Original Research Article

Estimation of Heritability and Genetic Advance in wheat (*Triticum aestivum*.L.)

ABSTRACT

An experiment was conducted to estimate the genetic variability, heritability and genetic advance in the 100 wheat genotypes including ten parents and 45 F_1 and 45 F_2 for obtained through half diallel mating design in pea during 2021-22 at Oil Seed Farm, Kalyanpur, C.S. Azad University of Agriculture and Technology, Kanpur-208002 (U.P.) Quantitative analysis were carried out for all the parameters which are directly or indirectly associated with the yield and yield contributing traits. Analysis of variance showed significant variability for all the studied characters for parents. In F1 significant variability was observed in all the traits except spike length, number of grains per spike and protein content reflecting considerable amount of heterotic response in these attributes. High heritability was observed in all the characters in F_1 and F_2 in both the generations. Highest value of GCV and PCV were observed for grain yield per plant (20.01) in F_2 indicating the presence of high genetic variation. High heritability coupled with high genetic advance for protein content and yield per plant which indicate the presence of additive gene action and used for future population improvement. The genotypes with specific characters could be utilized for hybridization programme.

Key words: Wheat, Heritability, Genetic advance, GCV and PCV

INTRODUCTION

Wheat (Triticum aestivum L., 2n=42) belongs to the family Poaceae (Gramineae) and tribe Triticeae containing more than 15 genera and 300 species including wheat and barley. T. aestivum is a segmental allohexaploid (2n = 6x = 42, AABBDD) originated in the Fertile Crescent area of South-Western Asia (Lupton 1987), its geographical centre of origin and spread globally for cultivation and consumption. Allohexaploid wheat possesses three genomes and A, B, and D are three genomes. The genome "A" comes from wild einkorn wheat (Triticum monococcum var. urartu), "B" comes from an unknown species, and genome "D" comes from a weedy grass Squarrosa Aegilops.

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Hexaploid wheat (Triticum aestivum L., 2n = 42) has a haploid DNA content of around 1.7 x 1010 bp, which is almost 40 times that of rice. **(Bennett and Smith, 1976; Amuruganathan and Earle, 1991.** The world's most important centres of wheat and associated species variety are in Central Asia, the Near East, the Mediterranean, and Ethiopia. The Hindukush region is the epicentre of hexaploid wheat variability **(Kundu and Nagarajan, 1996).** Wheat is grown on around 221.24 million hectares worldwide, with a record yield of 771.64 million tonnes of grain and productivity is 3.49 metric tons per hectare **(USDA 2023).** India has the most wheat-growing land (14 percent), followed by Russia (12.43 percent), China (11.14 percent), and the United States (6.90 percent), accounting for around 45 percent of the global total. China, on the other hand, is the world's largest wheat producer, with 136 million tonnes produced, followed by India (98.51 million tonnes), Russia (85 million tonnes), and the United States (47.35mt). Global wheat production in 2022 is predicted to decline from the 2021 record level by 0.8 per cent, reaching 771.64 million tonnes and marking the first drop in four years. Year-on-year falls in production in Australia, India, Morocco and Ukraine will likely outweigh expected increases in Canada, Iran and Russia Further; it said that in Asia, wheat production in India is forecast at 105.5 million tonnes, down nearly 4 per cent from the record crop gathered in 2021. **(Business Standard 2022-23).**

Wheat production in 2022-23 is expected to be between 98 million and 106 million tonnes, down from 107.9 million tonnes in 2020-21 **(USDA report, 2022).** Wheat demand is anticipated to rise by 50% by 2050 compared to current levels. Meanwhile, new and more aggressive pests and viruses, dwindling water resources, limited accessible land, and unpredictable weather are all threatening the crop (heat in particular). For Africa, Asia, and Latin America, the CIMMYT's Global Wheat Program is one of the most significant public sources of high-yielding, nutritious, disease-resistant, and climate-resilient wheat varieties **(Wheat Research, CIMMYT).**

The success of our wheat varieties is up to a considerable extent due to incorporation of the Norin 10 genes *i.e.* Rht_1 and Rht_2 in wheat. These dwarfing genes changed the wheat plants type and it becomes more responsive to higher application of fertilizer and better crop management under practices. **In 1966, Dr. N.E. Borlaug**, a noble laureate introduced the Mexican dwarf wheat genotypes and provides the way for green revolution in India.

