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Genetic analysis of advanced wheat genotypes for yield and its attributing traits under late sown condition of Kymore hills central zone

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Abstract

The current study was carried out for the thirty advanced lines of wheat, evaluated under late sown condition *Rabi* 2014 in a randomized block design for seventeen traits under wheat improvement project at seed breeding farm JNKVV, Jabalpur. Analysis of variance resulted into significant differences among all the studied traits. Genetic variance were found highest among the traits *viz*; harvest index followed by the number of grains plant⁻¹ and plant height. The value of PCV and GCV were high for the characters *viz*; number of effective tillers plant⁻¹ number of ears plant⁻¹, number of grains plant⁻¹, ear weight, yield plant⁻¹ and the number of tillers plant⁻¹. The remaining characters exhibited moderate to low value of PCV and GCV estimates. Estimates of heritability and genetic advance were observed higher for the characters *viz.*, number of grains ear⁻¹, number of grains plant⁻¹, ear weight, peduncle length, yield plant⁻¹, number of leaves plant⁻¹, 1000 grain weight, harvest index, and biological yield plant⁻¹. This study showed that broad-sense heritability showed a high level of genetic control above examined traits. It is concluded that more fertile tiller number and ear weight of main spike are major yield contributing factors in selecting high yielding wheat lines.

Keywords: Wheat (*Triticum aestivum* L.), PCV, GCV, Heritability and genetic advance

Introduction

Bread wheat (*Triticum aestivum* L.) is one of the most widely grown crops worldwide. Increasing wheat yield remains one of the important goals of wheat breeding efforts, and wheat yield is a particularly a complex trait. Number of grains per spike plays an important role in improvement of wheat yield. It is also a cereal crop, able to cope with different environmental situations. Thus, this type of ability present in wheat genotypes, exploits the existing variability in developing high yielding varieties that may provide high productivity under changing climatic scenario. Yield is a complex trait and many, developmental and morpho-physiological characters have been suggested as being important to yield. However, yield can be considered in terms of metric characters and to achieve higher yields was an important goal of wheat breeders. So, cereal crop improvement depends upon the continuous supply of new germplasm material for various genes of agronomic importance. The development of high yielding wheat cultivars is the main objective of any breeding programs in the world (Ehdaie and Waines, 1989) [7]. Identification of better genotypes with desirable traits and their subsequent use in breeding program and establishment of suitable selection criterion can helpful for successful varieties improvement program. Analysis of variability among the traits and the association of a particular character in relation to other traits contributing to yield of a crop would be great importance in planning a successful breeding program (Mary and Gopalan, 2006) [21].

The priority of this wheat improvement programme is to increase grain yield along with identification and improvement in important yield traits. Any improvement programme, selection efficiency of breeder for increasing yield requires sufficient information on variability with respect to contribution, towards grain yield and yield contributing character. Development of high-yielding varieties requires a thorough knowledge of the existing genetic variation for yield and its components. The observed variability is a combined estimate of genetic and environmental causes, of which only the former one is heritable.

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The heritability of metric traits such as grain yield directly controls the efficiency of selection for that trait and that with high heritability is easier to be improved than those with lower heritability, as showed the presence of additive genetic variance in highly heritable traits (Sabal *et al.* 2001) [25].

However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic advance, the change in mean value between generations (Shukla *et al.*, 2006) [28]. Those traits, which illustrate simple inheritance and governed by few major genes suggested that they are under control of additive gene action and selection for such trait will be effective and if a non-additive gene action governing a trait, it may give high heritability along with low genetic advance, then selection for such a trait may be unproductive. Thus, estimates of heritability along with the study of genetic advance may help the breeders for identification of those characters having maximum selection efficiency.

Many investigators analysed variation for yield and its contributing metric traits in wheat. Being a complex trait, grain yield, depend upon yield attributing characters and their relations. One of the main objectives of any breeding program is to produce high yielding and better quality lines for release as cultivars to farmers. The prerequisite to achieve this goal is to find sufficient amount of variability, in which desired lines are to be selected for further manipulation to achieve the target. Introduction of new populations can be made from one region to the other easily and may be used for further manipulation to develop breeding lines (Jamal *et al.*, 2009) [13]. The present study was conducted to evaluate the performance of thirty wheat lines in order to assess the presence of variability for desired traits and a significant amount of variation for different parameters.

