

## Full Length Research Paper

# Inheritance of grain yield and its correlation with yield components in bread wheat (*Triticum aestivum* L.)

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The genetic effect of grain yield plant<sup>-1</sup> and its correlation with yield components were investigated in a 7 × 7 incomplete diallel cross of seven wheat parents during the crop season of 2009 to 2010. Mean square of general combining ability (GCA) effect was 2.90 for grain yield plant<sup>-1</sup>, which was highly significant (P<0.01), indicating that additive effect played important role in the inheritance of the trait. Specific combining ability (SCA) effect was highly significant (P<0.01) for grain yield plant<sup>-1</sup> (0.68), suggesting that the trait was also controlled by non-additive effect. The estimates of GCA showed that the best combiner for grain yield plant<sup>-1</sup> was Ningmai 9. The additive-dominance model was partially adequate for grain yield plant<sup>-1</sup> and it was controlled by the over dominance type of gene action. Ningmai 8 possessed maximum dominant genes, whereas Yangmai 9 had maximum recessive genes. Grain yield plant<sup>-1</sup> might be controlled by two groups of genes and exhibited moderately high value of narrow sense heritability (h<sup>2</sup><sub>N</sub>=69.51%). The statistical analysis revealed that grain yield plant<sup>-1</sup> was positively and significantly correlated with tillers plant<sup>-1</sup> (r<sub>p</sub>=0.584, r<sub>g</sub>=0.595) and number of grains spike<sup>-1</sup> (r<sub>p</sub>=0.528, r<sub>g</sub>=0.507) at phenotypic and genotypic levels. The information obtained from the study might be helpful for wheat breeders trying to develop new varieties with high-yielding potential.

**Key words:** Combining ability, diallel cross, grain yield, inheritance, *Triticum aestivum* L.

## INTRODUCTION

Wheat (*Triticum aestivum* L.) is an important cereal crop next to rice in both acreage and production constituting about 22% of the staple food in China (Lu et al., 2010). Wheat has been cultivated in an area of 24.2 million hectares with the total production of 115 million metric tons in the year of 2010 to 2011 (Shen, 2012). The average yield of wheat in China is 4.75 t ha<sup>-1</sup>, which is low compared to other leading wheat producers in the world like Germany and France where average yields are 7.4 t and 7.2 t /ha, respectively. The yield is generally insufficient to fulfill the domestic requirements due to the

increase in population (Xiao, 2006). Therefore, it is necessary to develop the new wheat cultivars, having wider genetic base capable of producing better yield under a wide range of agro-climatic conditions to enhance the grain. The grain yield of wheat is determined by three yield components: productive spikes per unit area, number of grains spike<sup>-1</sup> and 1000-grain weight (Tian et al., 2012). The grain yield and its components are controlled by many genes, whose expression is greatly influenced by the varying environments (Groos et al., 2003). In most of the diallel studies of wheat, grain

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**Table 1.** Genetic background and yield traits of the seven parents.

Parent	Pedigree	Released year	Grain yield plant <sup>-1</sup> (g)	Tillers plant <sup>-1</sup>	Number of grains spike <sup>-1</sup>	1000-grain weight (g)
Ningmai 8	Yangmai 5/Yang 86-17	1996	7.43	4.53	51.17	32.51
Ningmai 9	Yang 86-17/Xifeng	1997	9.03	4.97	55.52	32.86
Yangmai 158	Yangmai 4/st1472-506	1993	9.39	4.80	48.96	39.75
Yangmai 9	Jian 3/Yangmai 5	1996	7.80	4.77	47.98	34.12
Jimai 17	Lingfen 5064/Lumai 13	1999	7.12	5.13	39.40	35.70
Zheng 9023	[83(2)3-3/84(14)43//Xiaoyan 6/Xinong 65]F3/3/Shannong 13	2001	8.05	4.93	37.81	43.45
Yumai 18	Zhengzhou 761/Yanshi 4	1990	7.17	4.93	42.43	34.72

