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Full Length Research Paper

Study of phenotypic variances for quantitative traits among wheat varieties (*Triticum aestivum* L.)

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ABSTRACT

The wheat varieties (*Triticum aestivum* L. var. HUW 234, HUW 468 and HUW 533) were used to study the inheritance pattern of yield and its components. The yield components were studied like Leaf area (LA, cm square), Shoot length (SL, cm), Shoot Biomass (SB, g^{-1}FW and DW), Number of Seeds per inflorescence (SI) and Seed weight (SW, g) per inflorescence. The total phenotypic variance (V_P), covariance, heritability (H^2) and the genotypic components of the wheat varieties were illustrated to locate the strong genes or alleles for the parameters studied. The Hardy-Weinberg equilibrium was used to predict the gene frequencies percent for Dominant and Recessive alleles. The results obtained suggested that the wheat variety (HUW 533) has strong genes or alleles for the parameters studied as compared to the other two. Therefore, the HUW 533 might be used in limited type of environment for the good yield of its components like LA, SL, SB (FW/DW), Number of seeds per inflorescence and Seed Weight per inflorescence.

Key words: *Triticum aestivum L., Heritability, alleles, total phenotypic variance, gene frequency*

INTRODUCTION

Wheat (*Triticum aestivum* L.) represents an important source of food and energy. The life cycle of wheat is of short duration but the crop has multipurpose utility owing to its richness in carbohydrates, proteins, starch and vitamins which makes it most important cereal crop of the world. It is the main staple food of the rapidly increasing population of Asian countries, especially India that is why it occupies a prominent position in the cropping pattern of the country. Therefore, it is the basic aim of all wheat breeding programmes to improve wheat yield. The basic information on the genetic control of yield and yield components is very much helpful in designing a breeding programme (Aghee et al. 2010, Ahmad et al. 2011).
Grain yield is a complex trait made up of the interaction between different yield components of the crop plant and its environmental effects (Ahmad et al. 2007). Van de Wouw et al. (2010) reported that additive gene action was involved in plant height, grain yield and other yield components. Ojaghi et al. (2010) reported partial dominance with additive gene action for most of the yield components in wheat.

The variation of characters in a plant might be genetic or environmental but the variation should be heritable because the efficiency of plant selection mainly depends on additive genetic variance, influence of the environment and interaction between genotype and environment (Akhtar & Chowdry 2006, Awan et al. 2005).

The present studies were carried out to have information on inheritance of yield and its components in wheat varieties (*Triticum aestivum* L, var. HUW 234, HUW 468 and HUW 533). The varieties were double dwarf gene variety and developed at Institute of Agricultural Sciences, Banaras Hindu University, Varanasi by Pedigree method. The variety HUW234 is developed from pedigree method by cross involving HUW 12 × Sparrow first then their F1 backcrossed with HUW 12. The variety HUW 468 of wheat is developed from the pedigree method by cross involving CPAN 1962 × TON 1 producing F1 progeny LIRA 'S'. This LIRA 'S' is crossed with PRL 'S' producing the variety. The HUW 533 variety of wheat is developed from pedigree method by cross involving Unnath-c-306 × HUW 81 first then their F1 crossed with K8027 producing the variety. The yield components were studied like Leaf area (cm square), Shoot length (cm), Shoot Biomass (g^{-1}FW and DW), Number of Seeds per inflorescence and Seed weight (g) per inflorescence. The total phenotypic variance (V_P), covariance, heritability (H^2) and the genotypic components of the wheat varieties were illustrated to locate the strong genes or alleles for the parameters studied. The Hardy-Weinberg equilibrium was used to predict gene frequencies percent for Dominant and Recessive alleles. The information so derived (available genetic variability and quantitative traits) could be of great value for wheat breeding programmes.