Materials and Methods

Present experimentation with thirty wheat genotypes (*Triticum aestivum*) [Table-1] were studied at the AICRP on wheat improvement project, JNKVV, Jabalpur and were seeded in the *Rabi* late season of 2014. The genotypes were grown in six row plot with three replications according to randomized complete block design. Suggested package of practices were followed. Following seventeen characters were studied [Table-2]

The data were analyzed to determine significant variation among the characters by studying phenotypic coefficient of variation and genotypic coefficient of variation, heritability estimates along with the genetic advance were estimated for the selection of those effective traits, which were not under the influence of environmental effect. The analysis of variance was done according to the method suggested by Burton (1952) [4] in order to estimate variance among the different characters. Following analysis were carried out accordingly as mentioned below:

Genetic Parameters Estimates

Genotypic and phenotypic coefficient of variation was computed, using formula given by Burton (1952) [4].

$$\text{Genotypic coefficient of variation (GCV \%)} = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV\%)} = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100$$

Where,

$$\begin{aligned} \sqrt{\sigma^2_g} &= \text{Genotypic standard deviation} \\ \sqrt{\sigma^2_p} &= \text{Phenotypic standard deviation} \\ \bar{X} &= \text{General mean of particular character} \end{aligned}$$

Heritability (h^2 Bs)

Heritability in broad sense was calculated by the method proposed by Johnson *et al.*, (1955) [14] and Hanson *et al.* (1957) [10].

$$h^2 (Bs) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

$$\begin{aligned} h^2 (bs) &= \text{Heritability in broad sense} \\ \sigma^2_g &= \text{Genotypic variance} \\ \sigma^2_p &= \text{Phenotypic variance} \end{aligned}$$

Genetic advance

The estimation of genotypic and phenotypic variances and heritability were used to determine the expected genetic advance as suggested by Johnson *et al.*, (1955) [14] and expressed as-

$$GA = K \times \sigma^2_p \times h^2$$

Where,

$$\begin{aligned} K &= \text{Selection intensity (2.06 at 5\% level)} \\ \sigma^2_p &= \text{Phenotypic standard deviation} \\ h^2 &= \text{Heritability (Bs) in fraction} \end{aligned}$$

Genetic advance as percentage of mean

This was expressed by following formula:

$$\text{Genetic advance (as \% of mean)} = \frac{GA}{\bar{X}} \times 100$$

Where,

$$\begin{aligned} GA &= \text{Genetic advance} \\ \bar{X} &= \text{Mean} \end{aligned}$$

Statistical Analysis of variance: By using completely randomized block design, was computed for all the characters evaluated by data entry and processing using Microsoft Office Excel 2007. Standard statistical procedures were used to analyze the average data by using Windostat software (Windostat version 9.2).

Results

High significant variance was obtained from analysis of variance among all the studied traits [Table-3]. Mean sum of squares due to genotypes was high for all the traits under investigation except number of tillers plant⁻¹ (5.15). Whereas, harvest index (8.02) followed by, number of spikelets plant⁻¹ (4.46) and number of grains plant⁻¹ (3.84) reported highest value of mean sum of squares due to error. The differences between GCV and PCV were high for number of tillers plant⁻¹ (PCV =20.1 & GCV =11.32), followed by a number of spikelets ear-1 (PCV =12.54 & GCV =4.67), number of effective tillers plant-1 (PCV =29.16 & GCV =22.54) and number of ears plant⁻¹ (PCV =26.11 & GCV =20.09) as presented in Table-3. The phenotypic coefficient of variation showed that number of effective tillers plant-1 (29.16)