yield plant<sup>-1</sup> seemed to be controlled by over dominance type of gene action (Singh and Sharma, 1976; Hussain et al., 2008; Akram et al., 2009; Ojaghi and Akhundova, 2010; Ahmad et al., 2011). However, researchers like Riaz and Chowdhry (2003), Samiullah et al. (2010) and Farooq et al. (2010) observed partial dominance with additive type of gene action for grain yield plant<sup>-1</sup>. Zhang and Xu (1997) reported that grain yield plant<sup>-1</sup> could result from additive and dominant genes with the possibility of epistatic genetic effects. Heritability estimate is a valuable parameter for determining the magnitude of genetic gain from selection. Low, medium, and high narrow sense heritability estimates were reported for grain yield plant<sup>-1</sup> (Mckendry et al., 1998; Novoselovic et al., 2004; Liu and Wei, 2006; Erkul et al., 2010; Ahmad et al., 2011). Grain yield plant<sup>-1</sup> is a complex trait including number of fertile tillers plant<sup>-1</sup>, number of grains spike<sup>-1</sup> and 1000-grain weight, and it is closely associated with its components ( Khaliq et al., 2004; Munir et al., 2007; Ali et al., 2008). The objective of this study was to investigate combining ability, and gene action for grain yield plant<sup>-1</sup>, and its correlations with yield components in a 7×7 incomplete diallel cross experiment in wheat. This study can be of

great importance in the selection of desirable parents for an effective breeding program to develop the new wheat varieties with high yield potential.

## MATERIALS AND METHODS

### Plant materials

The experimental material comprised seven wheat varieties: Ningmai 8, Ningmai 9, Yangmai 158, Yangmai 9, Jimai 17, Zheng 9023, and Yumai 18. The parents were chosen based on their broad genetic background and large variations for grain yield plant<sup>-1</sup> and yield components (Table 1). These genotypes were crossed in an incomplete diallel fashion during April, 2009. For each of the cross, 15 spikes were emasculated and bagged to avoid contamination with foreign pollen. Pollination with the pollen collected from the specific male parent was done in the morning when the ovaries became receptive. At maturity, the seeds from each cross were harvested and stored separately.

### Experimental design

The seeds of seven parents and 21 F<sub>1</sub> hybrids were sown in the field area of Jiangsu Academy of Agricultural Sciences, Nanjing, China, in the first week of November in 2009 and tested in a randomized complete block design with three blocks. Plant-to-plant and row-to-row spacing

was 6.5 and 25 cm, respectively. Within each block, each genotype occupied a plot of two rows of 2 m-long. All the other cultural operations including weeding, fertilizers and disease control were carried out uniformly. At maturity, in late May 2010, ten plants were randomly selected from each of the parents and F<sub>1</sub> progeny to determine fertile tillers plant<sup>-1</sup>, number of grains spike<sup>-1</sup>, 1000-grain weight and grain yield plant<sup>-1</sup>.

### Statistical analysis

To assess the differences among parents and F<sub>1</sub> progeny, the data were subjected to analysis of variance using the SAS software. The general and specific combining ability values were estimated using Method II, Model I of Griffing (1956). Two scaling tests (Mather and Jinks, 1982) were applied to test the validity of the additive-dominance model. Further, the Hayman (1954) method was used for estimation of gene actions. Correlation coefficients between grain yield plant<sup>-1</sup> and yield components were determined using the data processing system (Tang and Feng, 2002).

## RESULTS AND DISCUSSION

### Analysis of variance

Analysis of variance revealed highly significant differences ( $P \leq 0.01$ ) among the genotypes for grain yield plant<sup>-1</sup> (Table 2). These results

**Table 2.** Analysis of variance for combining ability for grain yield plant<sup>-1</sup>.

Source of variation	Degree of freedom	Sum of square	Mean of square	F
Replications	2	7.329	3.664	4.339*
Genotypes	27	95.131	3.523	4.172**
Error	54	45.609	0.845	
GCA	6	17.424	2.904	10.315**
SCA	21	14.287	0.680	2.416**
Error	54	15.203	0.282	

\*, \*\* Significance at P≤0.05 and P≤0.01 levels, respectively.

