Agricultural Sciences, 2023, 14, 485-498
https://www.scirp.org/journal/as
ISSN Online: 2156-8561
ISSN Print: 2156-8553

The Relation between Genetic Difference for Parents of Hybrid Rice and Heterosis

Xudong Zhu[1*], Xieli Tong[2], Ju Zhao[1], Ziliang Zhu[1], Dan Zhu[1], Qingming Zhou[1]

[1]College of Agronomy, Hunan Agricultural University, Changsha, China
[2]Agricultural and Rural Bureau, Hengshan County, Hengyang, China
Email: *zxdzhaoju@126.com

How to cite this paper: Zhu, X.D., Tong, X.L., Zhao, J., Zhu, Z.L., Zhu, D. and Zhou, Q.M. (2023) The Relation between Genetic Difference for Parents of Hybrid Rice and Heterosis. *Agricultural Sciences*, **14**, 485-498.
https://doi.org/10.4236/as.2023.144032

Received: February 17, 2023
Accepted: April 9, 2023
Published: April 12, 2023

Abstract

Exploring the *indica-japonica* differentiation in parents of hybridization can provide theoretical bases for utilizing inter-subspecific heterosis. In this study, 5 sterile lines and 18 self-bred restorer lines were used as female parents and male parents respectively. Then 90 combinations were constructed by incomplete diallel cross followed by relationship analysis between parental Cheng's index difference value and Euclidean distance and heterosis. The results showed a significant correlation between several phenotype values, super male parent heterosis and control heterosis and Euclidean distance or Cheng's index difference value. However, it was no significant correlation for yield. Further analysis found a common interval, 3.41 - 3.46 for Euclidean distance and 3 - 4 for cheng's index difference value of parents, which was significant or high significant positive correlated with phenotype value, super male parent and control heterosis of main yield traits. This illustrates that the larger the genetic difference of parents was, the stronger the heterosis combinations were, when the genetic differences of parents were in an appropriate range.

Keywords

Indica and *Japonica* Subspecies, Heterosis, Cheng's Index, Euclidean Distance

1. Introduction

Rice is an important food crop; nearly half of the world's population depends on rice as the main food. Breeding rice varieties with high yield and high quality are necessary to ensure global food security. In order to achieve this goal, a large number of rice varieties (combinations) with high yield and high quality have been bred, greatly increasing rice yield per unit area. However, the genetic background is relatively narrow for the parents of rice varieties (combinations) pro-

moted in the current production, which limits the utilization of intervarietal heterosis, and increasing rice production has met a bottleneck. The hybrid F1 of *indica-japonica* subspecies contains huge biology heterosis [1] [2]. Exploitation of inter-subspecific heterosis in rice is recognised as an effective approach to further improving the rice yield [3] [4]. There was high degree genetic differentiation between *indica-japonica* subspecies genome [5] [6], and has closely relation with the strong heterosis [7] [8]. But because of a farther genetic relationship, there were four major problems for hybrid F1: low seed-set rate, high plant height, long growth period, and grain not full [9] [10], so the degree of difficulty for breeding hybrid rice combinations with strong heterosis was very larger.

The inter-subspecies hybrid fertility was controlled by interaction gene of a set of multiple alleles on S_5 site, and found that Ketan Nangka, CPSLO17 and Dular crossed with type typical *indica* or *japonica* varieties, seed setting rate of their offspring was normal. They put forward the theory of wide compatibility, the wide compatibility gene and are multiple alleles with *indica* and *japonica* subspecies hybrid sterility genes, their genetic fits a pattern of unit point sporophyte - gametophyte interactions, and located the wide compatibility gene [11] [12]. This theory was supported by follows a string of research [13] [14] [15], and found multiple hybrid sterility sites except S_5 site, and hybrid abortion was caused by female gamete abortion [16] [17] [18] [19] and also pollen abortion [19] [20] [21] [22].

"Building a bridge between *indica* and *japonica*" could partially solve the above problems [23]. The breeding goals of *indica*-compatible *japonica* lines was proposed [24] [25] Mixed with *japonica* in *indica* restorer line in southern China and mixed with *indica* in *japonica* in northern China. Up to now, a number of *indica-japonica* varieties with both wide compatibility gene and restoration gene have been developed [26] [27] [28]. Yu Yahui *et al.* studied the heterosis between *indica-japonica* subspecies by using *japonica* two-line hybrid rice parents and combinations as materials, and concluded that the difference of *indica-japonica* composition of parents was significantly and high significantly positively correlated with the yield and yield heterosis [29]. However, it was rarely for the report of successful matched *indica* type (or partial *indica* type) sterile lines with *japonica* type (or partial *japonica* type) restorer lines so far. The purpose of this study was aimed to explore the key technology of inter-*indica-japonica* subspecies combination to provide theoretical and practical reference for the breeding of *inter-indica* hybrid rice.