exhibited highest phenotypic coefficient of variation followed by number of ears plant⁻¹ (26.11), number of grains plant⁻¹ (23.77), ear weight (22.81), yield plant⁻¹ (21.01), number of tillers plant⁻¹ (20.1), biological yield plant⁻¹ (19.88), number of leaves, plant⁻¹ (19.87), harvest index (18.88), peduncle length (17.48), number of effective grains ear⁻¹ (15.92), ear head length (15.21) and number of spikelets ear⁻¹ (12.54) whereas remaining characters exhibit low PCV. The highest estimate of the genotypic coefficient of variation was found for a number of grains plant⁻¹ (23.77) followed by number of effective tillers plant⁻¹ (22.54), ear weight (21.55), number of ears plant⁻¹ (20.09), yield plant⁻¹ (26.22) and the number of leaves plant⁻¹ (19.44), showed

The estimated heritability (broad sense) and genetic advance expressed as percentage of mean have been presented in [Table-4]. High heritability associated with high estimates of genetic advance (GA) for characters *viz.*, number of grains ear⁻¹, number of grains plant⁻¹, ear weight, peduncle length, yield plant⁻¹, number of leaves plant⁻¹, 1000 grain weight, harvest index, biological yield plant⁻¹. The estimates of high broad sense heritability along with high genetic advance as a percentage of mean were observed for number of grains plant⁻¹ ($h^2= 101.86$ & $GA= 64.13$), followed by, biological yield plant⁻¹ ($h^2= 99.12$ & $GA= 57.77$), number of leaves plant⁻¹ ($h^2= 97.2$ & $GA= 56.07$), and harvest index ($h^2= 83.12$ & $GA= 45.35$). Whereas high heritability along with moderate genetic advance as a percentage of mean were reported by number of grains ear⁻¹ ($h^2= 97.43$ & $GA= 28.12$), ear head length ($h^2= 94.95$ & $GA= 20.45$), yield plant⁻¹ ($h^2= 90.25$ & $GA= 26.22$) and 1000 grain weight ($h^2= 88.24$ & $GA= 27.76$). Broad sense heritability was highest for number of grains plant⁻¹ (101.86), biological yield plant⁻¹ (99.12), number of grains ear⁻¹ (97.43), days to maturity (97.31), number of leaves plant⁻¹ (97.20), plant height (95.45) yield plant⁻¹ (90.25), ear head weight (94.95), peduncle length (89.51), 1000 grain weight (88.24), harvest index (83.12) and days to 50% flowering (83.14). The estimate of genetic advance as per cent of mean was noticed highest for number of grains plant⁻¹ (64.13), followed by biological yield plant⁻¹ (57.77), number of leaves, plant⁻¹ (56.07), harvest index (45.35), ear weight (41.94), number of tillers plant⁻¹ (36.01), number of ears plant⁻¹ (32.87), number of grains ear⁻¹ (28.18), 1000 grain weight (27.76), yield plant⁻¹ (26.22), peduncle length (20.26) and ear head length (20.45)

Discussion

The results from analyses of variance investigated for the traits are presented in Table 3. In this experiment, grain yield and some grain quality characteristics of the thirty promising wheat genotypes which were introduced from CIMMYT, Mexico were assessed and a high significant variability among the promising wheat genotypes were examined with respect to the studied genetic parameters (Table 4). Because of genotypic variations of the genotypes included in the investigation, their responses differ significantly. Such considerable range of variations provided a good opportunity for yield improvement.

Genetic Variability is used to find out the extent to which variation in yield contributing traits are responsible for differences in yield among various genotypes, it must be arises in mind that maximum variability depends on heritable and non-heritable components. While coefficients of variation measure the extent of variability present in a population,

estimates of heritability and genetic advances are important preliminary steps in any breeding program as they provide information needed in designing the most effective breeding program and the relative practicability of selection. Genotypic variance, phenotypic variance, genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), broad sense heritability, genetic advance and genetic advance expressed as percentage of mean for seventeen characters.

Estimates of Genotypic and Phenotypic Coefficients of Variation The results revealed considerable phenotypic and genotypic variances among the genotypes for the traits under consideration. In all traits a large portion of the phenotypic variance was accounted for by the genetic component except for number of tillers plant⁻¹.

