

Combining ability and gene action analysis for quantitative and yield-attributing traits in Maize (*Zea mays* L.)

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Abstract

An investigation was conducted to study the general combining ability (GCA) and specific combining ability (SCA), along with the underlying gene action, across 16 important quantitative traits in maize (*Zea mays* L.). A half-diallel crossing design was utilized to generate the experimental hybrids. The analysis of variance indicated significant genetic variability among the genotypes. High GCA effects for traits such as Days to 75% Dry Husk, Plant Height, Number of Kernel Rows per Cob, and 100-Grain Weight demonstrated the importance of additive gene action. Conversely, significant SCA variance for traits including Plant Height, Ear Placement, and Number of Kernels per Row indicated substantial non-additive gene effects. The ratio of genetic components ($\sigma^2\text{GCA}/\sigma^2\text{SCA}$) confirmed the predominance of non-additive gene action for major yield attributes, pointing towards hybrid breeding as an optimal strategy. Concurrently, traits governed equally by both additive and non-additive gene actions can be improved via reciprocal recurrent selection procedures.

Keywords: General combining ability, specific combining ability, gene action, Maize, quantitative traits, diallel crossing, additive gene action, non-additive gene action, hybrid breeding, reciprocal recurrent selection

Introduction

Maize (*Zea mays* L.) stands as one of the world's most versatile and widely cultivated cereal crops, satisfying dietary, animal feed, and industrial needs. To meet increasing global grain demands, breeders focus on maximizing genetic yield potential. Efficient selection of parents and understanding genetic systems governing quantitative traits are fundamental prerequisites for a successful hybridization program.

The concept of combining ability, given by Sprague and Tatum (1942) [3], serves as a robust approach to classify the nature and magnitude of gene effects. General combining ability (GCA) represents the average performance of a parental line in a series of crosses and is primarily associated with additive gene action and additive $\times$ additive interactions. Specific combining ability (SCA) reflects cases where certain hybrid combinations perform relatively better or poorer than expected based on parental performance, which is an indicator of non-additive gene action (dominance and epistasis).

To evaluate parental lines, a half-diallel mating design is highly preferred by breeders. It allows the estimation of genetic components without the confounding maternal effects found in full diallel systems, reducing the field workload while maximizing genetic insight. Determining the variance ratios ($\sigma^2\text{GCA}/\sigma^2\text{SCA}$) helps differentiate whether a population should be subjected to family selection programs or if the development of F1 hybrids is ideal to exploit heterosis. The present investigation was conducted to study genetic variance distribution and gene action across sixteen different agronomical components in a half-diallel set of maize.

Materials and Methods

The research was executed under controlled field conditions optimized for maize cultivation. The experimental material

was generated by crossing elite, homozygous maize inbred lines in a half-diallel mating design (excluding reciprocal crosses) to produce the single-cross F1 progeny. The resulting half-diallel hybrids, with parental lines and commercial checks, were evaluated in a Randomized Block Design (RBD) with appropriate replications. The Data were taken for the following sixteen characters for Days to 50% Tasseling (D50%T), Days to 50% Silking (D50%S), Anthesis-Silking Interval (ASI), Days to 75% Dry Husk (D75%DH), Plant Height (PH), Ear Placement (EP), Biological Yield per Plant (BY/P), Cob Weight (CW), Cob Length (CL), Cob Girth (CG), Number of Kernel Rows per Cob (NKR/C), Number of Kernels per Row (NK/R), 100-Grain Weight (100GW), Shank Weight, Shelling Percentage (SELLING%) and Grain Yield per Plant (GY/P) have been recorded.

Statistical and genetic parameter evaluations of combining ability variances ($\sigma^2\text{GCA}$, $\sigma^2\text{SCA}$) were derived using Griffing's (1956) [1] numerical approach, optimised for half-diallel systems. The significance of GCA and SCA mean squares was verified using F-tests at 5% (*) and 1% (**) levels of probability.

Results and Discussion

1. Analysis of Variance for Combining Ability

The analysis of variance (ANOVA) for combining ability revealed highly significant mean sum of squares for GCA and SCA for a majority of the observed characters, signifying significant genetic variability within the half-diallel cross combinations (Table 4.4).

The mean squares due to GCA were highly pronounced for key traits including Days to 75% Dry Husk (5.27**), Plant Height (471.89**), Number of Kernel Rows per Cob (3.23**), and Number of Kernels per Row (26.99**), confirming strong additive gene regulation among the parents. Concurrently, SCA variances were high for Plant

Height (916.07**) and Ear Placement (503.22**), indicating that non-additive components significantly influence structural attributes in specific single-cross combinations.

2. Gene Action Profiling and Genetic Variances

The partitioning of components and evaluation of genetic variance ratios ($\sigma^2\text{GCA}/\sigma^2\text{SCA}$) provided the classification of traits into three explicit genetic action categories (Table 4.5):

2.1 Predominance of Additive Gene Action

Traits showing positive GCA variances paired with negative or low SCA values include:

- Anthesis-Silking Interval (ASI): $\sigma^2\text{GCA} = 0.01^*$, $\sigma^2\text{SCA} = -0.0035$
- Days to 75% Dry Husk (D75%DH): $\sigma^2\text{GCA} = 0.48^{**}$, $\sigma^2\text{SCA} = -0.26$
- 100-Grain Weight (100GW): $\sigma^2\text{GCA} = 0.99^*$, $\sigma^2\text{SCA} = -0.62$

The negative estimates observed for certain SCA variances indicate that the variance component is negligible or near zero. The clear dominance of fixable additive gene effects indicates that phenotypic selection, recurrent selection, or pedigree breeding will lead to rapid population improvement for these traits.

