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Vikash Kumar Jalaj Department of Genetics and Plant Breeding, COA, CAU Imphal, Manipur, India

N Brajendra Singh

Department of Genetics and Plant Breeding, COA, CAU Imphal, Manipur, India

Samuel Jeberson

Department of Genetics and Plant Breeding, COA, CAU Imphal, Manipur, India

Th. Renuka Devi

Department of Genetics and Plant Breeding, COA, CAU Imphal, Manipur, India

Sakthivel G

Department of Genetics and Plant Breeding, COA, CAU Imphal, Manipur, India

Bireswar Sinha

Department of Plant Pathology, COA, CAU Imphal, Manipur, India

N Okendro Singh Department of Agriculture, Statistics COA, CAU Impha

Statistics COA, CAU Imphal, Manipur, India

Corresponding Author: Vikash Kumar Jalaj Department of Genetics and Plant Breeding, COA, CAU Imphal, Manipur, India

Diallel analysis of yield and its important components in wheat (*Triticum aestivum* L)

Vikash Kumar Jalaj, N Brajendra Singh, Samuel Jeberson, TH Renuka Devi, Sakthivel G, Bireswar Sinha and N Okendro Singh

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Abstract

This study was carried out in Andro Research Farm, CAU, Imphal to study diallel analysis of yield and its important components in 10 genotype of wheat during two consecutive *rabi* season 2017-2019. All the 10 genotype and their 45 $F_{1's}$ cross combination exhibited significant difference in characters under study Combining ability analysis showed that both gca and sca variances value were highly significant for most of traits studied in F_1 progenies which suggest importance of both additive as well as non-additive genetic components for the expression of characters under study. VL 3017 was found good general combiner for the characters like fifty percent flowering, days to eighty percent maturity, plant height, total number of tillers per hill, total number of spikelets per spike, spike length, total number of filled grains per spike and grain yield per plant. Among all 45 crosses, cross combination VL 3018 x HS 490 and VL 892 x UP 3017 were good specific combiners for the grain yield per plant character in F_1 generation.

Keywords: Wheat, Diallel analysis, combining ability, genotype, GCA, SCA

Introduction

Bread wheat (Triticum aestivum L.) is one of the oldest and most important cereal crops in the world. It is an allohexaploid (2n=6x=42, AABBDD). Wheat belongs to tribe Triticeae (Hordeae) under family Poaceae and genus is Triticum. In an effective breeding programme diallel analysis is an important tool to identify parents with better potential to transmit desirable characteristics to its progenies and to identify the best specific crosses for yield and various quality parameters. We should keen on selection of right parent for effective hybridisation as well as good knowledge of estimating genetic component of variation and their proportion. One of best method for complete information on nature and magnitude of comes through diallel observation. Here the combining ability analysis used as a tool which gives us all the information of genetic mechanism that influence the quantitative and qualitative traits and helped in selection of suitable genotype in hybrid combination for the commercial reason. The Study revealed that both gca and sca was significant therefore there was importance of both additive as well as non-additive gene effects in the inheritance of characters (Dinesh and Kerkhi 2015)^[1]. Keeping this in view, the present study was carried out with two objectives one is to study the gene action of the yield and its important components in wheat and second is to estimate the genetic components of variance for grain yield and its components in wheat.

Materials and Methods

This case study was conducted during rabi season 2017 and 2018 in the experimental farm at Andro research farm CAU, Imphal which is located at 24°. 77 N latitude and 94.° 06 E longitutde and an altitude of about 790 m above MSL. In this trial, ten genetically diverse varieties of wheat (Table 1) having different morphological and productive attribute were used. All the seeds were collected from AICW & BIP Imphal, Manipur. The whole experimental took two crop season. In the first crop season of 2017 the F_1 hybrid seed were produced using diallel mating design (mating design as per half diallel method of Griffing, 1956)^[4] in which ten genotypes of wheat crossed in all possible ways excluding reciprocal by

hand emasculation and pollination. The crossed seeds were harvested when the spikes turn golden colour and then sundried in order to avoid any storage damage. F_1 seeds obtained from 45 cross combinations along with their 10 parents were sown in a well prepared experimental field according to RBD experimental design with 3 replication in 2 rows of 1.25 m long. The data were recorded by randomly selecting 10 plant from each plot separately. Mean values of different characters of 45 F_{1 's progenies along with their 10 parents were arranged in diallel table. General combining ability (gca) and specific combining ability (sca) variances and effects were calculated as per Griffing (1956)^[4] Method II and Model 1.