2. Materials and Methods

2.1. Test Materials

Sterile lines: Minyuan A, Guangzhan 63S, 33S, Shen 97A, Hengfeng A, Denoted by A1, A2, A3, A4 and A5 respectively. Provide by Hunan Liusan seed industry Co. Ltd.

Restorer line: R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R11, R12, R13, R14, R15, R16, R17 and R18, all of them was bred by research group. The control combination was provided by Long Ping seed industry.

2.2. Test Design

A total of 114 materials (including 5 sterile lines, 18 restorer lines, 90 combinations and control combination Y Liangyou 1) were planted in the breeding base of Chang'an Village, Gansha Town, Changsha County. All combinations and parents material planted according to the method of contrast test design. Except for control combination, the other material planted more than 100 plants, and with a spacing of 16.7 cm × 16.7 cm with single seedling per hill, and the distance among materials was 33 cm. Field management was accorded to the production requirements of conventional hybrid rice planting.

2.3. Sampling

Selected 2 spots for each material in the middle of plot, 10 plants for each plot to count effective panicle of unit area, sampled according to the effective panicle of unit area each plot. Inspected plant height, panicle length, total grain number of per panicle, filled grains per panicle, setting rate, 1000 grain weight in doors, 50 plants were harvested from each plot and dried and weighed, converted to the actual yield of unit area.

2.4. Measure Cheng's Index

Identify the *indica-japonica* attribute of parental materials by Cheng's index method. The total score ≤ 8 is divided into *indica*, 9 - 13 divided into indicalinous, 14 - 17 divided into japonicalinous, 18 to 24 divided into japonica. The specific method was as below Table 1:

1) Glume hairiness: take ten grains randomly, and observe the morphological characters of glume hairness;

Table 1. The scores and identification character according to Cheng's index.

Index	0	1	2	3	4
Glume hairiness	short, neat, hard, straight, even	hard, sightly neat, sightly long, middle or longer	not neat, long, sightly soft	lack of neat or not neat	long, chaos, soft
Phenol reaction	black	gray black or brown black	grey	edge and arris tinging	no dye
the length of the 1 and 2 rachis	<2.0 cm	2.1 - 2.5 cm	2.6 - 3.0 cm	3.1 - 3.5 cm	>3.5 cm
Glume color	greenish white	whitish green	yellowish green	light green	green
Leaf pubescence	very much	much	middle	little	none
Shape of grain	>3.5	3.5 - 3.1	3.0 - 2.6	2.5 - 2.1	<2.0

2) Phenol reaction: take ten grains randomly, and soak them into 2% phenol solution in the petri dish for about 24 h, then observe the glume color;

3) Interval between the 1st and 2nd nodes of panicle axis: measure ten panicles randomly between the 1st and 2nd nodes;

4) Glume color at heading: take ten plances randomly, and identify the glume color at the heading stage;

5) Leaf pubescence: take ten leaves randomly, and judge how many leaf pubescences at the heading stage;

6) Shape of grain: take five grains randomly, measure their lengths and widths, then calculate the length-width ratio.

2.5. Data Processing

The data was calculated in Excel 2010, and the correlation analysis and Euclidean distance was calculated in DPS 9.5.

$$\text{Super male parents heterosis} = \frac{F_1 - P}{P} \times 100$$

$$\text{Control heterosis} = \frac{F_1 - CK}{CK} \times 100$$

3. Results

3.1. Analysis on Heterosis of Test Combinations

3.1.1. Super Male Parent Heterosis of Test Combinations

Super male parent heterosis of all eight traits were positive, among of them, the strongest super male parent heterosis was filled grains per panicle, was 22.00%, followed by total grains number per panicle, was 17.42%, the smallest was effective panicles per unit area, was 1.16% (Table 2); The number of test combinations with negative super male parent heterosis for plant height trait was 8.89%. The number of combinations with positive super male parent heterosis for effective panicles per unit area, filled grains per panicle, seed setting rate, 1000 weight,

Table 2. The over male heterosis for agronomic trats and yield of test combinations (Unit: %).

NO.	PH	PP	PL	NGP	FGP	SR	GW	YP
Mean value	10.73	1.16	6.85	17.42	22.00	3.91	3.06	9.01
Range	45.85	129.17	41.61	165.53	189. 50	50.69	61.74	123.86
Variable coefficient	0.88	19.74	1.27	2.01	1.72	2.37	3.58	2.51
Miximum	35.19	38.24	31.50	125.89	151.26	31.86	42.66	80.28
Minimum	−10.66	−90.94	−10.11	−39.64	−38.24	−18.83	−19.08	−43.58
Combinations with positive	80	54	67	60	64	61	59	59
Combinations with negtative	8	35	23	30	26	28	31	31
Combinations with zero heterosis	2	1	0	0	0	1	0	0

Note: PH: Plant height, PP: Effective panicles per unit area, PL: Panicle leight, NGP: total number of grains per panicle, FGP: Filled grains per panicle, SR: setting rate, GW: 1000 weight, YP: Actual yield unit area, the same bellow.

and the actual yield unit area were 60.00%, 74.44%, 66.67%, 71.11%, 67.78%, 65.56% and 65.56% respectively (Table 2). The results showed that the combinations with positive super parent heterosis was common, It is possible for selecting out the combinations with the stronger super male parent heterosis.