Generally, maximum of the observable variability was due to the genetic variation. Which indicates existence of immense inherent variability that may not influence by environment, which in turn be more useful in exploitation for selection and hybridization programs. The PCV values were higher than GCV values for all the traits which reflect the influence of environment on the expression of traits. The genotypic coefficient of variation along with heritability estimates provide reliable estimates of the amount of genetic advance to be expected through phenotypic selection (Burton, 1952) [4]. The results of the present study indicated that moderate heritability values were recorded for number of effective tillers per plant, number of tillers per plant and harvest index. PCVs were slightly higher than GCVs for all selection parameters were indicative of the presence of environmental effect on the expression of characters [Table-3] as earlier reported by Sharma and Garg (2002) [27] and Kumar and Tyagi (2002) [18]. The remaining traits reporting lower estimation in the their genetic parameters taken in this study and offered less scope for selection as they are very much under the influence of environment

The expected genetic advance values for twelve characters of the genotypes evaluated is presented in Table 4. These values are also expressed as percentage of the genotypes mean for each character so that comparison could be made among various characters, which had different units of measurement. High heritability along with high genetic advance is an important factor for predicting the resultant effect for selection the best individuals. In the present investigation, High heritability accompanied with high genetic advance as percent of the mean in case of number of grains ear⁻¹, number of grains plant⁻¹, ear weight, peduncle length, yield plant⁻¹, number of leaves plant⁻¹, 1000 grain weight, harvest index, biological yield plant⁻¹ which in fact due to the presence of additive genes action representing efficacy of selection for the enhancement of these characters in early generation. Similarity with the findings were supported by Atta *et al.*, (2008) [2]; Bhoite *et al.*, (2008) [3] Manal (2008) [19]; Waqar-ul-haq *et al.*, (2008) [30]; Manal (2009) [20]; Ferdous *et al.*, (2010); Tsegaye and Dessalegn (2012) [29]; Hassan *et al.*, (2013) [11, 12]; Hussain *et al.*, (2013) [11, 12] and Farshadfar and Estehghari (2014) [8] Singh M., *et al.*, (2016) [26]. From the above discussion, number of grains ear⁻¹, number of grains plant⁻¹, ear weight, peduncle length, yield plant⁻¹, number of leaves plant⁻¹, 1000 grain weight, harvest index, biological yield plant⁻¹ were shown to have high to moderate genotypic variance, high to moderate heritability and greater genetic gain. Selection can therefore be based on these traits and their

phenotypic expression can be a good indicator of their genotypic potential. Whereas, High heritability for maturity days, heading days and plant height coupled with low genetic

advance indicates non-additive gene effects. Therefore, there seems a limited area for improvement in this trait

Table 1: List of genotypes of wheat under investigation:

S. No	Genotype	S. No	Genotype	S. No	Genotype
1.	JW-3269	11	PBW-343/CDWR-9563-1	21	CIMMYT-2
2.	GW-366	12	MP-3349/MP-3222	22	CIMMYT-4
3.	LOK-1	13	MP-3342/PBW-343/K-9924	23	CIMMYT-5
4.	JW-3211	14	PBW-343/CDWR-9563-6	24	CIMMYT-6
5.	JW-3336	15	MP-3368/MP-4669	25	CIMMYT-7
6.	HD-2864	16	MP-3359/WH-1092	26	CIMMYT-8
7.	HD-2932	17	MP-3372/NTAW-1395	27	CIMMYT-9
8.	HI-1544	18	MP-3360/RAJ-4213	28	CIMMYT-10
9.	MP-3324/MP-3092/MP-322	19	CIMMYT-3	29	CIMMYT-11
10.	401-136/JW-17-1	20	CIMMYT-1	30	CIMMYT-12