Result and Discussion

Analysis of variance was calculated for all the characters under this trial. According to ANOVA (Table 2) all the characters of genotypes were found significant differences which indicate all the genotype were differ from each other.

Analysis of variance for combining ability of parents and F_1 : On the analysis of variance for combining ability, it revealed that mean square due to general combining ability as well as specific combining ability were highly significant for all the characters in F_1 under study(Table 3). This indicate that the importance of both additive as well as non-additive gene action for the expression of characters under study (Dinesh and kerkhi, 2015)^[1].

Components of genetic variance in F₁

Here sca variance were higher than gca variances (Table 4), it means that there was preponderance of non- additive gene action (dominance and epistasis). All the characters studied viz. days to 50% flowering, days to 80% maturity, plant height, total no. of tillers, spike length, no. of spikelets per spike, no. of grains per spike and grain yield per plant the estimates due to gca i.e. $\sigma^2 g$ and due to sca i.e. $\sigma^2 s$ effects along with their ratios i.e. $\sigma^2 g/$ $\sigma^2 s$ ratio indicate that nonadditive gene effect was higher than additive gene effect for all above mentioned characters. However the mean square for gca was significant, the non- additive component may be predominant for all the characters. Both gca (σ^2 g) and sca $(\sigma^2 s)$ variance data analysis revealed many important idea about additive as well as non-additive about various characters under study. The gca variances appears if there is difference in gca effects of parents whereas in case of sca variance arises from differences in sca effects of crosses. Here, the value of gca variance represents the variance of the breeding value which means additive genetic variance ($\sigma^2 a$). But non-additive genetic variance ($\sigma^2 d$) is due to *sca* variance which is mainly dominance variance. The relative importance of additive or non-additive genetic variance is assist by information given by variance of *gca* and *sca*. Both additive and non-additive genetic variance is of equal importance if value is equal to unity. Here both genetic variance play a vital role in an expression of gene. This result was also seen by Arya *et al.* (2017)^[1], Kohli (2019)^[8] and Khan (2019)^[9].

General combining ability effects of F1

The *gca* effects (Table 5) for all ten parents revealed which parent was good general combiner in F_1 progenies on the basis of magnitude and direction of combining ability effects. Based on the analysis, VL 3017 and VL 892 are good general combiner for most of characters that come under this study. However not a single parent show good general combiner for all the characters at a same time. This result shows that VL 3017 and VL 892 could be most promising parent having good general combiner for grain yield and others yield contributing characters. This type of result corroborated with result of Hammad (2013) ^[5] and Desale (2014) ^[3] and Dedaniya *et al.* (2019)^[2].

Specific combining ability effects of F1

The highest and positive significant sca effects (Table 6) was observed in VL 3018 x HS 490 followed by other cross viz. VL 892 x UP 3017, HPW 459 x VL 3017, VL 3018 x HS 660 and HS 660 x HS 662 for grain yield per plant in their F₁ progenies. However some of other yield contributing character like total number spikelets per spike, spike length, number of grains per spike and number of tiller per spike is also imparts in productivity. In most of cases, cross combination having good specific cross combination for different characters involved either both parent or one of them was with good gca effects for the yield and its important components characters. However it is not mandatory that parents having highest estimates of gca effects would also produce highest *sca* effects. Most probably highest *sca* effects is due to crosses having diverse parents. The cross between two different genotype having high x high gca denotes about possibility of complementary epistasis that directing along the direction of additive effects. In case of cross combination having two different genotype with high and low gca with positive sca effects may be effect of dominant x recessive interaction effects, most likely complementary, however it may be also possible that in poor x poor crosses combination it perform better as compare to both high x high as well as high x low cross combination. Here productive of traits having poor x poor cross only denotes a high value of nonadditive components and reason conferring the top-tier to the pertinent cross combination and can be used as resource for heterosis breeding or multiple crosses, followed by inter among the productive segregates. Similar mating experimental findings also observed by Hannachi et al. (2013) ^[6], Dinesh and kerkhi (2015)^[1] and Kohli (2019)^[8].

