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Genetic variability analysis of yield and its attributes in F1 and their parent of bread wheat (*Triticum aestivum* L.) over environment

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Abstract
A diallel cross study comprising of ten bread wheat (*Triticum aestivum* L.) cultivars was carried out with parents and F1 progeny to determine genetic variability analysis for yield and its attributes. The result showed that higher estimate of phenotypic and genotypic coefficient of variation for grain yield per plant and biological yield per plant followed by grains per plant, number of leaves per plant, effective tillers per plant, spike per plant, revealed presence of exploitable genetic variance which can be improved through direct selection. Also the above traits reported high heritability coupled with high genetic advance over percentage of mean reporting selection will be rewarding and effective as traits were likely to governed by additive genes. It also provides information on the correlated response to directional selection to predict genetic advancements and so, can be used as selection indices for the functioning of a more efficient selection program. The results obtained from this study might be helpful for wheat breeders trying to make efficient breeding programme to develop new varieties.

Keywords: Genotype, genetic variability, diallel, environment, selection indices

Introduction
Lentil (*Lens culinaris* Medik) is a member of Leguminaceae family and it is commonly known Wheat is one of the most important grain food crops of India, which provides 20% of the total food calories of human requirement (Bhawsar, 1993) [2]. Both in terms of area and production, India is the second largest wheat growing country in the world. In acreage it is next to rice in India and world. From a meagre 5.6 million tons produced during 1947-48, marking an increase up to 98.61 million tons in 2019-20. Partly this is the result of increase in area under wheat. However, the major part of this increase has resulted from increased productivity from 7 quintal to 33 quintal since freedom of nation. This is primarily due to the introduction and development of dwarf Maxican high yielding wheat varieties. Madhya Pradesh is the second largest producing state of wheat with 17.58 million tonnes from the 5.46.69 million hectares area and 2627 kg/ha (Source: DES, MoA & FW, India 2021) but geometrical increase in India's population has been a challenge for agricultural scientists. To feed the ever-increasing population of India, there is a need of improving genotypes for better wheat yield potential per unit area basis. This could be achieved by exploring the maximum genetic potential from the available germplasm of wheat.

Grain yield improvement is one of the most challenging objective in wheat breeding due to complex genetic architecture and low heritability. Identification of gene for grain yield and related traits and genetic study are important for yield improvement. Genetic study provides the experimental means to functionally characterize genetic determinants by suppressing or enhancing gene activities. This knowledge can then be used for targeted improvements tailored to the specific needs of the diverse and changing environments in which wheat is grown across the world. This offers the potential to tackle yield gaps wherever they exist, for a variety of causes, enabling this global crop to finally reach its full potential.

Breeders should concentrate on development of productive wheat varieties by crossing good general combining lines for grain yield and selecting transgressive segregants from the resulting hybrids. Information regarding general and specific combining ability of wheat genotypes is a prerequisite to launch a successful wheat-breeding program. Diallel and partial diallel mating design has been extensively used to analyze the combining ability effects of wheat genotypes and also to provide information regarding genetic mechanisms controlling grain yield and other traits.

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Materials and Methods

An experiment was conducted in a completely randomized block design with three replications at Zonal Agricultural Research Station, Powarkheda, Madhya Pradesh in black cotton soils during *Rabi* 2020-21. Each plot comprised 2 rows of 2 meter length with 20 cm distance between rows and 10 cm between plants. The all good agronomic practices for crop management are applied. Ten varieties and 45 crosses in dialle passion of wheat along with 2 checks were used in the experiment. The parents obtained from AICRP on wheat, ZARS Powarkheda and crosses were made in Rabi 2019-20 (Table 1).