MATERIALS AND METHOD

The seeds of *Triticum aestivum* L. varieties HUW 234, HUW 468 and HUW 533 were collected from the Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University (BHU), Varanasi, India. The wheat varieties were grown in randomly designed plots at the field laboratory of Department of Botany, BHU Varanasi. The experiment was set up in the 1st week of October and the data were collected at the end of March during the harvesting time or at the maturation of the plants every year. The average data of yield and quality contributing parameters of 10 random

plants were recorded. The parameters were taken as leaf area (LA, cm square), shoot length (SL, cm), shoot biomass (SB, g/FW and DW), number of seeds per inflorescence (SI) and seed weight (SW, g) per inflorescence. The experimental design was completely randomized and all the experiments were repeated thrice. Statistical analyses (SPSS ver. 16 and Curve expert 140) and manual calculations were done to compute each parameter.
The formulae used in calculations were:

Total Phenotypic Variance (V_P) were calculated by $\sigma^2=\Sigma (x-\bar{x})^2/N$

Total Genetic Variance (V_G)= $\frac{(\text{Mean of each parameter} - \text{Mean of all parameters studied})2+\cdots\ldots}{\text{Total Parameters}}$

Total Environment Variance (V_E)= $\frac{\text{Variance of Each Parameter}}{\text{Total Parameters}}$

Broad Sense Heritability (H^2)= $\frac{VG}{VP}$

Chi square test (χ^2)= $\frac{(O-E)2}{E}$

Covariance (COV) = $\frac{\text{Standard Deviation of all parameters studied}}{\text{Total Mean of all parameters studied}} \times 100$

Correlation and Regression lines were computed with the help of curve expert ver 140

Hardy-Weinberg equilibrium (Hardy 1908, Weinberg 1908):

$p+q=1$

$(p+q)^2=p^2+2pq+q^2=1$

Allele frequency of DD or dd= frequency of homozygotes+1/2×frequency of heterozygotes

{For H-W equilibrium, 180 plants (10 plants for each parameter×6 Total parameters studied×3 Hybrid wheat varieties) were used for dominant (D) and recessive (d) allele frequency determination and prediction with base population of 1000}.

RESULT AND DISCUSSION

The three wheat varieties (*Triticum aestivum* L. var HUW 234, HUW 468 and HUW 533) were studied for their quantitative traits inheritance for Leaf Area (cm square), Shoot length (cm), Shoot Biomass (g-1FW/DW), Number of seeds per inflorescence and Seed weight (g) per inflorescence. The quantitative traits of inheritance and its mean, variance and standard error was presented in Table I.

Table 1. Means, Standard Errors and Variance of wheat varieties for quantitative traits

	Parameters											
	LA		SL		FW		DW		SI		SW	
Triticum aestivum L. var.	Mean ± S.E.	Variance	Mean ± S.E.	Variance	Mean ± S.E.	Variance	Mean ± S.E.	Variance	Mean ± S.E.	Variance	Mean ± S.E.	Variance
HUW234	37.55± o.800	6.402	71.94± 0.859	7.380	6.07± 0.877	7.698	3.95± 0.809	6.554	44.82± 0.922	8.515	2.35±0.122	0.150
HUW468	33.38± 0.888	7.894	69.47± 0.818	6.692	8.89± 0.733	5.378	5.76± 0.589	3.477	41.89± 0.603	3.642	1.99±0.184	0.340
HUW533	43.42± 0.916	8.408	73.35± 0.678	4.598	11.61 ±0.731	5.353	7.56± 0.231	0.537	45.76± 0.776	6.025	2.58±0.123	0.154

The *Triticum aestivum* L. var. HUW 533 has the maximum variance in leaf area as compared to other two varieties (Chandra et al. 2010). It might be suggested that parent plant of HUW 533 (Unnath-c-306, HUW 81 and K8027) had such kind of character and passed to the progeny. On the other hand shoot length, Shoot Biomass (g-1FW/DW), Number of seeds per inflorescence has maximum variance in *Triticum aestivum* L. var. HUW 234. The parents of HUW 234 includes HUW 12 and Sparrow variety of wheat and the traits were dominating in HUW12, therefore, when backcrossed F1 with HUW 12 the traits were appeared in HUW 234.

The comparison of variance and covariance among wheat varieties indicated that the parents of varieties were not related or close to each other and distinct (Dere & Yildirim 2006). The parents had their own traits influenced by environment or genetic and these characters passed to the progeny.