3.1.2. Control Heterosis of Test Combinations

The control heterosis mean value was positive for effective panicles per unit area, total grain number per panicle and actual production. The control heterosis of effective panicles per unit area was strongest, was 4.69%, followed by total number of grain per panicle, was 3.27%; The control heterosis of plant heitht was weakest, was −11.75%. Combinations with negative control heterosis occupied 93.33%. It indicated that the plant height was shorter than control combination common. The number of combinations with positive control heterosis were effective panicles per unit area, filled grains per panicle, 1000 weight and the actual yield traits were 65.56%, 17.78%, 51.11%, 43.33%, 10.00%, 23.33%, 51.11% respectively. The results showed it was possible for selecting combinations with good comprehensive traits and strong control heterosis (Table 3).

3.2. Genetic Difference between the Parents of Combinations

3.2.1. Euclidean Distance between the Parents

The Euclidean distance between parents of the test combinations was in the interval 1.4 - 5.19. The range of Euclidean distance between the parents of the test combination was 3.72. Among of them, the number of combinations was 5 for the Euclidean distance greater than or equal to 5; 11 for greater than or equal to 4 and less than 5; 41 for greater than or equal to 3 and less than 4; 27 for greater than or equal to 2 and less than 3, 8 for less than 2 (Table 4). This result indicating the parents of the test combinations had certain genetic differences.

3.2.2. The Cheng's Index Value and the Difference Value between the Parents of Combinations

Among 5 sterile lines, Cheng's index value of A1 and A5 less than 8, was *indica*,

Table 3. The control heterosis for agronomic trats and yield of test combinations. Unit: %.

No	PH	PP	PL	NGP	FGP	SR	GW	YP
Mean value	−11.75	4.69	−7.13	3.27	−3.10	−5.87	−6.37	0.34
Range	26.85	65.24	29.90	94.84	102.39	29.10	40.04	163.60
Variable coefficient	−0.57	2.71	−1.02	7.04	−7.25	−0.96	−1.30	62.91
Mixmum	1.74	40.24	8.93	54.72	53.51	6.04	12.45	111.22
Minimum	−25.11	−25.00	−20.97	−40.12	−48.88	−23.06	−27.59	−52.38
Combinations with positive	4	59	16	46	39	9	21	46
Combinations with negtative	84	24	74	44	51	81	69	44
Combinations with zero heterosis	2	7	0	0	0	0	0	0

Table 4. The Euclidean distance between two parents.

Parents	A1	A2	A3	A4	A5
R1	3.13	3.92	3.42	4.36	3.69
R2	1.52	2.72	1.44	2.09	3.44
R3	3.85	3.44	3.59	3.43	4.29
R4	2.98	2.23	3.46	3.16	2.78
R5	2.21	3.73	2.53	3.86	5.16
R6	2.15	3.47	3.45	4.16	4.48
R7	1.87	3.13	3.46	4.00	4.25
R8	2.14	3.73	2.38	3.47	3.88
R9	1.87	3.06	2.24	3.17	3.40
R10	2.00	2.83	2.90	3.41	5.05
R11	2.24	3.75	1.73	3.37	4.11
R12	1.40	2.71	2.05	2.83	3.88
R13	1.75	2.79	2.98	3.64	4.45
R14	2.02	2.92	2.19	2.80	3.58
R15	3.20	3.86	3.29	3.93	3.40
R16	2.42	3.47	3.93	4.40	3.87
R17	2.51	3.52	3.52	4.33	4.55
R18	2.46	3.72	1.73	3.08	5.19

Cheng's index value of A2, A3 and A4 was in the interval 9 - 13, were the indicalinous. Among of 18 restorers lines, Cheng's index value of R4, R12, R14 less than 8, were *indica*, Cheng's index value of R3, R5, R6, R8, R9, R10, R13, R16, R17 and R18 was in the interval 9 - 13, were the indicalinous, Cheng's index value of R1, R2 and R15 was in the interval 14 - 18, were japonicalinous. The number of combinations were 4, 17, 19, 17, 13, 3, 5, 6, 4 and 2 for the parent Cheng's index difference value 9, 8, 7, 6, 5, 4, 3, 2, 1 and 0 respectively (Table 5).

3.3. Analysis on the Relation between Difference of Parents and Heterosis

3.3.1. The Correlation Analysis between Differences of Parents and Heterosis

From the phenotypic value, the phenotype values of plant height, total number of grains per panicle and filled grains per panicle were high significantly positive correlation with the Euclidean distance between the parents. The phenotype values of total number of grains per panicle and filled grains per panicle were significantly or high significantly positively correlation with the cheng's index difference value between the parents (Table 6). From the super male parent

Table 5. The difference value between two parents.

