Journal of Pharmacognosy and Phytochemistry

Gite VD
Genetics and Plant Breeding Group, MACS- Agharkar Research Institute GG Agarkar Road, Pune, Maharashtra, India

Bankar DN
Genetics and Plant Breeding Group, MACS-Agharkar Research Institute GG Agarkar Road, Pune, Maharashtra, India

Yashavantha kumar KJ
Genetics and Plant Breeding Group, MACS-Agharkar Research Institute, GG Agarkar Road, Pune, Maharashtra, India

Baviskar VS
Genetics and Plant Breeding Group, MACS-Agharkar Research Institute, GG Agarkar Road, Pune, Maharashtra, India

Honrao BK
Genetics and Plant Breeding Group, MACS-Agharkar Research Institute, GG Agarkar Road, Pune, Maharashtra, India

Chavan AM
Genetics and Plant Breeding Group, MACS-Agharkar Research Institute, GG Agarkar Road, Pune, Maharashtra, India

Surve VD
Genetics and Plant Breeding Group, MACS-Agharkar Research Institute, GG Agarkar Road, Pune, Maharashtra, India

Raskar SS
Genetics and Plant Breeding Group, MACS-Agharkar Research Institute, GG Agarkar Road, Pune, Maharashtra, India

Khairnar SS
Genetics and Plant Breeding Group, MACS-Agharkar Research Institute, GG Agarkar Road, Pune, Maharashtra, India

Bagwan JH
Genetics and Plant Breeding Group, MACS-Agharkar Research Institute, GG Agarkar Road, Pune, Maharashtra, India

Khade VM
Genetics and Plant Breeding Group, MACS-Agharkar Research Institute, GG Agarkar Road, Pune, Maharashtra, India

Correspondence
Baviskar VS
Genetics and Plant Breeding Group, MACS-Agharkar Research Institute, GG Agarkar Road, Pune, Maharashtra, India

Genetic variability parameters and correlation study in elite genotypes of bread wheat (*Triticum aestivum* L.)

Gite VD, Bankar DN, Yashavantha kumar KJ, Baviskar VS, Honrao BK, Chavan AM, Surve VD, Raskar SS, Khairnar SS, Bagwan JH and Khade VM

Abstract
Thirty-six genotypes of wheat were studied for generating scientific information on nature and magnitude of genetic variability, heritability, genetic advance and correlation for designing breeding programme. The field experiment was conducted at Experimental Research Farm, Hol, MACS-Agharkar Research Institute during 2016-17. The data were recorded on days to heading, plant height (cm), reproductive period, days to maturity, 1000-grain weight (g), biomass (g), grain yield (g) and harvest index (%). Analysis of variance revealed significant differences among the genotypes for all the characters except biomass. High heritability coupled with high genetic advance was observed for plant height (cm), days to heading, 1000-grain weight (g), grain yield (g) and harvest index (%), indicating the presence of additive gene action and direct selection for such characters would be more effective. Biomass, harvest index and days to maturity gave the positive association with grain yield. Correlation of these traits will be useful to breeders in selecting genotypes possessing group of desired traits. From this study it was concluded that, the high grain yielding genotypes GW 491, HI 1624, HI 1625 and GW 498 were observed and these genotypes could be utilized in further breeding programme. Genotypes HI 1624 was found to be early maturing with high yielding, can be utilized as parent in crossing programme for further crop improvement or can be tested further to consider it for commercial cultivation.

Keywords: Wheat, Variance, Heritability, Genetic Advance, Correlation, Elite Genotypes