Table 1: List of Wheat (Triticum aestivum L) genotypes and their source of origin

S. No.	Genotypes	Source
1.	VL 3017	AICW & BIP
2.	UP 3017	AICW & BIP
3.	VL 306	AICW & BIP
4.	HS 662	AICW & BIP
5.	HS 490	AICW & BIP
6.	VL 892	AICW & BIP
7.	HS 661	AICW & BIP
8.	HS 660	AICW & BIP
9.	VL 3018	AICW & BIP
10.	HPW 459	AICW & BIP

S. No.	Characters	Mean	Mean sum of square			
		Replication	Genotype	Error		
1	Days to 50% flowering	62.62	112.38*	3.52		
2	Days to 80% maturity	13.48	42.69*	5.44		
3	Number of tiller/ plant	0.57	1.00*	0.17		
4	Number of spikelets/ spike	0.43	1.39*	0.20		
5	Number of grain/ spike	1.99	5.02*	0.63		
6	Grain yield /plant	0.04	4.43*	0.28		

Table 1	2: /	Analysis	of	variance	for	different	characters	in	wheat
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 $\label{eq:combining} \textbf{Table 3:} Analysis of variance for combining ability of parents and F_1$

Source	4 f	Mean sum of square								
Source	u.1.	50% F	80% MA	NT/ P	NSPKL/SPK	NG/ SPK	GY/P			
Gca	9	95.64*	24.73*	0.43	4.03	74.66	1.08			
Sca	45	25.81*	12.12*	0.31	1.19	38.00	1.55			
Error	108	1.17	1.81	0.05	0.21	0.93	0.09			
c.d.		0.87	1.09	0.18	0.37	0.78	0.49			

50% F -Days to 50% flowering, 80% MA- Days to 80% maturity, NT/ P-Number of tiller/ plant, NSPKL/SPK -Number of spikelets/ spike, NG/ SPK-Number of grain/spike and GY/P- Grain yield /plant

Table 4: Estimation of components of variance and their ratio for various characters in wheat

Components	50% F	80% MA	NT/ P	NSPKL/SPK	NG/ SPK	G Y/P
	F_1	F_1	F_1	F_1	F_1	F_1
$\sigma^2 g$	7.87	1.91	0.03	0.31	6.14	0.08
$\sigma^2 s$	24.64	10.31	0.25	0.98	37.7	1.46
GCA/SCA Ratio	0.13	0.18	0.12	0.32	0.16	0.56

50% F -Days to 50% flowering, 80% MA- Days to 80% maturity, NT/ P-Number of tiller/ plant, NSPKL/SPK -Number of spikelets/ spike, NG/ SPK-Number of grain/spike and GY/P- Grain yield /plant