The Cheng's index index of female parent		A1	A2	A3	A4	A5
The Cheng's index vaule of male parent		6	11	9	10	6
R1	14	8.0	3.0	5.0	4.0	8.0
R2	14	8.0	3.0	5.0	4.0	8.0
R3	13	7.0	2.0	4.0	3.0	7.0
R4	7	1.0	4.0	2.0	3.0	1.0
R5	12	6.0	1.0	3.0	2.0	6.0
R6	9	3.0	2.0	0.0	1.0	3.0
R7	12	6.0	1.0	3.0	2.0	6.0
R8	9	3.0	2.0	0.0	1.0	3.0
R9	10	4.0	1.0	1.0	0.0	4.0
R10	8	2.0	3.0	1.0	2.0	2.0
R11	10	4.0	1.0	1.0	0.0	4.0
R12	7	1.0	4.0	2.0	3.0	1.0
R13	8	2.0	3.0	1.0	2.0	2.0
R14	7	1.0	4.0	2.0	3.0	1.0
R15	15	9.0	4.0	6.0	5.0	9.0
R16	13	7.0	2.0	4.0	3.0	7.0
R17	8	2.0	3.0	1.0	2.0	2.0
R18	13	7.0	2.0	4.0	3.0	7.0

Table 6. The correlation analysis between the difference of parents and heterosis.

Item	correlation coefficient	PH	PP	PL	NGP	FGP	SR	GW	YP
Phenotypic value	Euclidean distance	0.3411**	0.1692	0.1428	0.3004**	0.3298**	0.1126	0.1533	0.0411
	Cheng's index difference value	−0.1822	0.1242	0.1515	0.2861**	0.2472*	−0.1360	−0.1873	−0.0050
Super male parents heterosis	Euclidean distance	0.1451	−0.2437*	0.2196*	0.3406**	0.3293**	−0.0103	0.1293	0.0001
	Cheng's index difference value	0.1004	−0.1091	0.3234**	0.1420	0.1931	0.1056	0.0261	−0.0414
Control heterosis	Euclidean distance	0.4554**	−0.1109	0.2273*	0.3478**	0.4233**	0.2074*	0.2052	0.1148
	Cheng's index difference value	−0.2336*	0.0924	0.1664	0.3783**	0.3066**	−0.0999	−0.1898	−0.0667

Note: *means a = 0.05, r = 0.2072, 0.05 significant level, **means a = 0.01, r = 0.2702, 0.01 significant level.

heterosis. The super male parents heterosis of panicle length, total number of grains per panicle and filled grains per panicle were significantly or high significantly positive correlation with the Euclidean distance between the parents, while the super male parent heterosis of effective panicle unit area was significantly negatively correlation with the Euclidean distance between the parents. Panicle length traits was significant positive correlation between super male parents heterosis and the difference value of cheng's index of the parents, while for other traits, there was no significant correlation between super male parents heterosis and the difference value of cheng's index between parents (**Table 6**).

From the control heterosis, the control heterosis of plant height, panicle length, total number of grains per panicle, filled grains per panicle and seed setting rate trait were significantly or high significantly positively correlation with the Euclidean distance between the parents. The control heterosis of effective panicle per unit area, panicle leight, total number of grains per panicle, filled grains per panicle trait were significantly or high significantly positively correlation with Cheng's index difference value of parents, it was significantly negatively correlated between control heterosis and Cheng's index difference value of parents for plant height (**Table 6**).

The above results showed there were significant or high significant positive correlation between parental Euclidean distance and phenotype value, super male parent heterosis and control heterosis of total grain of per panicle and filled grains per panicle. The positive significant or high significant correlation between parental Cheng's index difference value and phenotype value and control heterosis of total number grain of per panicle and filled grains per panicle, but it was no significant correlation for yield. Therefore, it was not larger for Euclidean distance and Cheng's index difference value of parents, the stronger for actual yield heterosis of combinations.

3.3.2. The Correlation Analysis between the Different Parental Genetic Difference Interval and the Heterosis

To further understanding the relationship between parental genetic difference and heterosis, we analyzed the correlation between different intervals of parental genetic differences and heterosis, hoped to find out the parental genetic difference interval closely related with heterosis. The parental Euclidean distance in the interval of 3.41 - 3.52, it was high significant negative correlation between the parental Euclidean distance and the phenotype value of plant height. it was significant or high significant positive correlation between the parental Euclidean distance and the phenotype value of effective panicles per unit area, filled grains per panicle, 1000 - grain weight and actual yield and parental (**Table 7**). It was possible for selecting the combinations with good comprehensive performance and plant height is shorter, When the Euclidean distance of the parents in the interval of 3.41 - 3.52.

In the interval of 3 - 5 for Chen's index difference value, there was a significant negative correlation between the phenotype value of plant height and

Table 7. The correlation analysis on interval of the difference for parents and the heterosis for agronomic trats and yield of combinations.

