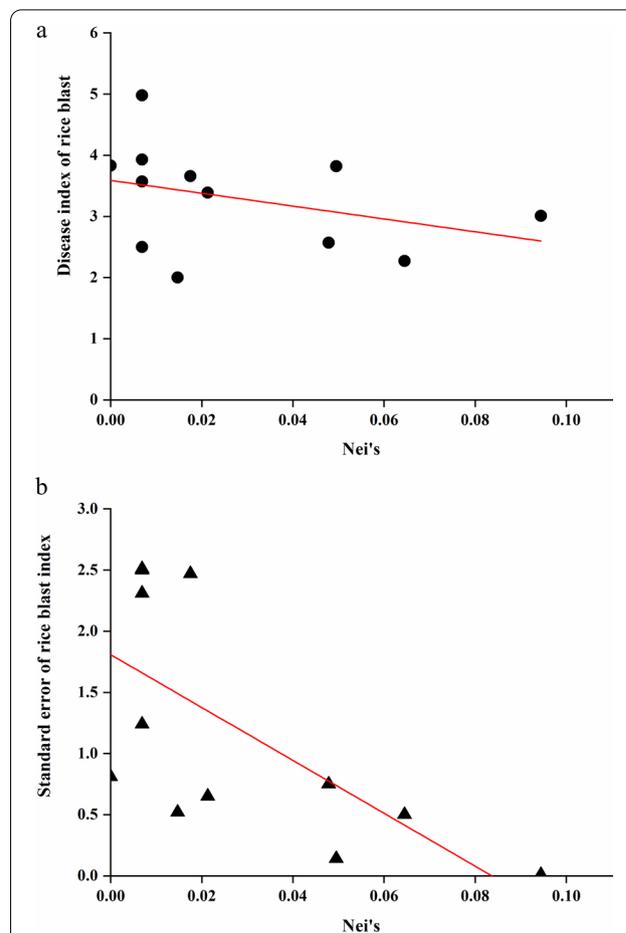


Fig. 3 The correlation between rice blast disease and Nei's diversity. **a** The correlation between disease index of rice blast and Nei's diversity index. **b** The correlation between standard error of rice blast disease index and Nei's diversity index. Red straight lines indicate the trend line. Black solid cycles indicate the mean disease index of multi-genotype varieties (4 varieties: YQ3, YQ5, YQ6, YQ11), component lines (CP-YQ3: 3-1, 3-2, 3-3, 3-4, 3-5; CP-YQ5: 5-1, 5-2, 5-3, 5-4, 5-5, 5-6, 5-7; CP-YQ6: 6-1, 6-2, 6-3, 6-4, 6-5; CP-YQ11: 11-1, 11-2, 11-3, 11-4, 11-5) and the control variety YiXiangYou2115 (four replicates, each corresponding to one of the four multi-genotype varieties). Black solid triangles indicate standard error of disease index

on YQ6 in Wenshan in 2015 (Fig. 4a and Additional file 2: Table S4).

For rice false smut, the occurrence of the disease was more severe in Chuxiong than that in other planting regions for all the tested rice varieties including CK; YQ6 and NBN in 2015, GD18 and GY1 in 2016, YQ1 and DJX6 in 2017 exhibited a moderate resistance (MR , $10 \leq DI \leq 30$) in Chuxiong. GD18 and GY1 in Qujing also showed a moderate resistance in 2016. The tested multi-genotype varieties in other planting regions were high resistant (HR , $DI \leq 3$) or resistant (R , $DI \leq 10$) to the disease. HY7 (CK) was high-resistant to rice false smut

The above data suggest that most of the multi-genotype varieties that we tested here have a good performance in disease resistance in different rice-planting regions, comparable or even superior to that of CK (a local disease-resistant variety) and exhibiting relatively stable disease resistance.