Introduction
Bread wheat (*Triticum aestivum* L.) is the second most important food crop after rice in terms of both area and production. In India during 2015-16 area under wheat cultivation was 30.23 Mha with an average productivity of 30.93 q/ha. In Maharashtra it occupies an area of 6.29 lakh ha with an average productivity of 12.05 q/ha (DES, MoA & FW, India 2015-16). This crop provides more nutrition to the human being in comparison to other food crops; hence, it is considered staple food of the world's population. It is a challenging task to the breeders to enhance the present level of production, as the growing population of the country will require much more food as compared to the present day requirement. It is not possible to increase the area under production. Hence, only alternative is to increase the productivity per unit area by evolving superior genotypes and better management of crop production to fulfill increasing demands of food. Analysis of variability among the traits and the association of a particular character with other traits contributing to yield of a crop would be great importance in planning a successful breeding programme (Mary and Gopalan, 2006). Genetic variability among wheat genotypes can be estimated based on quantitative traits. The choice of parents is of paramount importance in breeding programme. For effective selection, information on nature and magnitude of variation in population, association of character with yield and among themselves and the extent of environmental influence on the expression of these characters are necessary (Yagdi and Sozen, 2009). The presence of considerable genetic variability in the base material ensures better chances of evolving desired plant types (Sabharwal and Lodhi, 1995). The knowledge of genetic parameters *viz.,* heritability and genetic advance among characters under selection is very useful for predicting genetic progress in breeding programme and developing efficient breeding strategies (Falconer and Mackay, 1996). Yield is complex character which is controlled by poly genes thus, the effective selection for yield is a complex process. Association between yield and its component characters themselves can improve the efficiency of selection. Selection for an optimum genetic advance should be based on judiciously computed parameters. More variation within species are useful for selection of parents. As a multivariate statistical technique, the principal components analysis (PCA) has the ability to transform a number of possibly correlated variables into a smaller number of

variables called principal components (Ziegel E., 2002), the principal components are linear transformations of the original variables and could be respective of a particular meaning (Jobson D., 1991). This approach is very helpful in deciding which agronomic traits of crop contributing most to yield, subsequently, these agronomic traits should be emphasized in the breeding program. Keeping in view, an effort has been made in the present study to evaluate a set of 36 bread wheat genotypes with an aim, to analyze the genetic variability, heritability, genetic advance, correlation and the principal components analysis for yield and its component traits.

Materials and Methods
The experimental material consists of 36 genotypes including two checks received from IIW&BR, Karnal (Haryana) as part of NIVT (National Initial Varietal Trial) to evaluate under timely sown condition. The source details of selected genotypes were given in Table 1. Two check varieties MACS 6222 and HI 1544 were used in the conduction of the experimental trial. The trial was sown in a simple lattice design with two replications at Experimental Research Farm, Hol during *rabi* 2016-17. The Farm is located at $18^0 04'$N; $74^o 21'$E; 549 m above sea level. The trial was sown in 18th November 2016 with plot of 6-meter length of 6 rows. The

row to row and plant to plant distance maintained at 20 and 10 cm, respectively. Net plot harvested was 4 rows of 6-meter length with 20 cm spacing. Fertilizers were applied at the rate of 120:60:40 NPK kg/ha. The full dose of P, K and half dose of N applied as basal dose at the time of sowing and remaining half dose of N as top dressing after 25 days sowing. The recommended agronomic practices were followed for good crop condition of wheat. The observations were recorded on five randomly selected competitive plants from each genotype in each replication for plant height (cm) and plot observation recorded on agro-morphological characters *viz.,* and days to heading, days to maturity, reproductive period, 1000-grain weight (g), biomass (g), grain yield (g) and harvest index (%). The analysis of variance and Principle Component Analysis (PCA) was performed by using STAR (IRRI) software. The test of significance done by F test. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were analyzed by adopting the procedure suggested by Burton & Devane (1953). Heritability in broad sense h² (b) and genetic advance as percent of mean were estimated by the formula as suggested by Hanson *et. al.,* (1956) and the correlation coefficient was estimated according to Al-Jibouri *et al.,* (1958)