**Table 3.** Mean grain yield plant<sup>-1</sup> and general combining ability (GCA) effects.

Parent	GCA	Mean (g)
Ningmai 9	0.915 <sup>aA</sup>	9.031 <sup>aA</sup>
Yangmai 158	0.480 <sup>abAB</sup>	9.387 <sup>aA</sup>
Zheng 9023	0.143 <sup>bcBC</sup>	8.045 <sup>bcABC</sup>
Yangmai 9	0.006 <sup>bcBCD</sup>	7.799 <sup>cBC</sup>
Jimai 17	- 0.325 <sup>cdCD</sup>	7.123 <sup>cC</sup>
Yumai 18	- 0.594 <sup>dD</sup>	7.169 <sup>cC</sup>
Ningmai 8	- 0.625 <sup>dD</sup>	7.434 <sup>cC</sup>
r (GCA, mean)	0.900**	

The values followed by different capital or small letters within the same column are significantly different at the 0.01 and 0.05 probability levels, respectively. \*\* Significance at P≤0.01 level. r correlation coefficient.

permitted further analysis of combining abilities. Both general combining ability (GCA) and specific combining ability (SCA) variances were highly significant for grain yield plant<sup>-1</sup> (Table 2), indicating the importance of both additive and non-additive gene effects. These results are in agreement with earlier findings (Wang et al., 2003; Farooq et al., 2006; Hussain et al., 2012). However, Akram et al. (2011) illustrated that the additive effects were more important for the genetic control of grain yield plant<sup>-1</sup>.

### Performance of parents and combining ability

Mean grain yield plant<sup>-1</sup> and GCA effects of the parents are given in Table 3. Significant differences were found for grain yield plant<sup>-1</sup> among parents. Yangmai 158 and Ningmai 9 had significant higher grain yield plant<sup>-1</sup> than the other five parents and they can be considered as high yielding parents. Zheng 9023 had moderately high yield capacity while Ningmai 8, Yangmai 9, Jimai 17 and Yumai 18 had medium and low yield capacity. Estimates of GCA effects of parents ranged from - 0.625 to 0.915 (Table 3). The highest positive-valued GCA was exhibited in Ningmai 9 followed by Yangmai 158. The GCA value of Ningmai 9 was significantly higher than that of Zheng

9023, Yangmai 9, Jimai 17, Yumai 18 and Ningmai 8 except Yangmai 158. This result indicate that Ningmai 9 was the best combiner for grain yield plant<sup>-1</sup> and may serve as genetic sources in breeding programs for increased grain yield. The highest negative-valued GCA was shown in Ningmai 8 followed by Yumai 18. The positive and significant correlation ( $r = 0.900$ ,  $P \leq 0.01$ ) between GCA and parental performance (Table 3) suggested that selection of parents for grain yield plant<sup>-1</sup> could be made on the basis of their performance *per se*. The high grain yield plant<sup>-1</sup> of certain crosses (Ningmai 8 × Jimai 17, Ningmai 9 × Zheng 9023, and Ningmai 9 × Yangmai9) showed strong positive SCA effects (Table 4). Because in most cases at least one good combining parent was included in these crosses, their progenies had higher grain yield plant<sup>-1</sup> than the overall means and yielded desirable transgressive segregations.

### Assessment of grain yield plant<sup>-1</sup> for additive-dominance model

The data were assessed for additive-dominance (AD) model by exploiting various adequacy parameters given in Table 5. According to Mather and Jinks (1982), the data will be only valid for genetic interpretation if the value of

**Table 4.** Effects of specific combining ability for grain yield plant<sup>-1</sup> in 21 crosses.

Parent	Ningmai 9	Yangmai 158	Yangmai 9	Jimai 17	Zheng 9023	Yumai 18
Ningmai 8	- 0.267	- 0.843	- 0.439	1.377	0.274	0.052
Ningmai 9		0.641	0.999	- 0.152	1.023	0.877
Yangmai 158			0.701	0.664	- 0.693	0.196
Yangmai 9				0.132	0.733	- 0.176
Jimai 17					0.381	- 0.424
Zheng 9023						0.287

$S.E.(\hat{S}_{ij}-\hat{S}_{ik})$ : Standard error of differences for SCA effect among crosses with a communal parent;  $S.E.(\hat{S}_{ij}-\hat{S}_{kl})$ : Standard error of differences for SCA effect among crosses without a communal parent.  $S.E.(\hat{S}_{ij}-\hat{S}_{ik}) = 0.708$ ,  $LSD_{0.05} = 1.415$ ,  $LSD_{0.01} = 1.882$ ;  $S.E.(\hat{S}_{ij}-\hat{S}_{kl}) = 0.662$ ,  $LSD_{0.05} = 1.324$ ,  $LSD_{0.01} = 1.760$ .