The covariance among varieties indicated that HUW 533 was very near to the origin (zero) of the x-y axis graph and could be suggested as strong dominancy of the characters in this variety followed by HUW 468 and HUW234 (Figure 1a-b).

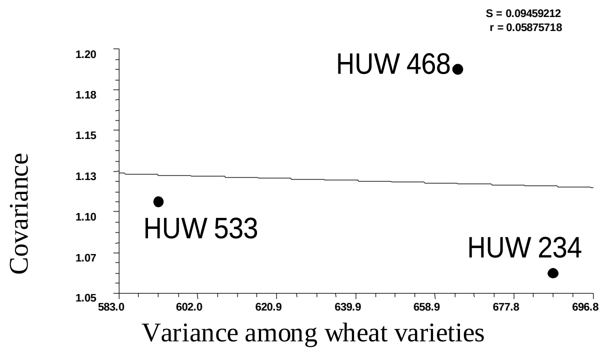

Figure 1a. Comparison of Variance and Covariance among wheat varieties

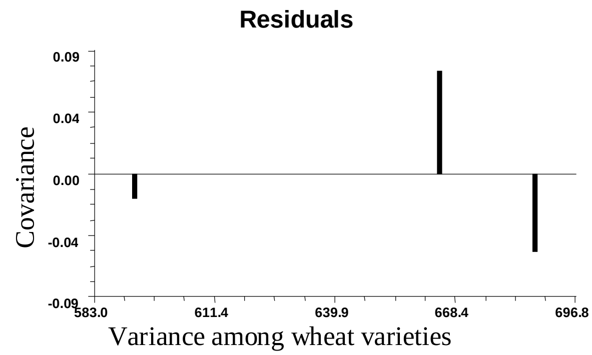

Figure 1b. Residual bar graph of variance and covariance for parameters

The variance comparison for shoot length and leaf area among varieties showed negative correlation (r=0.848) with the regression line (y=1.136-6.099x). The variance is inversely proportional to the shoot length and leaf area means the maximum variation in LA had affect the shoot length variation and vice-versa (Figure 2a-b).

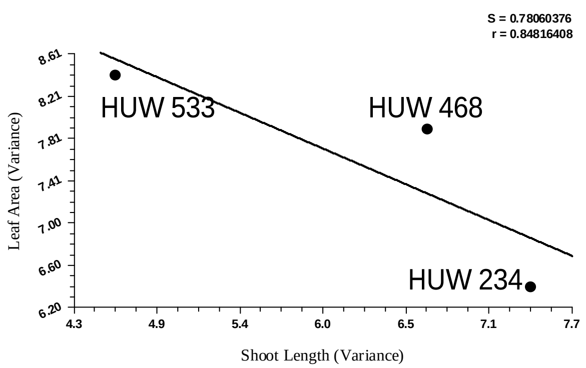

Figure 2a Variance comparison for shoot length and leaf area among the varieties

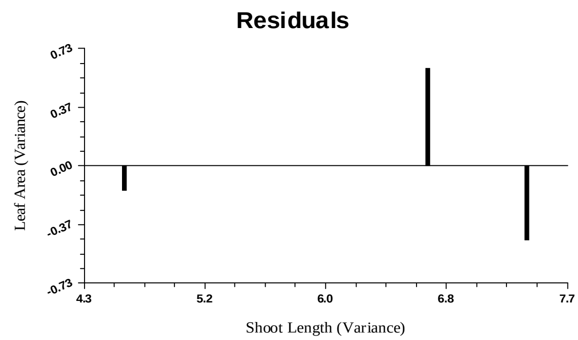

Figure 2b. Residual bar graph for the shoot length and leaf area variance

The variance comparison of shoot length with shoot biomass showed partially positive correlation (r=0.697) as the regression line (y=2.105+6.487x) does not pass through the origin (zero) of the x-y axis graph and suggested that there must be some biomass for the shoot length growth and variation. It might be suggested as the effect of environmental factors on the shoot length and shoot biomass, therefore, the plant must be acquainted with good quality nutrition, edaphic factors, light, space, fertilization and other factors for growth and development (Figure 3a-b).