Table 1. List of bread wheat genotypes used in the study

Sr. No.	Genotype	Parentage	Developed by/Source
1	HI 1622	BAJ#1*2//ND643/2*WBLL1	IARI, New Delhi
2	MACS 6703	KINGBIRD#1//INQALAB91*2/TUKURU	ARI, Pune
3	MP 1339	STAR//KAUZ/STAR/3/GW241	JNKKV, Powerkheda
4	PBW 770	PBW585/4/BABAX//IRENA/KAUZ/3/HUITES	PAU, Ludhiana
5	GW 498	K9507/GW322	JAU, Junagadh
6	K 1610	K0402/PBW502	CSAUA&T, Kanpur
7	AKAW 4924	DL-9-65-2/AKW1071-1-2	PDKV, Akola
8	UAS 391	GW344//UAS239/UAS304	UAS, Dharwad
9	GW 493	HW2045//HI1183/PCE2555	SDAU, Vijapur
10	MACS 6709	ROLF07/4/BOW/NKT//CBRD/3/CBRD/5/FRET2/TUKURU//FRET2	ARI, Pune
11	DBW 235	MELON//FILIN/MILAN/3/FILIN/4/TRCH/SRTU//KACHU	IIWBR, Karnal
12	NIAW 3161	ROLF07*2/5/FCT/3/GOV/AZ//MUS/4/DOVE/BUC	MPKV, Niphad
13	MP 1337	BECARD/QUAIU#1	JNKKV,Powerkheda
14	MP 3471	PFAU/MILLAN/3/SKAUZ/KS94U215//SKAUZ	JNKKV, Jabalpur
15	GW 492	RAJ4040/HD2808	SDAU, Vijapur
16	HI 1623	KAUZ/PASTOR//PBW343/3/KIRITATI/4/FRNCLN	IARI, New Delhi
17	GW 495	LOK54/RAJ4083	JAU, Junagadh
18	UAS 389	RAJ4083/DWR195	UAS, Dharwad
19	WH 1234	CHIBIA//PRLII/CM65531/3/MISR2*2/4/QUAIU	CCSHAU, Hissar
20	JWS 152	RAJ4133/MP4033	JNKKV, Sagar
21	NIAW 3173	CNO79//PF70354/MUS/3/PASTOR/4/BAV92/5/FRET2/KUKUNA/ /FRET2/6/ MILAN/KAUZ//PRINIA/3/BAV92	MPKV, Niphad
22	UAS 390	CNO79//PF70354/MUS/3/PASTOR/4/BAV92/5/FRET2/KUKUNA// FRET2/6/MILAN/KAUZ//PRINIA/3/BAV92	UAS, Dharwad
23	UP 2983	WBLL1*2/BRAMBLING/5/BABAX/LR42//BABAX*2/4/ SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ	GBPUA&T, Pantnagar
24	HD 3263	KACHU//KIRITATI/2*TRCH	IARI, New Delhi
25	HI 1624	GW322/PBW498	IARI, New Delhi
26	DBW 236	BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/ CASKOR/3/CROC1/AE.SQUARROSA(224)// OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92	IIWBR, Karnal
27	MACS 6708	MILAN/KAUZ//DHARWAR DRY/3/BAV/92/4/DANPHE#1	ARI, Pune
28	RAJ 4501	RAJ4037/PBW568	SKRAU, Durgapura
29	CG 1024	1447/PASTOR//KRICHAUFF/3/ATTILA*2/PBW65	IGKKV, Bilaspur
30	GW 491	HD2808/HI1516//PBW573	SDAU, Vijapur
31	HI 1625	GAINT3/HW2045	IARI, New Delhi
32	UAS 388	DWR162/NIAW301//UAS326	UAS, Dharwad
33	MP 1338	MILAN/KAUZ//DHARWAR DRY/3/BAV92/4/PAURAQ	JNKKV, Powerkheda
34	RAJ 4502	RAJ4037/PBW568	SKRAU, Durgapura
35	MACS 6222	HD2189*2/MACS2496	ARI, Pune
36	HI 1544	MACS2496*2/MC10/CPAN2099	IARI, RS, Indore

Statistical Analysis

The statistical analysis of the data on individual character was carried out on the mean values over two replications. The statistical methods adopted were as follows.

$$\text{i) General mean (X)} = \frac{\text{Sum of observations of all the plants for each genotype}}{\text{Number of plants}}$$

ii) Range = the minimum and maximum values for each trait within population

$$\text{iii) Coefficient of variation (CV \%)} = \frac{\sigma p}{\overline{X}} \times 100$$

Analysis of variance (ANOVA)

The structure of ANOVA

Source of variation	d.f.	M.S.S.	Expected values of M.S.S.
Replication (r)	r-1	M1	-
Genotypes (g)	g-1	M2	$\sigma e^2 + r\sigma g^2$
Error (r-1)	(g-1)	M3	σe^2
Total	(rg-1)	M1 + M2 + M3	-

Where,
r = number of replications
g = number of genotypes

Estimation of genetic parameters

In order to assess and quantify the genetic variability among the genotypes for the characters under study, the following parameters were estimated.