	Item	PH	PP	PL	NGP	FGP	SR	GW	YP
Phenotypic value	Interval of parental Euclidean distance	1.40 - 5.19	3.41 - 3.59	3.44 - 3.64	1.40 - 5.19	1.40 - 5.19	3.47 - 5.05	3.29 - 3.52	3.06 - 4.40
	correlation coefficient	−0.3411*	0.5211*	0.5779*	0.3004**	0.3298**	0.3523*	0.4826*	0.3012*
	Interval of parental Cheng's index difference value	0 - 9	1 - 9	3 - 8	0 - 9	0 - 9	3 - 5	5 - 6	2 - 7
	correlation coefficient	−0.2400*	0.2504*	0.3506*	0.2861**	0.2472*	0.4670*	0.8563	0.3366*
Super parent heterosis	Interval of parental Euclidean distance	2.98 - 3.64	3.41 - 3.59	1.40 - 5.19	1.40 - 5.19	1.40 - 5.19	3.45 - 3.58	2.24 - 3.88	3.41 - 3.59
	correlation coefficient	−0.4530*	0.4500*	0.2196*	0.3406**	0.3293**	0.7798*	0.2711*	0.6025*
	Interval of parental Cheng's index difference value	3 - 8	3 - 4	0 - 9	7 - 9	1 - 6	1 - 9	3 - 4	2 - 6
	correlation coefficient	−0.3024*	0.5025*	0.3234**	0.6572*	0.3024*	0.2356*	0.5131*	0.3159*
Control heterosis	Interval of parental Euclidean distance	3.47 - 3.64	3.41 - 3.46	1.40 - 5.19	1.40 - 5.19	1.40 - 5.19	1.40 - 5.19	1.44 - 5.16	2.02 - 5.16
	correlation coefficient	−0.7242**	0.7000*	0.2273*	0.3478**	0.4223**	0.2074*	0.2327*	0.2546*
	Interval of parental Cheng's index difference value	0 - 9	4 - 9	3 - 8	0 - 9	0 - 9	3 - 4	3–6	2 - 7
	correlation Coefficient	−0.2336*	0.4365*	0.3326*	0.3783**	0.3066**	0.4575*	0.3023	0.3411**

Note: *means 0.05 significant level, **means 0.01 significant level.

parental Cheng's index difference value. the phenotype values of effective panicles per unit area, total number of grains per panicle, filled grains per panicle, setting rate and the actual yield was significant or highly significant positive correlation with Cheng's index difference value of parents, that when Cheng's index difference value of the parents in the range of 3 - 5, it was possible for screening out combinations with good comprehensive properties, and plant height is short.

When the Euclidean distance of parents was in the interval 3.45 - 3.58, the super male parent heterosis of plant height was negatively correlated with the Euclidean distance of parents, there was significant or highly significant positive correlation between the super male parent heterosis of parents effective panicle per unit area, total number of grains per panicle, seed setting rate, 1000 - grain weight and actual yield and the parental Euclidean distance. This indicated that when the Euclidean distance of parents was 3.45 - 3.58, it was completely possible to screen out the combinations with better comprehensive properties and shorter plant height than the male.

When Cheng's index difference value of parents was in the interval of 3 - 4, the super male parent heterosis of plant height was negatively correlated with the Cheng's index difference value of parents, the super male parents heterosis of ef-

fective panicle per unit area, total number of grains per panicle, setting rate, 1000 - grain weight and actual yield was significant positive correlated with the Cheng's index difference value of parents. It showed when Cheng's index difference value is in the interval of 3 - 4, it is possible to screen out the combinations with stronger super male parent heterosis and shorter plant height than the parent.

When the Euclidean distance of parents was in the interval 3.41 - 3.46, the control heterosis of plant height traits was highly significant negative correlation with the Euclidean distance of parents, the control heterosis of effective panicles per unit area, filled grains per panicle, setting rate and the actual yield was significant or highly significant positive correlation with Euclidean distance of parents. This indicated when the Euclidean distance of parents was in the interval of 3.41 - 3.46, it was completely possible to select combinations with better comprehensive traits and shorter plant height than the control combination.

When Cheng's index differences of parents was in the interval of 3 - 4, the control heterosis of plant height was significant negative correlation with the Cheng's index difference value of parents, The control heterosis of effective panicles per unit area, filled grains per panicle, setting rate and the actual yield were significantly or highly significant positive correlation with Cheng's index difference value of parents. When Cheng's index difference value of parents was in the interval of 3 – 4, this indicated that it was completely possible to select combinations with better comprehensive traits and shorter plant height than the control combination, when Cheng's index difference value between parents was in the intervals 3 and 4.