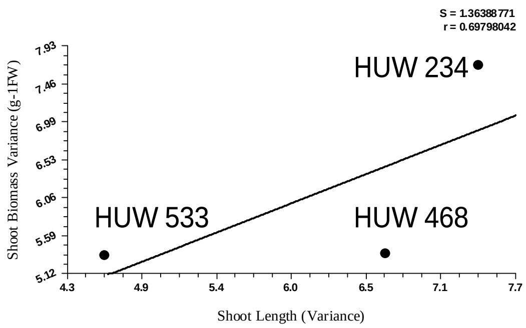

Figure 3a Variance comparison for shoot length and shoot biomass

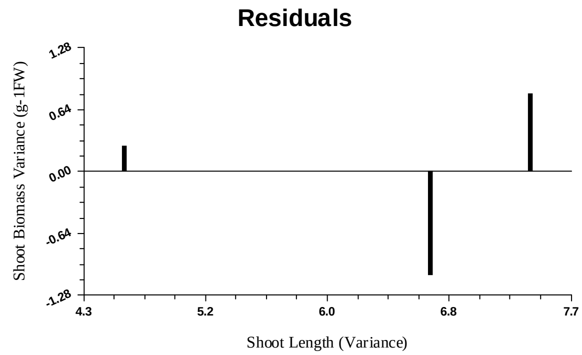

Figure 3b Residual bar graph for shoot length and shoot biomass variance

The variance comparison for shoot length and number of seeds per inflorescence showed the positive correlation (r=0.913) among the wheat varieties with regression line (y=8.788+9.409x). This could be suggested as the healthy competition among the varieties with environmental factors and showed directly proportional to the shoot length and number of seeds per inflorescence (Figure 4a-b).

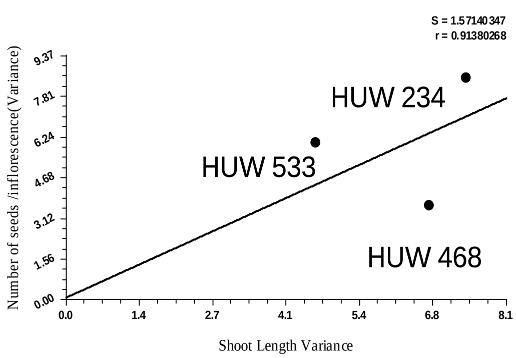

Figure 4a. Variance comparison for shoot length and number of seeds per inflorescence

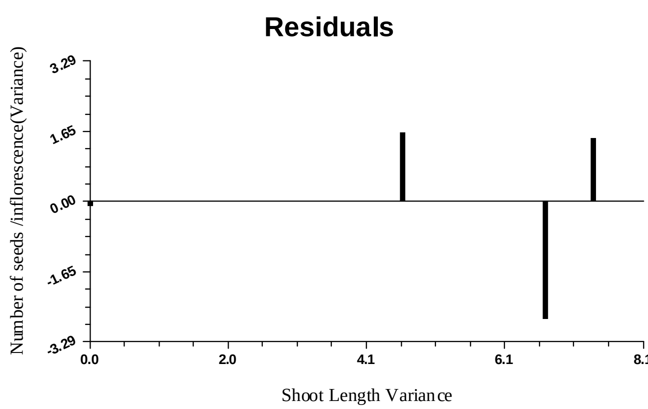

Figure 4b. Residual bar graph for shoot length and number of seeds per inflorescence

The comparison of variance for number of seeds per inflorescence and seed weight per inflorescence showed negative correlation (r=0.868) with the regression line y=1.0247-1.9502x (Figure 5a-b).