Estimation of variance components

Phenotypic and genotypic variances were estimated using the following formula,

$$\text{Genotypic variance } (\sigma g^2) = \frac{\text{MSS (genotypes) - MSS (error)}}{\text{Number of replications}} = \frac{M2 - M3}{r}$$

$$\text{Phenotypic variance } (\sigma p^2) = \sigma g^2 + \text{MSS error} = \frac{M2 - M3}{r} + M3$$

Genotypic and phenotypic coefficient of variation

1. Genotypic coefficient of variability (GCV)

$$\text{GCV (\%)} = \frac{\sigma g}{\overline{X}} \times 100$$

2. Phenotypic coefficient of variability (PCV)

$$\text{PCV (\%)} = \frac{\sigma p}{\overline{X}} \times 100$$

Where, σg = Genotypic standard deviation
σp = Phenotypic standard deviation
X = General mean of the character

GCV and PCV values were categorized as low, moderate and high as indicated by Sivasubramanian and Menon (1973). It is as follows,
0-10%: Low
10-20%: Moderate
20% and above: High

Heritability

Heritability in broad sense was estimated as the ratio of genotypic to the phenotypic variance and was expressed in percentage.

$$\text{Heritability (h}^2) \text{ (\%)} = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

The heritability was categorized as low, moderate and high as given by Robinson et al. (1949).
0% : Low
30-60%: Moderate
60% and above: High

Genetic Advance (GA): The extent of genetic advance to be expected from selecting five per cent of the superior progeny was calculated by using the following formula.
Genetic Advance (GA) = ih2σp
Where,
i = Intensity of selection
h^2 = Heritability in broad sense
σp = Phenotypic standard deviation
The value of i was taken as 2.06 assuming 5% selection intensity.

Genetic Advance over mean (GAM): Genetic advance over mean was estimated using the following formula,

$$\text{GAM (\%)} = \frac{GA}{\overline{X}} \times 100$$

Genetic advance as percent mean was categorized as low, moderate and high as given by Johnson et al. (1955). It is as follows.
0-10% : Low
10-20% : Moderate
20% and above: High

Result and discussion

Analysis of variance

Analysis of variance revealed that all the characters showed highly significant differences among the genotypes under study except biomass (Table 2), thereby it has suggested the presence of sufficient variability among the genotypes and provides ample scope for further improvement. Similar results were also reported by Tazeen and Naqvi et al. (2009). The presence of large extent of variability might be due to diverse sources of breeding materials collected as well as environmental effects on phenotypes.

Range and mean

The variability exploited in breeding programme is desired from the naturally occurring variants and wild relative of main crop species as well as from strains and genetic stocks artificially developed by human efforts. Through this study, an attempt was made to assess the mean performance and

extent of variability in wheat germplasm. In Table 4 shows the mean values for grain yield showed a wide variation which ranged from 1759 g (UAS 391) to 3107 g (GW 491) with mean value of 2365.17 g. Biomass showed a wide variation which ranged from 6114 g (UAS 391) to 8526 g (AKAW 4924) with mean value of 7013.50 g. 1000 grain weight showed a wide variation which ranged from 27 g (NIAW3161) to 40 g (RAJ 4502) with mean value of 34.61 g. Maqbool *et al.*, (2010) reported wide range of variation for plant height, reproductive period, biomass, grain yield and 1000 grain weight. However, Sajjad *et al.*, (2011) reported large variation for grain yield and 1000 grain weight. Earlier reports are in congruity with some of our results in the present experiment. A wide range recorded for maximum characters also indicated that there are differences among the genotypes in terms of performance for yield and component traits. On the basis of mean performance, the highest grain yield was observed for genotype GW 491 (3107 g) followed by HI 1624 (3101 g), HI 1625 (2874 g) and GW 498 (2386.5 g) among 36 genotypes and other contributing characters. These high yielding genotypes could be utilized in further breeding programme.