Multi-genotype varieties have stable performance in yield traits in field investigations

We also investigated rice yield, plant height and some yield-associated agronomic traits of the aforementioned 6 multi-genotype varieties at different ecological regions in Yunnan Province during 2015–2017. In 2015, the average rice yield of NBN (9.19 t/ha) at the four trial regions was higher than those of YQ6 (7.03 t/ha) and the control variety HY7 (7.14 t/ha). Among different rice-planting regions, multi-genotype varieties planted in Honghe had the highest average yield (8.86 t/ha). NBN planted in Dehong had the highest yield (10.02 t/ha) in all varieties and planting regions. In 2016, YQ1 performed greatest at all the four rice-planting regions (8.10 t/ha) and had a higher yield than those of GD18 (6.42 t/ha) and HY7 (7.85 t/ha). Multi-genotype varieties had the highest average yield in Qujing (9.51 t/ha), with yields significantly higher than those in Chuxiong (5.06 t/ha), Dehong (7.81 t/ha) and Wenshan (7.34 t/ha). In 2017, YQ1 produced higher yields at the four rice-planting regions (7.6 t/ha) than other varieties. Among different rice-planting areas, the average yield of three multi-genotype varieties were highest in Honghe (9.06 t/ha) and lowest in Chuxiong (6.28 t/ha), NBN planted in Honghe reached highest yield (9.81 t/ha) (Fig. 5 and Additional file 2: Table S5).

Plant height is an important agronomic trait for crop production. We found that the plant height of multi-genotype varieties in Dehong was significantly higher than that in other regions (Fig. 5 and Additional file 2: Table S5,

$P < 0.05$). A low coefficient of variation in plant height of multi-genotype varieties indicated that these varieties had good adaptability in Yunnan Province ($SE = 0.23 - 2.85$, Additional file 2: Table S5). The thousand-grain weights of NBN (2015), YQ1 and DJX6 were highest in Dehong (30.45 g, 30.14 g and 31.40 g, respectively), and those of YQ6 and NBN (2017) were highest in Honghe (32.07 g and 37.23 g, respectively) (Additional file 2: Table S5). The seed-setting rates of NBN (2015), GD18, GY1 and DJX6 in Dehong (81.59%, 80.37%, 81.78% and 81.32%, respectively) were significantly higher than those in the other three rice-producing regions (67.86–78.20%, $P < 0.05$, Additional file 2: Table S5). GD18 and NBN (2017) had the highest seed-setting rates in Wenshan (80.67% and 82.21%, respectively), and YQ6 had the highest seed-setting rate in Honghe (84.73%). YQ6 had the highest panicle length (31.56 cm) in all the planting areas (panicle length = 18.88–22.70) (Fig. 5 and Additional file 2: Table S5).

From these results, we concluded that during our three-year investigation, the yields of multi-genotype varieties were relatively stable in different rice-planting regions of Yunnan Province, and some varieties had a higher yield than the local high-yielding variety HongYou-7 (CK). There was also a high degree of uniformity in plant height. The performance of other yield-associated agronomic traits was also relatively stable. This shows that multi-genotype varieties have both a strong environmental adaptability and a high-yield potential.

Discussion

Multi-parental convergent hybridization is a new breeding strategy to develop multi-genotype varieties (Cavanagh et al. 2008). Since there is an unlimited source of parental materials, multi-genotype varieties derived from parental varieties/lines with complementary traits