**Table 5.** Adequacy test of additive-dominance model for grain yield plant<sup>-1</sup>.

Parameter	Grain yield plant <sup>-1</sup>
Joint regression (b)	0.963±0.253
Test for b=0	3.806**
Test for b=1	0.146 NS
Mean squares of Wr + Vr between arrays	1.334 NS
Mean squares of Wr - Vr between arrays	0.230 NS
Fitness of the data to Additive-Dominance model	Partial

\*\* Significance at P≤0.01 level, NS=non significant.

regression coefficient (b) must deviate significantly from zero but not from the unity. The regression analysis revealed that regression coefficient for grain yield plant<sup>-1</sup> departed significantly from zero but not from unity, suggesting the absence of non-allelic interactions in genetic behavior of grain yield plant<sup>-1</sup> which in turn attested the data valid for AD model for the trait. The appropriateness of the model data analysis was also verified by the analysis of variance of (Wr + Vr) and (Wr - Vr). The lack of significant variation in the (Wr - Vr) arrays suggested that any kind of epistasis was not involved in the phenotypic expression of the trait. Although the value of regression coefficient (b) proved the fitness of the data of grain yield plant<sup>-1</sup> for AD model, mean square value of (Wr + Vr) for the trait indicated no significant deviation, thus emphasizing partial validity of the trait. This was also confirmed by Ahmad et al. (2011), Farooq et al. (2011) and Nazeer et al. (2011). The partially adequate model for grain yield plant<sup>-1</sup> may be due to the presence of non-allelic interaction, linkage and non-independent distribution of the genes in the parents as suggested by Mather and Jinks (1982).

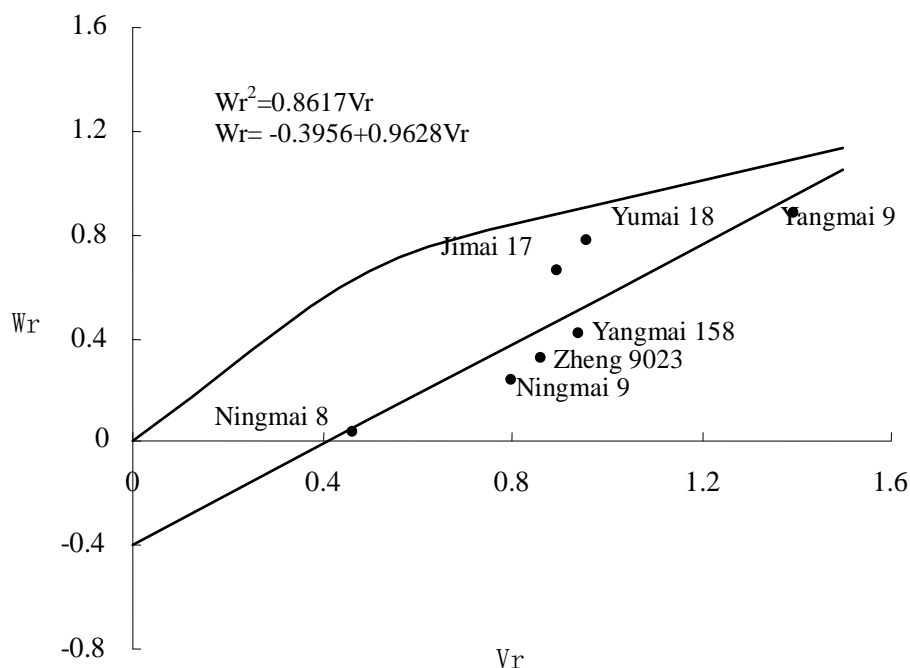
#### Genetic components of variation for grain yield plant<sup>-1</sup>

Genetics of grain yield plant<sup>-1</sup> was evaluated by calculation of the genetic components of variation D, H<sub>1</sub>, H<sub>2</sub> and F (Table 6). Additive (D) and non-additive (H<sub>1</sub> and