Table 2: Traits included for the investigation

S. No	Character name	S. No	
1	Days to 50% flowering (DF)	10	Ear head length (cm) (EHL)
2	Days to maturity (DM)	11	Ear weight (g) (EW)
3	Plant height (cm) (PH)	12	Peduncle length(cm) (PL ⁻¹)
4	Number of tillers plant ⁻¹ (TP ⁻¹)	13	Number of leaves plant-1(LP ⁻¹)
5	Number of effective tillers plant-1 (ETP ⁻¹)	14	1000 grain weight (g) (GW)
6	Number of spikelets ear-1 (SE ⁻¹)	15	Biological yield plant ⁻¹ (g) (BYP ⁻¹)
7	Number of ears plant ⁻¹ (EP ⁻¹)	16	Yield plant ⁻¹ (g) (YP ⁻¹)
8	Number of grains ear ⁻¹ (GE ⁻¹)	17	Harvest index (%) (HI)
9	Number of grains plant ⁻¹ (GP ⁻¹)		

Table 3: Analysis of variance for the present investigation

SV	Df	MSS																
		DF	DM	PH	TP ⁻¹	ETP ⁻¹	SE ⁻¹	EP ⁻¹	GE ⁻¹	GP ⁻¹	EHL	EW	PL	LP ⁻¹	GW	BYP ⁻¹	YP ⁻¹	HI ⁻¹
R	2	31.33*	28.23*	46.51*	6.82*	2.95*	13.37*	15.37*	43.95*	73.49*	2.92*	1.62*	46.87*	42.5*	10.28*	22.86*	30.16*	132.14*
G	29	25.29	53.54	93.75	5.15	5.52	5.17	6.28	164.51	17701.12	6	1.92	29.18	88.75	51.62	146.4	20.07	96.12
E	58	2.95	2.05	3.3	3.1	2.08	4.46	2.26	3.73	3.84	1.34	1.25	2.48	2.64	3.75	2.59	2.02	8.02

Table 4: Various parameters of genetic variability studied in the investigation

	MEAN	RANGE		C.V.	PCV	GCV	h ²	GA as % of mean
		MIN.	MAX.					
DF	67.57	59.9	71.23	3.89	6.51	6.06	83.14	11.58
DM	123.84	115.23	131.56	2.64	5.38	5.3	97.31	10.94
PH	99.39	81.06	107.3	3.37	7.72	7.53	95.45	12.54
TP ⁻¹	10.69	7.43	12.23	17.46	20.1	11.32	28.68	36.01
ETP ⁻¹	7.09	4.5	9.3	19.71	29.16	22.54	59.21	20.06
SE ⁻¹	19.41	16.76	21.63	12.17	12.54	4.67	8.68	9.97
EP ⁻¹	8.26	4.63	10.6	17.87	26.11	20.09	58.37	32.87
GE ⁻¹	55.34	42.93	69.2	4.86	15.92	15.6	97.43	28.18
GP ⁻¹	353.14	205	497.83	2.36	23.77	23.77	101.86	64.13
EHL	11.61	9.6	15.1	5.4	15.21	14.74	94.95	20.45
EW	4.3	3.38	5.4	9.03	22.81	21.55	90.26	41.94
PL	22.35	17.56	29.23	7.38	17.48	16.49	89.51	20.26
LP ⁻¹	32.45	22.43	44.46	5.79	19.87	19.44	97.20	56.07
GW	45.34	38.66	53.29	5.55	11.8	11.1	88.24	27.76
BYP ⁻¹	40.93	25.61	51.45	4.89	19.88	19.63	99.12	57.77
YP ⁻¹	15.56	11.23	20.92	8.42	21.01	19.86	90.25	26.22
HI	37.32	27.49	53.28	9.25	18.88	17.2	83.12	45.35

Conclusion

The heritability in a broad sense for yield and metric characters were moderate as well as high. The high value of these characters in irrigated timely sown condition was indicative of the presence of an additive type of gene action, thus selection for such traits would be useful in the improvement of these advance genotypes of wheat. The

selection of genotype having higher 1000-grain weight and higher number of grains plant-1 would ultimately be helpful for improving grain yield during procreation for yield enhancement in the wheat breeding programme.

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