Based on the above analysis, we could find the Phenotypic value, super parent and control heterosis of effective panicles per unit area, filled grains per panicle, seed setting rate, 1000 - grain weight and the actual yield traits were significantly or highly significant positive correlation with Euclidean distance and Cheng Shi index difference value of parents, when Euclidean distance of parents was in the interval 3.41 - 3.46 and Cheng's index difference value of parents was in the interval 3 - 4. This indicated that the greater the genetic difference was, the stronger the heterosis was, as long as the genetic difference of the parents was in the proper range.

4. Conclusions and Discussion

The hybrid F1 of *indica-japonica* subspecies contains huge biology heterosis [28] [30], which is closely related to the genetic differences between the parents, but the former research results were not consistent. Some scholars believed that the seed setting rate of *indica-japonica* hybrid F1 was significantly negatively correlated with the Cheng's index difference of parents [30] [31] [32] [33]. The fertility index of F1 would show a peak value, and the *indica-japonica* intermediate type parents with moderate genetic differentiation could make up a high heterosis combination within a certain range of genetic differentiation of parents [34].

It was relatively moderate that the cheng's index difference value of parents was in the interval 6 - 13. At this interval, the biological and economic heterosis was stronger, the parental Cheng's index difference value was significantly negatively correlated with the setting rate of F1, while was significantly positive correlated with the biological yield of F1 (Yang *et al.*, 1991. Liu *et al.*, 1992.) [31] [35]. When Cheng's index difference value of parents was in the interval 1 - 6, the performance was excellent for main yield characters of combinations including effective panicle per plant, grain number per panicle, seed setting rate and yield per plant, and the super male and control heterosis were strong [36]. However, some people believed that the genetic difference between parents of three-line hybrid rice was not closely related to heterosis, and the yield of hybrid rice was closely related to the yield of both parents, especially the average yield of both parents [37].

In this study, 18 restorer lines with different degrees of *indica and japonica* were crossed with 5 *indica* sterile lines, and 90 combinations were prepared. The Euclidean distance between parents ranged from 1.40 to 5.19, and the difference in Cheng's index ranged from 0 to 9. The relationship between the Euclidean distance and Ching's index between parents and heterosis was explored. Results showed that Euclidean distance and Cheng's index difference value of parents were significantly or highly significantly positively correlated with the phenotypic value and control heterosis of total number grains and filled grains per panicle of test combinations. The parental Euclidean distance were significantly or highly significant positive correlation with super male parent heterosis of total number grains and filled grain per panicle, significantly negative correlation with super male parent heterosis of effective panicles per unit area, significantly positive correlation with control heterosis of setting rate, but not significantly correlation with the phenotype of value actual yield, super parent and control heterosis.

Further analysis showed that the Euclidean distance and Cheng Shi index difference value were in the interval 3.41 - 3.46 and 3 - 4 respectively, effective panicles per unit area, total grain number per panicle, filled grain per panicle, seed setting rate, 1000 - grain weight and the actual yield of the phenotypic value, super parent and contrast heterosis were significantly or high significantly positive correlated with Euclidean distance and Cheng's index difference value of parents. The results indicated that the greater the genetic difference, the stronger the heterosis, when the genetic difference of parents was in the proper range.

Acknowledgements

The research was supported by the National Key Research and Development Project (2017YFD301500) of China.

Authors' Contributions

Z. X., and Z. Q. conceived and designed the study. Z. X., T. X., and Z. J., per-

formed the experiments. Z.X. wrote the paper.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

References

[1] Zeng, S.X., Yang, X.Q. and Lu, Z.W. (1980) The Heterosis of F_1 Hybrids between *Oryza sativa* Subsp. Hsien and *O. sativa* Subsp. Keng. *Acta Agronomica Sinica*, **6**, 193-202.

[2] Xiao, J.H. and Yuan, L.P. (1988) Study on the Heterosis of *Indica-Japonica* Hybrid F1s and the Correlation with Their Parents. *Hybrid Rice*, **3**, 5-9.

[3] Yuan, L.P. (1987) The Strategic Ideas of Hybrid Rice Breeding. *Hybrid Rice*, **2**, 1-3.

[4] Yuan, L.P., Wu, X.J., Yan, Y.C. and Luo, X.H. (1997) A Strategy for Developing Wide Spectrum Compatibitly Rice Line. *Scientia Agricultura Sinica*, **30**, 1-8.

[5] Li, R.H., Jiang, T.B., Xu, C.G., Li, X.H. and Wang, X.K. (2000) Relationship between Morphological and Genetic Differentiation in Rice (*Oryza sativa* L.). *Euphytica*, **114**, 1-8. https://doi.org/10.1023/A:1003664528131

[6] Han, B. and Xue, Y.B. (2003) Genome-Wide Intraspecific DNA-Sequence Variation in Rice. *Current Opinion in Plant Biology*, **6**, 134-138. https://doi.org/10.1016/S1369-5266(03)00004-9

[7] Li, R.H., Xu, C.G., He, Y.Q., Yuan, L.P. and Wang, X.K. (1998) Relationship between the Extent of Genetic Differentiation in Parenta Lines and Heterosis of *Indica-Japonica* Hybrid Rice. *Acta Agronomica Sinica*, **24**, 564-576.