Table 1: Details of parents

S. No.	Genotype/Crosses	Pedigree of parents	Source of parent
1.	GW -322	GW 173//GW 196	RARS, Vijapur
2.	MP-3382	CHOIX/STAR/3/HE1/3*CNO79//2*SERI/4/GW273	JNKVV, Jabalpur
3.	MP-3336	HD 2402/GW 173	JNKVV, Jabalpur
4.	HD-2967	ALD/COC/URESH/HD2160M/HD2278	IARI, New Delhi
5.	HI-1544	HINDI62/BOBWHITE/ CPAN2099	IARI, RWRS, Indore
6.	MP-3288	DOVE/BUC/DL 788-2	JNKVV, Jabalpur
7.	HD-3098	1455/2*PASTOR	IARI, New Delhi
8.	GW-173	TW 275/7/6/1LOK-1	RARS, Vijapur
9.	MP-4010	ANGOSTURA 88	RVSKVV, Gwalior
10.	GW 366	DL 802-3/GW 232	JAU, Junagadh

The data on nine morphological characters *viz*., Days to 50% heading, Days to maturity, Plant height (cm), Peduncle length(cm), No. of effective tillers plant^{-1}, Number of leaves plant^{-1}, Spike length (cm), No. of spike plant^{-1}, No. of spikelets spike^{-1}, Spike weight (g), Grain weight spike^{-1} (g), No. of grains spike^{-1}, Biological yield plant^{-1} (g), Number of grains plant, 1000-grain weight (g), Harvest Index (%) spike, Harvest index (%), Grain yield plant^{-1} (g) were recorded.

Analysis of variance, correlation coefficients and path coefficients for the observations were calculated by windostat version 9.2 form Indostat services, Hyderabad.

Results and Discussions
Analysis of variance

The Analysis of variance for different quantitative traits of 55 entries along with the checks revealed that the component of variance with the genotypes was significant at 1% level of probability in all the traits namely Days to 50% heading, Days to maturity, Plant height (cm), Peduncle length(cm), No. of effective tillers plant^{-1}, Number of leaves plant^{-1}, Spike length (cm), No. of spike plant^{-1}, No. of spikelets spike^{-1}, Spike weight (g), Grain weight spike^{-1} (g), No. of grains spike^{-1}, Biological yield plant^{-1} (g), Number of grains plant, 1000-grain weight (g), Harvest Index (%) spike, Harvest index (%), Grain yield plant^{-1} (g). The variation among these traits can be utilized in further breeding programme for improvement and selection of traits. Therefore, genes for such important trait may be utilized from other source such as from germplasm and other diverse genotypes. Similar results were reported by Nagar *et al*. (2018) [9] and Singh *et al*. (2020) [10].

Estimates of genetic parameter

The Mean values and the range of all the eighteen morphological traits representing maximum and minimum of all traits were presented in table no. 3.

(a) Phenotypic and genotypic coefficient of variation

Generally, the phenotypic coefficients of variability were higher than corresponding genotypic coefficients of variability for the observed traits which indicates the impact of environment upon the traits (Table 3). The higher estimate of phenotypic and genotypic coefficient of variation (PCV and GCV i.e., more than 20%) were observed for grain yield per plant and biological yield per plant followed by grains per plant, number of leaves per plant, effective tillers per plant, spike per plant and, with less difference between observed PCV and GCV estimates, indicating presence of exploitable genetic variance for these traits and suggested possible improvement through direct selection. Moderate phenotypic and genotypic coefficient of variation (10 to 19%) was observed for harvest index (%), grain weight per spike and grains per spike, which suggested that there is considerable scope of improvement in these traits in desired direction through a selection processes. The Low estimates of phenotypic and genotypic coefficient of variation were observed for the parameters days to maturity, peduncle length(cm), plant height (cm), 1000-grain weight (g), days to 50% heading, harvest Index (%) spike, No. of spikelets spike^{-1}, and spike weight (g) indicating the major role of genetic factors changing the expression of these traits. The above findings were accordance with the findings of Mohanty *et al*. (2016) [11], Arya *et al*. (2017) [1].

(b) Heritability and Genetic advance as a % of mean

Heritability estimates along with genetic advance were more helpful than heritability alone in predicting the resultant gain under selection of best individual. Heritability and genetic advance as percent of mean were estimated to get a clear picture for improvement in various traits through selection. In the results of the present investigation, high heritability were observed for the traits (>70%) days to 50% heading (83%), followed by No. of spikelets spike^{-1} (75%), and grain yield plant^{-1} (72%), the high value of heritability indicates that though the trait is least influenced by environmental effect, the selection for such character may not be useful because heritability is the estimate of both fixable and non-fixable variances. Whereas, moderate heritability (50-70%) were observed in biological yield plant^{-1} (69%) followed by No. of grains spike^{-1} and spike weight (68%), spike length, grain weight spike^{-1}, No. of grains plant, plant height, No. of spike plant^{-1}, No. of effective tillers plant^{-1}, days to maturity, harvest index (%) spike, No. of leaves plant^{-1} and 1000-grain weight. The lowest estimates of heritability were observed in harvest index (49%) and Peduncle length (36%) this reveals that character is highly influenced by environmental effect and genetic improvement through selection will be difficult

due to masking effect of environment. Similar results were reported by Laala *et al.* (2021) [8] and Kumar *et al*. (2013) [6].