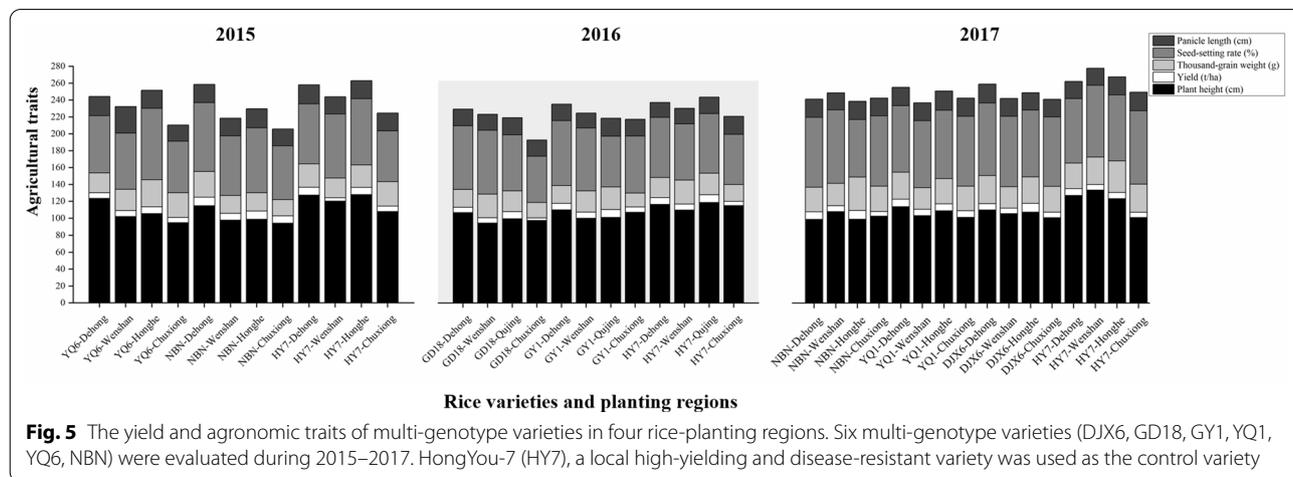


Fig. 5 The yield and agronomic traits of multi-genotype varieties in four rice-planting regions. Six multi-genotype varieties (DJX6, GD18, GY1, YQ1, YQ6, NBN) were evaluated during 2015–2017. HongYou-7 (HY7), a local high-yielding and disease-resistant variety was used as the control variety

can fuse their high-yield, strong disease-resistance and some other good agricultural traits together (Li et al. 2013). From the perspective of genetics, multi-genotype varieties are endowed with plentiful genetic diversity (Li et al. 2013). Several multi-genotype varieties were used in this study. Among them, YouQun-3 and YouQun-5 are derived from an 8-parent convergent cross; YouQun-6 and YouQun-11 are from a 12- and 3-parent convergent cross, respectively. SSR markers have been widely used to detect genetic diversity of rice plants (Aljumaili et al. 2018). Our SSR analysis showed that the levels of genetic diversity of multi-genotype varieties are significantly higher than those of the component lines and common rice varieties (Fig. 3 and Additional file 2: Table S3), indicating that the number of donor parents correlates with the genetic diversity of their derived varieties. Biparental lines have only two alleles at a locus, which limits the richness of single nucleotide polymorphism (Morrell et al. 2012). Multi-genotype varieties are constructed by paired hybridization between multiple parental lines (2^n) and subsequent multi-generational inbreeding, and therefore they have a greater genetic diversity and a higher allele frequency (Han et al. 2020; Ayaad et al. 2020). Accordingly, multi-genotype varieties are considered to be ideal for efficient and rapid DNA profiling and fine genetic mapping, and this provides the possibility of efficient molecular breeding on many complex agronomic traits (Mackay and Powell 2007).

Improving genetic richness is a good practice for controlling crop diseases in environment-friendly ways (Han et al. 2016). Correa-Victoria et al. (2004) performed a correlation analysis between blast resistance and genetic diversity in rice plants, and found that the occurrence of rice blast disease is significantly negatively correlated with the Shannon index, percentage of polymorphic loci and expected heterozygosity of rice varieties. This indicates that the resistance levels of rice varieties to rice blast increase with their increased genetic diversity. Our study also demonstrates that the good performance of multi-genotype varieties in disease resistance is conferred by their distant parents with broad genetic background (Figs. 3, 4 and Additional file 2: Tables S3, S4). Multi-genotype varieties have a rich genetic diversity, so compared with mono-genotype varieties, they have an increased resistance to environmental stress and a relative low disease severity.

An important characteristic for quality evaluation of rice varieties is their ecological adaptability in different environments (Yang et al. 2013). In this study, disease resistance and yield potential of rice multi-genotype varieties under different ecological environments in Yunnan Province were determined. The results showed that multi-genotype varieties have an enhanced disease

resistance, allowing a moderate or mild disease occurrence, and meanwhile, they have a stable yield production that is superior to local high-yielding japonica rice variety (Fig. 5 and Additional file 2: Table S5). Previous studies have also shown that the MAGIC populations have obvious advantages in improving disease resistance, rice quality and yield (He et al. 2019; Li et al. 2013). Among the 20 MAGIC populations derived from convergent crossing of 12 different rice parent materials, most populations exceed the control variety in yield and rice quality, but have a lower disease index for panicle blast (Li 2012; Li et al. 2013), consistent with the results of this study. Therefore, multi-genotype varieties can be deployed in different rice-producing regions with different environmental conditions according to this and other studies (Wang et al. 2016; Zhang et al. 2017, 2018; He et al. 2019).