H<sub>2</sub>) components were significant, indicating that both additive and dominance effects were important components of genetic variation for grain yield plant<sup>-1</sup>. However, dominance (H<sub>1</sub> and H<sub>2</sub>) effects were greater than additive (D), suggesting that non-additive gene action played a predominant role in controlling the genetic mechanism of the trait. The (H<sub>1</sub>/D)<sup>0.5</sup> was more than unity which confirmed the greater contribution of non-additive genes in the inheritance of grain yield plant<sup>-1</sup>. These results are in accordance with those of Arshad and Chowdhry (2003), Hussain et al. (2008), Akram et al. (2009), Nazeer et al. (2010) and Ojaghi and Akhundova (2010). Preponderance of dominance effects for grain yield plant<sup>-1</sup> suggested that the selection for the trait in early generations may not be useful and it had to be delayed till late segregating generations. Asymmetrical distribution of dominant genes was confirmed by unequal estimates of H<sub>1</sub> and H<sub>2</sub>, which was further supported by the value of H<sub>2</sub>/4H<sub>1</sub> (0.219). The F value, which estimates the relative frequency of dominant to recessive alleles in the parents, was negative. This suggests the excess of recessive alleles present in the parents, which was further supported by the small value (< 1.0) of [(4DH<sub>1</sub>)<sup>0.5</sup>+F]/(4DH<sub>1</sub>)<sup>0.5</sup>-F]. The mean dominance effect of the heterozygote locus (h<sup>2</sup>) was significant, suggesting that heterosis breeding could be rewarding for this trait. Significant environmental component (E) indicated that the trait was highly affected by environmental conditions (Ahmad et al., 2011). The number of gene groups

**Table 6.** Estimate of genetic parameters of grain yield plant<sup>-1</sup> in a 7×7 diallel cross of wheat.

Genetic parameter	Grain yield plant <sup>-1</sup>
D	0.487±0.118**
F	- 0.742±0.282**
H <sub>1</sub>	1.663±0.283**
H <sub>2</sub>	1.455±0.250**
h <sup>2</sup>	2.886±0.168**
E	0.315±0.042**
(H <sub>1</sub> /D) <sup>1/2</sup>	1.848
H <sub>2</sub> /4H <sub>1</sub>	0.219
[(4DH <sub>1</sub> ) <sup>1/2</sup> +F/((4DH <sub>1</sub> ) <sup>1/2</sup> -F)	0.416
K	1.984
h <sup>2</sup> <sub>N</sub> (%)	69.51
R[(Wr+Vr), Pr]	- 0.171

**Figure 1.** Vr versus Wr graph for grain yield plant<sup>-1</sup>.

differentiating the parents (k) was 1.984, suggesting that the inheritance of grain yield plant<sup>-1</sup> was controlled approximately by two groups of genes (Dere and Yildirim, 2006; Nazeer et al., 2010). Estimates of narrow sense heritability (h<sup>2</sup><sub>N</sub>) were moderately high for grain yield plant<sup>-1</sup>. Such moderately high heritable value for grain yield plant<sup>-1</sup> was also reported by other researchers (Novoselovic et al., 2004; Yang and Cao, 2005; Ajmal et al., 2009; Akram et al., 2009; Farooq et al., 2010). However, Mckendry et al. (1998), Liu and Wei (2006), Erkul et al. (2010) and Ojaghi and Akhundova (2010) found that the narrow sense heritability for grain yield

plant<sup>-1</sup> was low. Differences in the genetic material and analytical technique used in this study could account for these differences.

#### Graphical (Vr/Wr) representation for grain yield plant<sup>-1</sup>

The Vr/Wr graph (Figure 1) showed that the regression line intercepted the Wr-axis below the point of origin, suggesting that the trait was controlled by the over dominance type of gene actions and this was superbly maintained by the results provided by the higher values

**Table 7.** Phenotypic ( $r_p$ ) and genotypic ( $r_g$ ) correlation coefficient between grain yield plant<sup>-1</sup> and yield components.