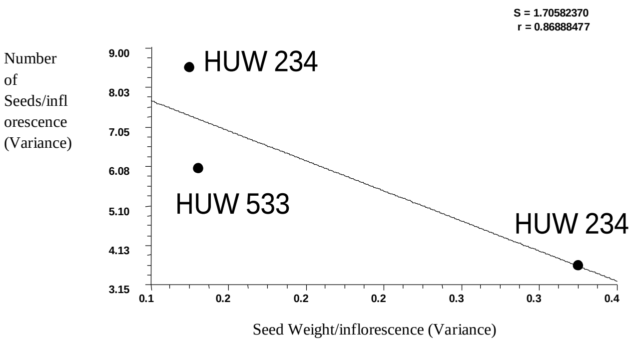

Figure 5a. Variance comparison for seed weight and number of seeds per inflorescence

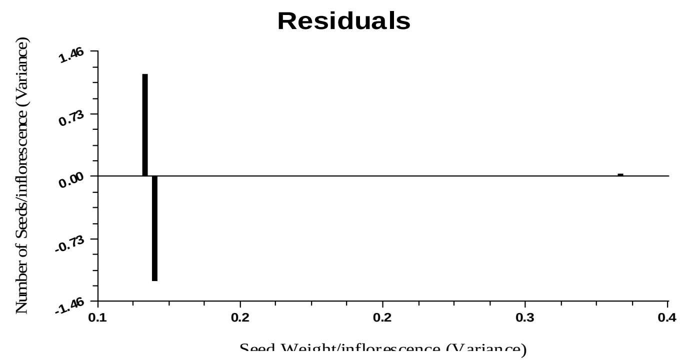

Figure 5b. Residual bar graph for seed weight and number of seeds per inflorescence

This might be suggested as the genetic variance among the reproductive organs and affected by the environmental factors, edaphic factors and time of sowing factors (Gupta et al. 2001, Kuchel et al. 2007, Maccaferi et al. 2008).

The total phenotypic variances (V_P) were estimated along with genetic (V_G) and environmental (V_E) variances in the three varieties (Table II).

Table 2. Estimates of Variance components and heritability in wheat varieties for quantitative traits.

Variance components of the parameters in wheat varieties						
Triticum aestivum L. var.	V_G	V_E	V_G+V_E	V_P	H^2	χ^2
HUW234	692.00	6.11	698.12	698.10	1.007	0.088*
HUW468	578.44	4.57	583.01	583.00	0.976	0.074*
HUW533	649.70	4.17	653.87	653.88	0.977	0.086*

Significant at 95%PL

The V_P was high in HUW 234. It could be suggested as the high impact of the environmental factors on the phenotype and less activity of the dominant alleles in the variety. HUW 468 showed less phenotypic variance and in HUW 533 observed intermediate phenotypic variance (Mohammadi et al. 2010, Sahu et al. 2005).

One hundred eighty individual plants were used to establish the dominancy of the alleles and gene frequencies among the wheat varieties and observed that 67% individuals were with homozygous dominant (DD), 3% with homozygous recessive (dd) and approximately 30% with heterozygous (Dd) alleles (Table III-IV).

Table 3. Types of random combinations among parents for wheat varieties.

Random Combinations	DD (0.6724)	Dd (0.2952)	dd (0.0324)
DD (0.6724)	DDDD (0.45212176)	DDDd (0.19849248)	DDdd (0.02178576)
Dd (0.2952)	DDDd (0.19849248)	DdDd (0.08714304)	Dddd (0.00956448)
dd (0.0324)	DDdd (0.02178576)	ddDd (0.00956448)	Dddd (0.00104976)

Table 4. Relative frequencies and ratios for dominant and recessive alleles among wheat varieties.

Parents		Dominant and Recessive alleles ratio and frequencies		
Types of combinations	Frequency of combinations	DD	Dd	dd
DD×DD	0.45212176	0.45212176		
DD×Dd	0.39698496	0.19849248	0.19849248	
DD×dd	0.04357152		0.04357152	
Dd×Dd	0.08714304	0.02178576	0.04357152	0.02178576
Dd×dd	0.01912896		0.00956448	0.00956448
dd×dd	0.00104976			0.00104976
		0.67240000	0.29520000	0.03240000

The percent of dominant and recessive alleles could be related to their parent plant from which the varieties were derived.