Some studies have revealed that intercropping and variety mixture planting have good effects on improving crop biodiversity and consequently controlling pests and diseases (Trutmann et al. 1993; Zhu et al. 2000, 2004; Han et al. 2016), but these studies only approach the issue from the perspective of cultivation, and don't change the genetic diversity of plant varieties. Although there is a concept of variety mixture (Kiær et al. 2012), the corresponding seed industry technology has not been developed, and there are no such commercial seeds that could be widely promoted. MAGIC breeding approach overcomes the limitations of existing breeding technologies, facilitating the creation of multi-genotype varieties. Moreover, in breeding practice, we can improve a specific trait of a multi-genotype variety via adjusting the construct of its component lines, which can further enlarge the adaptability and application range of this variety.

To date, through the MAGIC breeding approach, multi-genotype populations have been developed in approximate ten crops, such as rice, wheat, barley, maize, cotton and *Arabidopsis*, indicating the importance and acceptance of this breeding technology (Kover et al. 2009; Huang et al. 2011; Huang et al. 2012; Bandillo et al. 2013; Dell'Acqua et al. 2015; Sannemann et al. 2015; Islam et al. 2016). With more and more multi-genotype populations are developed in various crops, with the promotion of multi-genotype varieties in crop production, the genetic diversity and stability of agroecosystem will be much increased. The mechanism underlying the synergistic effect of component lines in enhancing stress resistance and yield-associated traits of multi-genotype varieties needs to be investigated in future researches.

Conclusions

In this study, we demonstrated that rice blast resistance and genetic diversity of multi-genotype varieties are superior to those of their component lines and mono-genotype varieties, and the occurrence of rice diseases decreases as genetic diversity increases. We further conducted a three-year field trial, and found that multi-genotype varieties have good disease resistance and possess the high-yield potential.

Methods

Rice varieties used in this study

The four multi-genotype varieties, YouQun-3 (YQ3), YouQun-5 (YQ5), YouQun-6 (YQ6) and YouQun-11 (YQ11), and their component lines were used to carry out plot experiments to assess disease resistance and genetic diversity in 2014. Six multi-genotype varieties, including YQ6, NanBaNuo (NBN), GuangYou-1 (GY1), GuangDuo-18 (GD18), DuoJiXin-6 (DJX6) and YouQun-1 (YQ1), were selected to conduct field experiments to assess their ecological adaptability in four different rice-producing areas during 2015–2017 (Table 1). The indica varieties YiXiangYou2115 (2014) and HongYou-7 (2015–2017) with high yield and good disease resistance were used as controls. The parental background information of multi-genotype varieties is presented in Additional file 2: Table S6.

Comparison of disease resistance among multi-genotype varieties and their component lines

Multi-genotype varieties and their component lines were subjected to plot experiments in 2014. Four plots were used, with each (6 rows \times 22 columns) having a size of 3.36 m² and a planting density of 16.7 cm \times 20 cm. For each rice variety/line, 100 individuals were grown. The planting order in plots is as follows: YQ3: CK, 3-1, 3-2, 3-3, 3-4, 3-5; YQ5: CK, 5-1, 5-2, 5-3, 5-4, 5-5, 5-6, 5-7; YQ6: CK, 6-1, 6-2, 6-3, 6-4, 6-5; YQ11: CK, 11-1, 11-2, 11-3, 11-4, 11-5. Throughout the growing season, pest instead of disease control was performed. Conventional irrigation and fertilization management was conducted. At the yellow ripening stage, 30 panicles were randomly investigated for the occurrence of rice diseases, including panicle blast, false smut and bacterial blight, in Dehong, Yunnan Province. Investigation of the incidence and disease index of rice diseases (rice blast, false smut and bacterial blight) was performed based on the Standard Evaluation System for Rice (International Rice Research Institute 2013; Additional file 2: Table S7).