Character	r	Tillers plant <sup>-1</sup>	Number of grains spike <sup>-1</sup>	1000-grain weight
grain yield plant <sup>-1</sup>	$r_p$	0.584**	0.528**	0.251
	$r_g$	0.595**	0.507**	0.261
Tillers plant <sup>-1</sup>	$r_p$		0.107	- 0.062
	$r_g$		0.132	0.002
Number of grains spike <sup>-1</sup>	$r_p$			- 0.552**
	$r_g$			- 0.614**

\*\* Significance at  $P \leq 0.01$  levels.

of dominance components  $H_1$  and  $H_2$  over the additive one D. Similar results have earlier been reported by Asif et al. (1999), Chowdhry et al. (2002), Arshad and Chowdhry (2003), Kashif and Khaliq (2003) and Saleem et al. (2005). However, these results were not in accordance with Riaz and Chowdhry (2003) and Samiullah et al. (2010). The distribution of array points along the regression line (Figure 1) revealed that parent Ningmai 8 contained maximum dominant genes being closest to the origin while parent Yangmai 9 carried maximum recessive genes being farthest from the origin. The other two parents Jimai 17 and Yumai 18 also had relatively high frequency of recessive genes. Negative  $r$ -value ( $r = -0.171$ ) between parental values ( $Pr$ ) with ( $Wr + Vr$ ) indicated that the parents with high grain yield plant<sup>-1</sup> may carry dominant genes. Similar results were reported by Inamullah et al. (2006) and Ojaghi and Akhundova (2010) while Dere and Yildirim (2006) reported that the parents with high grain yield plant<sup>-1</sup> may carry recessive genes.

### Correlation analysis

Correlation coefficients between grain yield plant<sup>-1</sup> and yield components are shown in Table 7. In general, correlation coefficients at genotypic level were higher than those of phenotypic level. It might be due to the depressing effect of environment on character association as reported earlier for wheat crop (Proda and Joshi, 1970). Grain yield plant<sup>-1</sup> had a highly significant positive genotypic correlation with tillers plant<sup>-1</sup> ( $r = 0.595$ ,  $P \leq 0.01$ ) and number of grains spike<sup>-1</sup> ( $r = 0.507$ ,  $P \leq 0.01$ ), and it showed positive and non-significant correlation with 1000-grain weight at both genotypic and phenotypic levels, suggesting that increase in tillers plant<sup>-1</sup> and number of grains spike<sup>-1</sup> would increase grain yield plant<sup>-1</sup>. These results are in agreement with those of Ali et al. (2008). Khaliq et al. (2004) and Munir et al. (2007) reported positive and significant genotypic and phenotypic correlation of grain yield plant<sup>-1</sup> with yield

components. Among the yield components, tillers plant<sup>-1</sup> was positive and had non-significant correlation with number of grains per spike and 1000-grain weight at genotypic level. Positive and non-significant correlation between tillers plant<sup>-1</sup> and number of grains spike<sup>-1</sup> at both genotypic and phenotypic levels was also reported by Khan and Dar (2010). Positive and non-significant correlation between tillers plant<sup>-1</sup> and 1000-grain weight was found at genotypic level, however the correlation was highly significant (Khokhar et al., 2010), whereas Kashif and Khaliq (2004) reported negative and significant association of tillers plant<sup>-1</sup> with 1000-grain weight. There was negative and significant correlation between number of grains spike<sup>-1</sup> and 1000-grain weight at both genotypic and phenotypic levels. Similar findings have also been reported by Khan et al. (2010). However, the results were contrary with the findings of Ashfaq et al. (2003).

### Conclusion

The results reveal that there was significant genetic variation for grain yield plant<sup>-1</sup> among the genotypes. Significant GCA and SCA effects for grain yield plant<sup>-1</sup> imply the role of both additive and non-additive gene actions in the genetic control of the trait. Ningmai 9 appeared to be a promising parent for improvement of grain yield plant<sup>-1</sup>. The additive-dominance model was partially adequate for grain yield plant<sup>-1</sup>. Dominant genes coupled with moderately high narrow sense heritability were involved in the inheritance of grain yield plant<sup>-1</sup>, suggesting that selection for the trait in early generations ( $F_2$ - $F_3$ ) may not be effective. Grain yield plant<sup>-1</sup> had significantly positive genotypic correlation with tillers plant<sup>-1</sup> and number of grains spike<sup>-1</sup>.

### Conflict of Interests

The author(s) have not declared any conflict of interests.

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