[8] Zhao, M.F., Li, X.H., Yang, J.B., Xu, C.G., Hu, R.Y., Liu, D.J. and Zhang, Q. (1999) Relationship between Molecular Marker Heterozygosity and Hybrid Performance in Inter-Subspecifie Crosses of Rice. *Plant Breeding*, **118**, 139-144. https://doi.org/10.1046/j.1439-0523.1999.118002139.x

[9] Chen, L.Y., Dai, K.G., Li, G.T. and Kang, C.L. (1992) A Comparative Study of Different Categories of F_1 Hybrids between *Indica* and *Japonica*. *Hybrid Rice*, **7**, 35-37.

[10] Zhang, Z.L., Wang, C.L., Tang, S.Z. and Shi, J.D. (1990) Rice Hybrids Derived by Crossing *Indica* CMS Lines with *Japonica* Widely Compatible Restorers. *Jiangsu Journal of Agricultural Sciences*, **6**, 10-16.

[11] Ikehashi, H. and Araki, H. (1984) Variety Screening of Compatibility Types Revealed in F_1 Fertility of Distant Cross in Rice. *Japanese Journal of Breeding*, **34**, 304-313. https://doi.org/10.1270/jsbbs1951.34.304

[12] Ikehashi, H. and Araki, H. (1986) Genetics of F_1 Sterility in Remote Crosses of Rice. In: IRRI, Ed., *Rice Genetics*, IRRI, Manila, Philippines, 119-130. https://doi.org/10.1142/9789812814265_0011

[13] Yanagihara, S., McCouch, S.R., Ishikawa, K., Ogi, Y., Maruyama, K. and Ikehashi, H. (1995) Molecular Analysis of the Inheritance of the S-5 Locus, Conferring Wide Compatibility in Indica/Japonica Hybrids of Rice (*O. sativa* L.). *Theoretical and Applied Genetics*, **90**, 182-188. https://doi.org/10.1007/BF00222200

[14] Liu, K.D., Wang, J., Li, H.B., Xu, C.G., Liu, A.M., Li, X.H. and Zhang, Q. (1997) A Genome-Wide Analysis of Wide Compatibility in Rice and the Precise Location of the S5 Locus in the Molecular Map. *Theoretical and Applied Genetics*, **95**, 809-814. https://doi.org/10.1007/s001220050629

[15] Liu, Y.S., Zhu, L.H., Sun, J.S. and Chen, Y. (2001) Mapping QTLs for Defective Female Gametophyte Development in an Inter-Subspecific Cross in *Oryza sativa* L. *Theoretical and Applied Genetics*, **102**, 1243-1251. https://doi.org/10.1007/s001220000520

[16] Qiu, S.Q., Liu, K.D., Jiang, J.X., Song, X., Xu, C.G., Li, X.H. and Zhang, Q.F. (2005) Delimitation of the Rice Wide Compatibility Gene S_5^n to a 40-kb DNA Fragment. *Theoretical and Applied Genetics*, **111**, 1080-1086. https://doi.org/10.1007/s00122-005-0033-0

[17] Ji, Q., Lu, J.F., Chao, Q., Gu, M.H. and Xu, M.L. (2005) Delimiting a Rice Wide-Compatibility Gene S_5^n to a 50 kb Region. *Theoretical and Applied Genetics*, **111**, 1495-1503. https://doi.org/10.1007/s00122-005-0078-0

[18] Li, D.T., Chen, L.M., Jiang, L., *et al.* (2007) Fine Mapping of S32(t), a New Gene Causing Hybrid Embryo Sac Sterility in a Chinese Landrace Rice (*Oryza sativa* L.). *Theoretical and Applied Genetics*, **114**, 5l5-524. https://doi.org/10.1007/s00122-006-0450-8

[19] Song, X., Qiu, S.Q., Xu, C.G., *et al.* (2005) Genetic Dissection of Embryo Sac Fertility, Pollen Fertility, and Their Contributions to Spikelet Fertility of Intersubspecific Hybrids in Rice. *Theoretical and Applied Genetics*, **110**, 205-211. https://doi.org/10.1007/s00122-004-1798-2

[20] Li, W.T., Zeng, R.Z., Zhang, Z.M. and Zhang, G.Q. (2002) Mapping of S-b Locus for F_1 Pollen Sterility in Cultivated Rice Using PCR Based Markers. *Journal of Integrative Plant Biology*, **44**, 463-467.