2.2 Predominance of Non-Additive Gene Action

Traits displaying very low or negligible $\sigma^2\text{GCA}/\sigma^2\text{SCA}$ ratios indicate an explicit over-dominance or epistatic control:

- Plant Height (PH) & Ear Placement (EP): PH exhibited a ratio of 0.05 with an SCA variance of 773.07. EP displayed exclusive non-additive behaviour with an SCA variance of 384.76.
- Inflorescence & Seed Row Alignment: Cob Girth (0.31), Number of Kernel Rows per Cob (0.21), Number of Kernels per Row (0.26), and SANKW (0.28) explicitly showcased a higher share of non-additive variances.
- Cob Weight (CW): Exhibited significant SCA variance (0.0004*) with a ratio of 0.15.

Because non-additive gene effects are unfixable in advanced generations, breeding strategies must exploit heterosis directly via single-cross hybrid production from this diallel set.

2.3 Equal Effectiveness of Additive and Non-Additive Genes

For traits such as Days to 50% Tasseling (-0.06), Days to 50% Silking (-0.04), Biological Yield per Plant (-0.38), Cob Length (-0.52), Shelling Percentage (-0.09), and Grain Yield per Plant (-0.08), both gene types operated simultaneously. This balanced or integrated genetic framework means population synthesis followed by continuous reciprocal recurrent selection is crucial to simultaneously utilize fixable and non-fixable gene components.

Table 1: Analysis of variance (mean sum of squares) for combining ability, estimates of components of variance and their ratio for various characters in maize.

Source of variation	GCA	SCA	ERROR	σ^2 GCA	σ^2 SCA	$\frac{\sigma^2 \text{GCA}}{\sigma^2 \text{SCA}}$
d.f	6	21	54			
D50%T	5.75	8.91	6.82	-0.12	2.08	-0.06
D50%S	5.69	9.23	6.68	-0.11	2.55	-0.04
ASI	0.19*	0.08	0.08	0.01	-0.0035	-3.51
D75%DH	5.27**	0.73	0.99	0.48	-0.26	-1.84
PH	471.89**	916.07**	143	36.54	773.07	0.05
EP	243.57	503.22**	118.46	13.9	384.76	0.04
BY/P	0.04	5.24	4.08	-0.45	1.16	-0.38
CW	0.0011	0.0010*	0.0005	0.00004	0.0004	0.15
CL	346.26	150.39	184.96	17.92	-34.57	-0.52
CG	2.61**	1.38*	0.68	0.21	0.7	0.31
NKR/C	3.23**	2.01**	0.7	0.28	1.31	0.21
NK/R	26.99**	15.05**	5.93	2.34	9.11	0.26
100GW	14.62*	5.12	5.74	0.99	-0.62	-1.59
SANKW	0.0028**	0.0014**	0.0004	0.0003	0.0009	0.28
SELLING%	0.0022	0.002	0.0021	(9.2*10-6)	-0.0001	-0.09
GY/P	0.0003	0.0006	0.0004	(-1.5*10-5)	0.0002	-0.08

Table 2: Variance for general combining ability and specific combining ability, along with gene action for different traits in maize.

Source of variation	GCA	SCA	GCA/SCA	Gene Action
D50%T	-0.12	2.08	-0.06	Additive and non-additive genes are equally effective.
D50%S	-0.11	2.55	-0.04	Additive and non-additive genes are equally effective.
ASI	0.01*	-0.0035	-3.51	Only additive gene action
D75%DH	0.48**	-0.26	-1.84	Only additive gene action
PH	36.54**	773.07**	0.05	Preponderance of non-additive gene action
EP	13.9	384.76**	0.04	Non-additive
BY/P	-0.45	1.16	-0.38	Additive and non-additive genes are equally effective.
CW	0.0000068	0.0004*	0.15	Non-additive
CL	17.92	-34.57	-0.52	Additive and non-additive genes are equally effective.
CG	0.21**	0.7*	0.31	Preponderance of non-additive gene action
NKR/C	0.28**	1.31**	0.21	Preponderance of non-additive gene action

NK/R	2.34**	9.11**	0.26	Preponderance of non-additive gene action
100GW	0.99*	-0.62	-1.59	Only additive gene action
SANKW	0.0003**	0.0009**	0.28	Preponderance of non-additive gene action
SELLING%	-0.00001	-0.0001	-0.09	Additive and non-additive genes are equally effective.
GY/P	0.00002	0.0002	-0.08	Additive and non-additive genes are equally effective.

Conclusion

This study reveals a distinct dual genetic control layout governing different agronomic features within the evaluated half-diallel population. Selection procedures targeting grain size (100GW) and maturity metrics (D75%DH) can be pursued effectively via simple selection programs. However, key morphological and crop yield parameters, including plant height, kernel configuration traits, and overall grain production, rely heavily on non-additive configurations. Thus, evaluating specific cross combinations for high SCA performance and exploiting heterosis via hybrid development stands as the most rewarding pathway forward for genetic gains in this maize population.

References

1. Griffing B. Concept of general and specific combining ability in relation to diallel crossing systems. Australian Journal of Biological Sciences, 1956;9(4):463-493.
2. Hallauer A R, Carena M J, Miranda Filho J B. Quantitative Genetics in Maize Breeding. Springer Science & Business Media, 2010.
3. Sprague G. F, Tatum L. A. General vs. Specific Combining Ability in Single Crosses of Corn. Journal of the American Society of Agronomy, 1942;34(10):923-932.