Higher estimates of Genetic Advance as a % over mean (i.e., >15%) were observed in grain yield plant-1 (53.3%), followed by biological yield plant-1 (51.5%), No. of grains plant (46.6%), No. of leaves plant-1 and No. of effective tillers plant-1(36.4), No. of spike plant-1 (34.4), harvest index (27.8), grain weight spike-1 (21.5), No. of grains spike-1 (21.4), No. of spikelets spike-1 (19.5), spike weight (19.4), days to 50% heading (16.5) and harvest index (%) spike (15.7%) this showed that character is governed by additive genes and selection will be rewarding. Moderate value of genetic advance as % over mean (10-15%) were observed in Spike length (13.6%), followed by Plant height (11.2%) and lowest value was observed in 1000-grain weight (g) (7.9%)followed by peduncle length (5.8) and days to maturity, the lowest value suggestion utilization heterosis breeding for improvement of this trait as it is governed by non-additive genes. The results were in accordance with Kumar *et al.* (2013) [6] and Bhushan *et al*. (2013) [3].

Hence, the high heritability and along with higher estimates of genetic advance over percentage of mean will be rewarding as likely it is governed by additive genes and selection will be

effective for such observed traits *viz*., grain yield plant-1 (g), biological yield plant-1, No. of effective tillers plant-1, No. of spike plant-1 and No. of leaves plant-1. These findings were supported by Fellahi *et al.* (2014) [4]. Although high estimates heritability and medium genetic advance over percentage of mean of were observed for days to 50% heading, grain weight spike-1 (g), spike weight (g) and No. of spikelets spike-1 and high heritability to low genetic advance were observed for days to maturity, plant height (cm) and harvest Index (%) spike, indicates that selection will be ineffective as the trait is under high influence of environment.

(c) Selection intensity
Highest selection intensity observed for grain yield per plant followed by biological per plant, No. of grains per plant, No. of effective tillers plant-1, No. of spike per plant and Harvest index (%). The high heritability of grain yield and its attributes warrants good progress from selection in early generations. The relatively lower heritability suggests the use of multiple replications during selection to limit environmental effects. These findings were supported by Ibrahim, and Quick (2001) [5].

Table 2: Analysis of variance of 18 yield and its attributes in diallel crosses of bread wheat

Trait	DF	Env	DH	DM	PH	PL	SL	G/S	S/P	S/S	ET/P	BY/P	HI	GW/S	SW (g)	HI(s)	NL/P	G/P	TGW	GY/P
Rep.	2	E1	1.0	7.2	8.0	0.2	0.02	3.3	0.6	0.2	0.9	13.6	36.6	0.01	0.01	7.3	0.2	1004.9	0.3	13.8
		E2	28.0	20.1	10.8	6.2	0.4	2.0	1.0	0.5	2.9	13.9	36.3	0.01	0.00	15.0	1.9	24.5	0.5	16.7
		E3	12.2	19.8	117.2	38.3	3.3	31.8	5.3	29.4	6.6	323.8	4.1	0.40	0.62	56.5	40.6	5378.2	38.4	28.6
Geno.	54	E1	116.7	70.0	190.6	11.9	1.45	58.8	8.3	9.2	9.3	1947.9	227.3	0.18	0.31	246.4	146.2	19489.5	13.8	163.4
		E2	121.5	67.9	193.6	21.9	2.3	170.4	21.8	13.2	17.0	2114.5	379.4	0.25	0.40	238.3	140.9	67894.5	34.7	504.3
		E3	52.4	33.6	37.3	20.1	1.8	86.2	9.4	8.3	6.6	3046.5	248.3	0.13	0.21	157.9	232.1	16818.8	34.8	156.4
Error	108	E1	0.8	0.8	2.4	0.6	0.05	1.6	0.2	0.3	0.2	2.9	2.9	0.00	0.01	8.1	1.8	620.9	0.6	1.1
		E2	0.9	0.8	4.2	1.3	0.1	1.5	0.4	0.9	0.6	12.9	5.9	0.01	0.02	10.3	1.8	1366.7	0.5	3.1
		E3	0.5	0.7	12.8	1.8	0.2	2.4	0.4	0.3	0.2	17.3	4.4	0.01	0.02	12.1	3.1	712.7	0.9	1.4