Table 5: Estimates of general combining ability effects for F1 in a ha	alf-diallel cross for various characters in wheat
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Genotypes	50% F	80% MA	NT/ P	NSPKL/SPK	NG/ SPK	G Y/P
VL 3017	-4.79**	-3.17 **	0.22 **	0.43 **	-0.36 ns	0.22 **
UP 3017	4.82**	1.08 **	-0.26 **	0.47 **	-0.13 ns	-0.32 **
VL 3016	-2.35**	-0.44 ns	-0.17 *	-0.48 **	-0.53 *	-0.09 ns
HS 662	3.57**	1.33 **	-0.03 ns	-0.68 **	-0.98 **	-0.57 **
HS 490	-0.02	0.28 ns	0.10 ns	-0.25 *	-0.60 *	0.20 *
VL 892	1.93**	0.97 **	0.35 **	1.04 **	5.63 **	0.38 **
HS 661	-0.82**	-1.03 **	-0.01 ns	0.02 ns	-0.01 ns	0.07 ns
HS 660	-0.10**	-0.56 ns	-0.02 ns	-0.06 ns	0.63 *	-0.21 *
VL 3018	-1.60**	-0.19 ns	0.03 ns	-0.82 **	-4.61 **	0.31 **
HPW 459	-0.63*	1.72 **	-0.21 **	0.33 **	0.97 **	0.02 ns

50% F -Days to 50% flowering, 80% MA- Days to 80% maturity, NT/ P-Number of tiller/ plant, NSPKL/SPK -Number of spikelets/ spike, NG/ SPK-Number of grain/spike and GY/P- Grain yield /plant

Table 6: Estimates of specific combining ability effects for F₁ in a half-diallel cross for various characters in wheat

Genotypes	50% F	80% MA	NT/ P	NSPKL/SPK	NG/ SPK	G Y/P
UP 3017 * VL 3017	-6.40 **	1.69 **	-0.78 **	-0.51 **	-3.81 **	-1.21 **
VL 3016 * VL 3017	11.10 **	4.22 **	-0.07 ns	0.37 *	-4.15 **	-1.09 **
HS 662 * VL 3017	0.85 *	3.11 **	-1.07 **	0.04 ns	4.56 **	0.23 *
HS 490 * VL 3017	-1.57 **	3.16 **	-0.01 ns	0.14 ns	8.51 **	1.61 **
VL 892 * VL 3017	-3.85 **	-2.53 **	0.41 **	-0.21 ns	-3.97 **	0.61 **
HS 661 * VL 3017	-1.10 **	3.47 **	-0.29 **	0.41 *	0.33 ns	-0.22 ns
HS 660 * VL 3017	-2.49 **	-3.34 **	-0.42 **	-0.18 ns	-5.64 **	-0.05 ns
VL 3018 * VL 3017	2.01 **	5.30 **	-0.67 **	0.51 **	-1.20 **	-0.14 ns
HPW 459 * VL 3017	-1.63 **	-1.62 **	0.44 **	1.30 **	6.82 **	2.39 **
VL 3016 * UP 3017	-0.52 ns	-1.37 **	1.14 **	1.20 **	5.70 **	1.83 **
HS 662 * UP 3017	-15.10**	-8.14 **	-0.06 ns	2.01 **	16.28 **	0.05 ns
HS 490 * UP 3017	0.82 *	0.58 ns	-0.59 **	0.17 ns	5.96 **	-0.91 **
VL 892 * UP 3017	-2.79 **	0.22 ns	0.88 **	0.82 **	4.07 **	2.70 **
HS 661 * UP 3017	6.96 **	-2.12 **	0.05 ns	-1.90 **	-8.43 **	0.75 **
HS 660 * UP 3017	3.57 **	-1.59 **	-0.08 ns	0.64 **	-3.60 **	-0.54 **
VL 3018 * UP 3017	-0.27 ns	-3.95 **	-0.13 ns	-1.46 **	-2.16 **	-1.78 **
HPW 459 * UP 3017	3.10 **	5.13 **	0.18 *	0.13 ns	1.00 **	-0.14 ns
HS 662 * VL 3016	4.73 **	3.05 **	-0.08 ns	0.22 ns	-4.92 **	-0.52 **
HS 490 * VL 3016	-2.35 **	-1.89 **	-0.15 ns	-0.08 ns	-2.24 **	0.54 **
VL 892 * VL 3016	2.04 **	3.41 **	-0.27 **	-1.23 **	9.00 **	-0.20 ns