Genotypic and phenotypic coefficient of variation
The magnitude of genotypic coefficient of variation was lower than phenotypic coefficient of variation for all the characters studied indicating ample of variability not only due to genotype but also environmental interaction in the expression of the characters. The findings were in agreement with previous study in wheat Singh *et al.*, (2012). The low value of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for days to heading (6.69 & 6.86%), days to maturity (1.99 & 2.33%), reproductive period (6.54 & 7.12%), plant height (6.15 & 6.46%), 1000-grain weight (9.47 & 9.63%), and biomass (5.77 & 8.40%) respectively. Low values of GCV and PCV suggested low variability for such characters among genotypes. These results were in conformity with the findings of Chaturvedi and Gupta (1995) for days to heading and plant height, while Jag Shoran (1995) for days to maturity. However, substantial difference between GCV and PCV was observed in grain yield and harvest index as compared to other characters and indicated suggested environmental effect was prominent for grain yield and harvest index. The least difference between PCV and GCV was noticed for 1000-grain weight, days to heading, plant height and days to maturity indicated that these characters were less influenced by environment. These results match with the finding of Shankararao *et al.* (2010). Moderate estimate of GCV and PCV were observed for grain yield and harvest index and these results similar with Jagshoran *et al.* (1995).

Heritability (H^2) in broad sense and genetic advance
Heritability decides the resemblance of progeny with their parents (Falconer, 1981). While, genetic advance provides knowledge about expected gain for a particular character after selection. In general, in self–pollinated crops, characters with high heritability possess high genetic advance, but when phenotypic variation in the population is low, genetic advance also tends to be low and vice–versa. This shows the variation and heritability are very much important for any breeding programme. In this concern, high estimates of heritability were observed for 1000-grain weight followed by days to heading, plant height, reproductive period, days to maturity, grain yield and harvest index, whereas moderate for biomass

(Table 5). Yadav *et al.* (2014) has been recorded high heritability for days to heading, days to maturity, 1000-grain weight and grain yield per plant. This shows the presence of additive gene effect and selection may be made for the improvement of these characters. It can be find out with greater degree of accuracy when heritability coupled with genetic advance is studied (Dudley and Moll, 1969). Therefore, to understand the type of gene action involved in the expression of various polygenic characters, estimation of heritability along with genetic advance is more useful. High heritability coupled with high genetic advance as percent mean were revealed for plant height, days to heading, 1000-grain weight, grain yield and harvest index similar findings were also reported by Khokhar *et al.*, (2010). This indicates substantial contribution of additive gene action in the expression of the characters. Hence, direct selection for such characters would be more effective. The character like, days to maturity and reproductive period exhibited high Heritability along with low genetic advance suggested predominance of non-additive gene action, hence direct selection for such characters would mislead the expected results.

Correlation coefficients
In the present investigation (Table 6) grain yield was found to be significant & positively correlated with biomass hence the breeding for increasing biomass and harvest index would be relevant to increase the grain yield. Harvest index was found to be significant and positively correlated with grain yield and negatively correlated with days to heading and maturity. Reproductive period is very much sensitive to temperature and water availability, hence date of sowing is important for coincidence of the reproductive period with the congenial temperature range. In the present study, the reproductive period has shown significant negative correlation with days to heading. Days to maturity has significant and positive correlation with days to heading. Over all from the present investigation, it was found that the days to heading, days to maturity, biomass, harvest index are important traits to consider for yield improvement because these traits have shown significant positive correlation either directly with grain yield and yield contributing traits. Similar results were obtained by Masood *et al.*, (2014). Correlation between the yield and yield components facilitate the choice of suitable breeding methods to be applied and selecting the parents for improving the crop
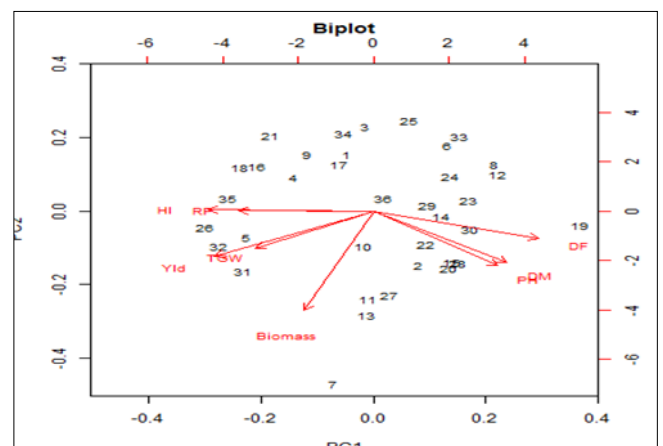
Principle Component Analysis (PCA)