[21] Zhuang, C.X., Fu, Y., Zhang, G.Q., Mei, M.T. And Lu, Y.G. (2002) Molecular Mapping of S-c, an F_1 Pollen Sterility Gene in Cultivated Rice. *Euphytica*, **127**, 133-138. https://doi.org/10.1023/A:1019973110467

[22] Wang, G.W., He, Y.Q., Xu, C.G. and Zhang, Q. (2005) Identification and Confirmation of Three Neutral Alleles Conferring Wide-Compatibility in Inter-Subspecific Hybrids of Rice (*Oryza sativa* L.) Using Near-Isogenic Lines. *Theoretical and Applied Genetics*, **111**, 702-710. https://doi.org/10.1007/s00122-005-2055-z

[23] Yang, Z.Y., Gao, Y., Zhao, Y.C., Wei, Y.L., Hua, Z.T., Zhang, Z.X. and Gao, R.L. (1996) Progress in Research on Utilization of Vigor in Hybrids between *Indica* and *Japonica* Rice Subspecies. *Acta Agronomica Sinica*, **22**, 422-429.

[24] Zhang, G.Q. and Lu, Y.G. (1999) Breeding of the Indica Compatible Japonica Lines and Their Use in the Breeding of Super High Yield Hybrid Rice. *Hybrid Rice*, **14**, 3-6.

[25] Zhang, S.G. and Xu, X.M. (2006) Breeding and Utilization of *Japonica* but Partial Indica Rice Restorer Line. *Fujian Science and Technology of Rice and Wheat*, **24**, 3-5.

[26] Yang, Z.Y., Zhang, Z.X., Wei, Y.L., Zhao, Y.C. and Gao, Y. (1998) Breeding and Characteristics of *Japonica* Type Wide Compatibility Line C418. *Hybrid Rice*, **13**, 31-32.

[27] Yang, C.N., Cai, X.G., Wu, M.L., Liu, Y.S., Cai, J. and Dong, S.B. (2004) Breeding and Application of Wide Compatibility Restorer Line D069 in Rice. *Hybrid Rice*, **19**, 15-16.

[28] Zhang, Y., Xu, D.Y., Han, Z.Y. and Shao, F.K. (2001) Selective Breeding and Application of T9530 of Wide Compatibility Restorer. *Journal of Nanjing Agricultural Technology College*, **17**, 30-33.

[29] Yu, Y.H., Sun, B., Xia, M., Qi, B., Wang, Y. Zheng, Y.J., Liu, Y., Li, Z., Che, G.,

Tang, L. and Xu, Z. (2014) Analysis of Relationship between *Indica-Japonica* Ingredient of Parents and Yield and Its Components of Japonica Two-Line Hybrid Rice by Cheng's Index. *Jiangsu Agricultural Sciences*, **42**, 61-63.

[30] Chen, H.Q., Huang, R.Y., Wang, T., Xie, W.Y., Chen, J.W., Xie, S.H., Wu, J. and Lin, L.H. (2016) Correlation between F_1 Seed-Setting and Genetic Differentiation of *Indica-Japonica* Progenies. *Fujian Journal of Agricultural Sciences*, **31**, 211-217.

[31] Liu, W.Y. and Yang, Z.Y. (1992) The Relation between Distance of Genetic Relationship of Rice Parents and Heterosis of F_1. *Liaoning Agricultural Sciences*, **1**, 8-12.

[32] Duan, Z.G., Wang, Y.Q. and Liang, C.Y. (2004) The Relationship of the Fertility of F_1 Hybrid Rice with Cheng's Index Difference and Isozyme Genetic Distance. *Journal of Tropical and Subtropical Botany*, **12**, 337-340.

[33] Zhang, Q., Liu, K.D., Yang, G.P., Saghai Maroof, M.A., Xu, C.G. and Zhou, Z.Q. (1997) Molecular Marker Diversity and Hybrid Sterility in *Indica-Japonica* Rice Crosses. *Theoretical and Applied Genetics*, **95**, 112-118. https://doi.org/10.1007/s001220050538

[34] Li, R.H., Xu, C.G., He, Y.Q., Yuan, L.P. and Wang, X.K. (1998) Relationship between the Extent of Genetic Differentiation in Parental Lines and Heterosis of *Indica-Japonica* Hybrid Rice. *Acta Agronomica Sinica*, **24**, 564-576.

[35] Yang, Z.Y. and Liu, W.Y. (1991) Classification of the F_1 Intersubspecific Hybrids between Indica and Japonica and Its Relation to the F_1 Hybrid Vigor. *Chinese Journal of Rice Science*, **5**, 151-156.

[36] Li, C., Zhu, X., Chen, L., Zhao, J. and Zhou, Q. (2020) Study on the Relationship between Genetic Difference and Heterosis of Hybrid Rice Parents. *Molecular Plant Breeding*, **18**, 7132-7142.

[37] Zou, X.Y., Fu, J.R., Peng, X.S., Zhu, C.L., He, X.P., Chen, X.R., He, H.H. and Liu, Y.B. (2007) Researching on Relation between the Genetic Distance of Three Lines Hybrid Rice Parents and Heterosis. *Proceedings of Academic Annual Conference in* 2007 *of the Crop Science Society of China*, Xianyang, 10 December 2007, 707-711.