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HS 661 * VL 3016	-1.21 **	-4.59 **	0.03 ns	-0.88 **	-8.50 **	-1.52 **
HS 660 * VL 3016	-4.93 **	0.27 ns	-0.03 ns	-0.01 ns	-2.60 **	0.96 **
VL 3018 * VL 3016	-4.43 **	0.91 ns	-0.15 ns	1.42 **	9.04 **	-0.09 ns
HPW 459 * VL 3016	-1.07 **	0.33 ns	-0.91 **	0.81 **	1.00 **	0.09 ns
HS 490 * HS 662	-1.93 **	1.66 **	-0.42 **	0.13 ns	0.74 *	-1.11 **
VL 892 * HS 662	0.46 ns	-1.03 *	-0.21 *	-0.29 ns	-9.82 **	-1.35 **
HS 661 * HS 662	0.21 ns	3.63 **	0.56 **	0.06 ns	2.35 **	-0.61 **
HS 660 * HS 662	3.82 **	1.49 **	0.70 **	0.13 ns	2.31 **	1.95 **
VL 3018 * HS 662	4.65 **	2.47 **	0.45 **	-1.04 **	-2.38 **	0.48 **
HPW 459 * HS 662	1.35 **	-0.12 ns	-0.51 **	-2.78 **	-11.89 **	0.09 ns
VL 892 * HS 490	5.04 **	0.02 ns	-0.41 **	0.27 ns	-1.14 **	-0.37 **
HS 661 * HS 490	2.88 **	-7.31 **	-0.24 **	-1.78 **	-2.37 **	-0.96 **
HS 660 * HS 490	6.73 **	2.88 **	0.03 ns	-0.10 ns	-0.80 *	-1.01 **
VL 3018 * HS 490	-5.43 **	-0.14 ns	0.58 **	1.06 **	-0.96 **	3.08 **
HPW 459 * HS 490	-2.40 **	-0.39 ns	-0.37 **	-0.02 ns	-0.14 ns	-1.18 **
HS 661 * VL 892	6.85 **	-1.34 **	0.17 ns	0.27 ns	0.41 ns	0.04 ns
HS 660 * VL 892	2.12 **	-0.14 ns	0.51 **	0.94 **	11.44 **	0.37 **
VL 3018 * VL 892	1.62 **	-1.84 **	-0.81 **	-0.76 **	-8.79 **	-0.79 **
HPW 459 * VL 892	5.65 **	3.91 **	-0.16 ns	-1.64 **	8.04 **	-1.69 **
HS 660 * HS 661	4.54 **	4.52 **	-0.32 **	0.96 **	6.48 **	-0.11 ns
VL 3018 * HS 661	-2.96 **	2.49 **	-0.57 **	0.72 **	0.18 ns	-1.18 **
HPW 459 * HS 661	-4.93 **	3.24 **	0.34 **	0.64 **	2.00 **	1.22 **
VL 3018 * HS 660	7.32 **	3.36 **	0.90 **	-1.00 **	6.35 **	2.08 **
HPW 459 * HS 660	-3.65 **	-1.56 **	-0.26 **	1.19 **	-2.30 **	-0.46 **
HPW 459 * VL 3018	3.85 **	-1.26 *	0.69 **	-1.92 **	0.48 ns	0.58 **

50% F -Days to 50% flowering, 80% MA- Days to 80% maturity, NT/ P-Number of tiller/ plant, NSPKL/SPK -Number of spikelets/ spike, NG/ SPK-Number of grain/spike and GY/P- Grain yield /plant

Conclusion

Based on the above result, we get that there is great significance of both additive as well as non-additive gene effects for grain yield and its contributing characters studied. Therefore it is suggested that there is considerable scope for improving these wheat genotype yield through pure line and heterosis breeding too. According to specific combining ability effects of all crosses for yield and their contributing characters advised that most of the good specific cross combination for different characters in between parents with either both good *gca* effects or one of them have good *gca* effects.

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