Days to 50% heading, Days to maturity, Plant height (cm), Peduncle length (cm), No. of effective tillers plant-1, Number of leaves plant-1, Spike length (cm), No. of spike plant-1, No. of spikelets spike-1, Spike weight (g), Grain weight spike-1 (g), No. of grains spike-1, Biological yield plant-1 (g), Number of grains plant, 1000-grain weight (g), Harvest Index (%) spike, Harvest index (%), Grain yield plant-1 (g)

Table 3: Estimates of parameters of genetic variability for 18 yield and its attributes in diallel crosses of bread wheat

Trait	Mean	Range		PV	GV	PCV %	GCV %	Heritability %	Genetic Advance	GA % over mean	Selection intensity (%)
		Min.	Max.								
DH	59.4	48.7	73.0	32.8	27.4	9.6	8.8	0.83	9.8	16.5	21.2
DM	115.8	104.8	121.2	19.6	11.9	3.8	2.9	0.61	5.5	4.8	6.1
PH	83.5	72.0	92.6	51.2	32.6	8.5	6.8	0.63	9.4	11.2	14.4
PL	34.2	31.1	38.3	6.8	2.5	7.6	4.6	0.36	1.9	5.8	7.4
SL	8.6	7.1	10.1	0.7	0.4	9.8	8.0	0.67	1.1	13.6	17.5
G/S	39.5	29.9	52.1	36.3	24.8	15.2	12.6	0.68	8.4	21.4	27.5
S/P	8.1	5.21	14.0	4.6	2.9	26.3	20.9	0.63	2.8	34.4	44.0
S/S	15.5	12.0	22.1	3.7	2.8	12.5	10.9	0.75	3.0	19.5	25.0
ET/P	7.0	4.3	12.5	3.9	2.4	27.9	22.2	0.63	2.5	36.4	46.7
BY/P	78.4	43.1	158.8	797.2	554.2	35.9	30.0	0.69	40.4	51.5	66.0
HI (%)	36.1	25.7	58.2	97.9	48.3	27.41	19.2	0.49	10.0	27.8	35.7
GW/S	1.6	1.2	2.1	0.06	0.04	15.7	12.8	0.66	0.35	21.5	27.5
SW(g)	2.4	1.8	3.0	0.1	0.07	13.8	11.4	0.68	0.4	19.4	24.9
HI(s)	68.9	46.0	81.1	78.2	46.6	12.8	9.9	0.59	10.8	15.7	20.1
NL/P	24.5	15.9	42.9	59.2	33.4	31.3	23.5	0.56	8.9	36.4	46.7
G/P	314.6	187.3	612.1	12178.2	7865.2	35.0	28.1	0.64	146.8	46.6	59.8
TGW	41.5	37.2	49.0	9.7	5.0	7.5	7.9	0.51	3.3	7.9	10.2
GY/P	27.0	17.9	62.9	92.8	67.5	35.5	30.3	0.72	14.4	53.3	68.3

Conclusion
The above experimentation concludes that the higher estimate of phenotypic and genotypic coefficient of variation for grain

yield per plant and biological yield per plant followed by grains per plant, number of leaves per plant, effective tillers per plant, spike per plant, revealed presence of exploitable

genetic variance which can be improved through direct selection. Also the above traits reported high heritability coupled with high genetic advance over percentage of mean reporting selection will be rewarding and effective as traits were likely to governed by additive genes. It also provides information on the correlated response to directional selection to predict genetic advancements and so, can be used as selection indices for the functioning of a more efficient selection program. Also, the above study was very useful for breeder in order to increase yield *per se* performance.

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