CONCLUSION

The varieties were shown the mixed response in respect to variance and covariance. The heritability of traits were totally influenced by environment in HUW 234 (H^2=1.007). The comparison of variance and covariance suggested that the variety (HUW 533) has strong genes or alleles for the parameters studied as compared to the other two varieties. Therefore, the variety could be suggested for a limited type of environment for the good yield of its components like LA, SL, SB (FW/DW), Number of seeds per inflorescence and Seed Weight per inflorescence.

REFERENCES

Aghee, M., Mohammadi, R., Nabovati. (2010) Agromorphological characterization of durum wheat accessions using pattern analysis. Aust. J. Crop Sci. 4: 505-514

Ahmad, F., Khan, S., Ahmad, S. Q., Khan, H., Khan, A., Muhammad, F. (2011) Genetic analysis of some quantitative traits in bread wheat across environments. Af. J. Agric. Res. 6(3): 686-692

Ahmad, F., Mohammad, F., Bashir, M., Saifullah, Khan, H. (2007) Inheritance of important traits in bread wheat over different planting dates using Diallel analysis. Sarhad J. Agric. 23(4): 954-964

Van de Wouw, M., Van Hintum, T., Kik, C., Van Treuren, R., Visser, B. (2010) Genetic diversity trends in Twentieth century crop cultivars: a meta analysis. Theor. Appl. Genet. 120: 1241-1252

Ojaghi, J. and Akhundova, E. (2010) Genetic effects for grain yield and its related traits in Doubled Haploid Lines of wheat. Int. J. Agric. Biol. 12(1): 86-90

Akhtar, N. and Chowdry, M. A. (2006) Genetic analysis of yield and some other quantitative traits in bread wheat. Int. J. Agric. Biol. 8: 523-527

Awan, S. I., Malik, M. F. A., Siddique, M. (2005) Combining ability analysis in inherital crosses for component traits in hexaploid wheat. J. Agric. Soc. Sci. 4: 316-317

Hardy, G. H. (1908) Mendelian proportions in a mixed population. Science 28 (706): 49–50

Weinberg, W. (1908) Über den Nachweis der Vererbung beim Menschen. Jahreshefte des Vereins für vaterländische Naturkunde in Württemberg 64: 368–382

Chandra, D., Sharma, R., Rani, S., Singh, D. K., Sharma, R., et al. (2010) Genetic variability for Quantitative traits in wheat [*Triticum aestivum* (L.) Em. Thell.]. Plant Archives 10(2): 871-874

Dere, S. and Yildirim, M. B. (2006) Inheritance of grain yield per plant, flag leaf width and length in an 8x8 diallel cross population of bread wheat (*Triticum aestivum* L.). Turkish J. Agric. For. 30: 339-345

Gupta, P. K., Balyan, H. S., Kulwal, P. L., Kumar, N., Kumar, A., Reyazul, M. A., Amita, M., Kumar, J. (2001) QTL analysis for some quantitative traits in bread wheat. J. Zhejiang Univ. Sci. B. 8: 807-814

Kuchel, H., Williams, K. J., Langridge, P., Eagles, H. A., Jefferies, S. P. (2007) Genetic dissection of grain yield in bread wheat. I. QTL analysis. Theor. Appl. Genetic 115: 1029-1041

Maccaferi, M., Sanguineti, M. C., Corneti, S., Ortega, J. L.A., Salem, M. B, Bort, J., DeAmbrogio, E., del Moral, L. F. G., Demontis, A., El-Ahmad, A., Maalouf, F., Machlab, H., Martos, V., Moragues, M., Motawaj, J., Nachit, M., Nserallah, N., Ouabbou, H., Royo, C., Slama, A., Tuberosa, R. (2008) Quantitative trait loci for grain yield and adaptation of durum wheat (*Triticum aestivum* Desf.) across a wide range of water availability. Genetics 178: 489-511

Mohammadi, A. A., Saeidi, G., Arzami, A. (2010) Genetic analysis of some agronomic traits in flax (*Linum usitatissimum* L.). Aust. J. Crop Sci. 4: 343-352

Sahu, Dhari, S. R., Joshi, A. K. (2005) Variability studies in wheat (*Triticum aestivum* L.) under late sown conditions. Indian J. Genet. 65(54): 309-310