Fig 1: Principle Component Analysis (PCA)

The average data was analyzed by using Principal Component analysis. Principal component analysis reflects the importance of the largest contributor to the total variation at each axis of differentiation. The eigen values are often used to determine how many factors to retain. The sum of the eigen values is usually equal to the number of variables (Sharma J. R. 1998). Two principal components showed more than one Eigen value and showed about 74.72% of variability. Table 7. PC-I showed 57.29% and PC-II 17.43% exhibited variability among different traits under experiment genotypes**.** Yield, 1000 grain weight, harvest index and reproductive period were in acute angle and the genotypes directed towards these traits were found to be top high yielders, viz., GW 498, HI 1624, GW 491, HI 1625 and HI 1544. Hence, 1000 grain weight, harvest index and reproductive period were very important for high yielding ability of genotypes. So, the breeding efforts to selection among these traits will encourage the yield of the genotypes.

Promising entries
In the present study sufficient variability among the genotypes were observed and it provides ample scope for further improvement. High grain yielding genotypes were GW 491 (3107g), HI 1624 (3101g), HI 1625 (2874g), HI 1544 (2844g) and GW 498 (2836.5g) among 36 genotypes. The genotypes GW 495 (105.5 days), HI 1544 (107 days), NIAW 3173 (108 days), HI 1624 (108 days) and MP 1338 (108 days) were early maturing as compared to mean value 111.13 days. The genotypes HI 1624 (40g), RAJ 4502 (40g), HI 1625 (39.5g), NIAW 3137 (39g) and MP 1337 (38g) were high 1000-grain weight. The genotypes AKAW 4924 (8526g), HI 1625 (8034g), DBW 235 (7788g), MACS 6222 (7782g) and GW 498 (7560g) were high biomass as compared to mean value was 7013.50g. Over all it has been observed that, the genotype HI 1624 was high yielding with high 1000-grain weight and early maturing when compared with the check variety HI 1544. Genotypes HI 1624 will be useful for crossing programme and further crop improvement.

Conclusion
On the basis of mean performance, the high grain yielding genotypes GW 491, HI 1624, HI 1625 and GW 498 was observed and these genotypes could be utilized in further breeding programme. High heritability coupled with high genetic advance was observed for plant height, days to heading, 1000-grain weight, grain yield and harvest index, indicates the presence of additive gene action and selection in early generation for these characters may be effective. Grain yield showed the positive association with biomass, harvest index, days to maturity and these traits were given more emphasis for increasing the grain yield in wheat. Biomass, harvest index, days to heading and days to maturity gave the positive association with grain yield. Correlation of these traits will be useful to breeders in selecting genotypes possessing group of desired traits. Genotypes HI 1624 was found to be early maturing with high yielding, can utilized as parent in crossing programme for crop improvement or directly released as varieties for cultivation.