DNA extraction and PCR amplification

Ten fresh leaves of each rice variety/line were collected for DNA extraction following the method as described

previously (Saghai Maroof et al. 1984). Twenty-four SSR markers distributed on 12 rice chromosomes were used in this study. PCR amplification was carried out in a final volume of 20 μ L, including 1 μ L of DNA template (25 ng), 0.5 μ L of each primer (forward and reverse primer), 2 μ L dNTP mix (2 mmol/L), 0.2 μ L *Taq* DNA polymerase (5U/ μ L, Sangon Biotech), 1.34 μ L MgCl₂ (25 mmol/L), 2 μ L PCR buffer (10 \times) and 12.46 μ L double distilled water. The PCR conditions were as follows: 1 cycle at 94 $^{\circ}$ C for 4 min; 36 cycles at 94 $^{\circ}$ C for 40 s, 55 $^{\circ}$ C for 30 s and 72 $^{\circ}$ C for 40 s; 1 cycle at 72 $^{\circ}$ C for 10 min. PCR products were separated on 6% denaturing polyacrylamide gel at 300 V for 80 min and then silver-stained as described previously (Creste et al. 2001). SSR data reading was performed according to the size of amplified products, and the products with the same size were regarded as an allele. Genetic diversity-related indexes such as observed alleles (Na), effective alleles (Ne), Shannon index (I), observed heterozygosity (Ho), expected heterozygosity (He) and Nei's gene diversity index (H) were calculated using PopGene (Version 1.32).

Investigation of the occurrence of rice diseases in multi-genotype varieties in different rice-planting regions

Ecological responses of multi-genotype varieties were evaluated in five counties with different ecological conditions in Yunnan Province during 2015–2017 (Table 1). The experiments were performed with a randomized complete block design with three replications. Each plot has a size of 1.33 \times 10⁻² ha and a planting density of 13.3 cm \times 20 cm. Throughout the growing season, pest control instead of disease control was performed; conventional irrigation and fertilization management were conducted. One hundred panicles were randomly investigated at the yellow ripening stage for the occurrence of rice blast, false smut and bacterial blight diseases at all experimental sites.

Evaluation of yield and agronomic traits

Yields of multi-genotype varieties were determined at the rice maturity stage during 2015–2017. Other agronomic characteristics, including plant height, seed-setting rate, thousand-grain weight and panicle length, were also determined following standard methods (Fang 1998).

Statistical analysis

SPSS 18.0 and Microsoft Office Excel 2019 were used for the analysis of variance and Fisher's least significant difference (LSD) test. The figures and tables were generated using ORIGIN 8.0 and CorelDRAW X8.

Abbreviations

DI: Disease index; DJX6: DuojiXin-6; GD18: GuangDuo-18; GY1: GuangYou-1; H: Nei's gene diversity index; He: Expected heterozygosity; Ho: Observed heterozygosity; HY7: HongYou-7; I: Shannon index; MAGIC: Multi-parent advanced generation inter-cross; Na: Observed alleles; Ne: Effective alleles; PCR: Polymerase chain reaction; SSR: Simple sequence repeats; YQ1: YouQun-1; YQ3: YouQun-3; YQ5: YouQun-5; YQ6: YouQun-6; YQ11: YouQun-11; YXY2115: YiXiangYou2115.

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s42483-021-00105-x>.

Additional file 1: Figure S1. Schematic diagram of breeding MAGIC lines. **Figure S2.** The occurrence of three main rice diseases on multi-genotype varieties and their component lines. **Figure S3.** A representative image of SSR assay.

Additional file 2: Table S1. Occurrence of three main rice diseases in plot experiments in 2014. **Table S2.** Yields and agronomic traits of multi-genotype varieties in plot experiments in 2014. **Table S3.** The genetic diversity index of multi-genotype varieties and their components. **Table S4.** Occurrence of three main rice diseases in field experiments during 2015–2017. **Table S5.** Yields and agronomic traits of multi-genotype varieties in field experiments during 2015–2017. **Table S6.** Parental information of multi-genotype varieties used in this study. **Table S7.** Grading criteria for evaluation of the severity of rice blast, false smut and bacterial blight.

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Authors' contributions

PH, YZ, GH and YYW designed the research; PH, CW, NZ, BL, YY and XY performed the experiments; XL developed the rice varieties; PH, YZ and GH analyzed the data; PH, GH and YYW wrote and revised the manuscript. All authors read and approved the final manuscript.

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Availability of data and materials

Not applicable.

Declarations

Ethic approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author details

¹State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, Ministry of Education Key Laboratory of Agriculture Biodiversity for Plant Disease Management, College of Plant Protection, Yunnan Agricultural University, Kunming 650201, Yunnan, China. ²Crop Genetic and Breeding Institute of Yangtze University, Jinzhou 434025, Hubei, China. ³Dehong Agricultural Technology Extension Center, Dehong 678400, Yunnan, China.

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