Acknowledgement

References
1. Al-Jibouri HA, Miller PA, Robinson HF. Genotypic and environmental variances in upland cotton cross of interspecific origin. Agron. J. 1958; 50:633-635.
2. Burton GW, Devane EH. Estimating heritability in table fercue from replicating clonal material. Agron J. 1953; 45:45-481.
3. 3rd Advance Estimates. from the directorate of Economics and Statistics (DES), Ministry of Agriculture and farmers Welfare (MoA & FW), India. 2015-16.
4. Chaturvedi BK, Gupta RR. Selection parameters for some grain and quality attributes in spring wheat. Agricultural Science Digest, 1995; 15:186-190.
5. Dudley JW, Moll RH. Interpretation and uses of estimates of heritability and genetic advance in plant breeding. Crop Sci. 1969; 9:257-262.
6. Falconer DS. Introduction to quantitative genetics. Longman, London and New York. pp.1981; 150-158.
7. Falconer DS and Mackay TFC. Introduction to Quantitative Genetics (4th ed.), Longman, Essex, UK, 1996.
8. Hanson GH, Robinson HF, Comstock RE. Biometrical studies on yield in segregating populations of Korean Lespidiza. Agorn. J. 1956; 48:268-272.
9. Jagshoran. Estimation of variability parameters and path coefficient for certain meteric traits in winter wheat (Triticum aestivum L.). Indian J. Genetics. & Plant Breeding, 1995; 55(4):399-405.
10. Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybean. Agron J. 1955; 47:314-318.
11. Khokhar MI, Hussain M, Zulkiffal M, Sabir W, Mahmood S, Jamil Anwar MW. Studies on genetic variability and inter-relationship among the different traits in wheat (Triticum aestivum L.). Krmiva. 2010; 52(2):77-84.
12. Maqbool R, Sajjad M, Khaliq I, Rehman AU, Khan AS, Khan SH. American-European Journal of Agric. Environ. and Sci. 2010; 8(2):216-224.
13. Mary SS, Gopalan A. Dissection of genetic attributes yield traits of fodder cowpea in F3 and F4. J. Appl. Sci, Res., 2006; 2:805-808.
14. Masood SA, Ahmad S, Kashif M, Ali Q. Correlation analysis for grain and its contributing traits in wheat (Triticum aestivum L.). Nat. Sci. 2014; 12(11):168-176.
15. Robinson HF, Comstock RE, Harvey PH. Genotypic and phenotypic correlations in corn and their implications in selection. Agronomy J., 1949; 43:282-287.
16. Sabhrawal PS and Lodhi GP. Germplasm evaluation for different traits in wheat (Triticum aestivum L.). HAU, J. of Agri. Res. 1995; 25 (4): 207-210.
17. Sajjad M, Khan SH, Khan AS. Exploitation of germplasm for grain yield improvement in spring wheat (Triticum aestivum L). Int. J. Agric. Biol. 2011; 13:695-700.
18. Shankararao BS, Mukherjee J, Pal AK. Estimation of variability for yield parameters in bread wheat (Triticum aestivum L.). J. of Plant Breeding, 2010; 1:764-768.
19. Singh AK, Singh SB, Singh AP and Sharma AK. Genetic variability, character association and path analysis for seed yield and its component characters in wheat (Triticum aestivum L.) under rainfed environment. Indian J. Agric. Res. 2012; 46:48-53.
20. Sivasubramanian S, Menon M. Heterosis and inbreeding depression in rice. Madras Agricultural J. 1973; 60:1139.
21. Statistical Tool. for Agricultural Research (STAR 2.0.1).

IRRI Headquarters, Los Banos, Laguna, Philippines, 2014.

22. Tazeen M, Naqvi FN. Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. J. of Food Agri. and Environ. 2009; 7(3, 4):278-282.

23. Yadav SK, Singh AK, Baghel SS, Jarman M, Singh AK. Assessment of genetic variability and diversity for yield and its contributing traits among CIMMYT based wheat germplasm. J. of Wheat Res. 2014; 6(2):154-159.

24. Yagdi K, Sozen E. Heritability, variance components and correlations of yield and quality traits in durum wheat (Triticum durum Desf.). Pak. J. Bot. 2009; 41(2):753-759.

25. Jobson D. Confidence Regions for the Mean Variance Set: An Alternative Approach to Estimation Risk. Review of Quantitative Finance and Accounting; 1991; 1:235-257.

26. Sharma JR. Statistical and Biometrical Techniques in Plant Breeding. New Age International (P) Limited Publishers, New Delhi, 198, 432.