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In most of the biometrical approaches for genetic evaluation of the crop , the diallel cross analysis become a proved and important system to provide maximum information on genetic parameters related to breeding programme of some important metric traits within considerable short time .To judge the stability performance over a wide range of environments, diallel cross analysis simultaneously evaluates the potentialities of the variance and predict the desirable types for further breeding programme. Various models of genetic analysis of diallel crosses have been given by **Jinks and Hayman 1953;Hayman 1954 a; 1954 b, Griffing, 1956 b; Gardner and Eberhart, 1966** and found suitable under limit facilities for achieving maximum genetic information . The objective of the study was to estimate the genetic variability, heritability and genetic advance in wheat genotypes including parents and F_1 and F_2 through half diallel mating design.

MATERIALS AND METHODS

The present investigation was conducted at Oil Seed Farm, Kalyanpur, C.S. Azad University of Agriculture and Technology, Kanpur-208002 (U.P.) during *Rabi*, 2021-22. The treatments comprised of forty five F_1s developed by crossing 10 lines *viz.*, DBW187, K1601, HD2967, HD3249, DBW321, K1317 K0307, HI 1563, DBW107 and HD3059 following half diallel mating design. A total of 100 treatments with 10 parents (45 F_1s and 45 F_2s) were evaluated for the study of twelve quantitative characters in wheat.

DIALLEL ANALYSIS:

Testing the validity of the hypothesis:

To test the validity of the hypothesis, i.e., the assumptions regarding diallel analysis as proposed by **Hayman (1954**), such as (i) diploid segregation (ii) no maternal effect, (iii) no linkage (iv) no multiple allelism, (v) independent action of non-allelic genes and (vi) hemozygosity of parents, the t^2 test was applied as suggested by **Hayman (1954a**):

$$t^2 = (n-2)/4\ [(Var\ Vr - Var\ Wr)^2 / Var\ Vr \times Var\ Wr) - Cov^2\ (Vr, Wr)]$$

which is an F test with 4 and (n-2) degree of freedom.

A significant value of t^2 would indicate the non-uniformity of Wr, Vr and thus, invalidates the hypothesis postulated. The failure of hypothesis is also indicated by non-significant regression coefficient.

$$b = \frac{\text{Cov (Wr,Vr)}}{\text{Var (Vr)}}$$

Where,

$$\text{Cov. (Wr, Vr)} = \left[\sum VrWr - \frac{\sum Vr \sum Wr}{n}\right] / (n-1) \text{ and}$$

$$\text{Var (Vr)} = \left[\sum Vr^2 - \frac{(\sum Vr)2}{n}\right] / (n-1)$$

The standard error of regression coefficient (b) was calculated as:

$$SE(b) = [(\text{Var Wr} - b \text{ Cov. Wr} - Vr) / \text{Var Vr} (n-2)]^{0.5}$$

Where,

N = number of parents

Now the significance of differences 'b' from zero and unity was tested by using 't' value of (b-0)/SE (b) and (1-b)/SE (b) with (n-2) degree of freedom.

Variance component analysis:

The components of variance in diallel cross were computed in F_1 by the use of equation given by **Hayman (1954a).**

Expectation for F_1 diallel crosses is as follows:

$$Vp = \hat{D} + \hat{E}$$

$$Vr = (1/4)\hat{D} + (1/4)\hat{H}_1 - (1/4)\hat{F} + [(n+1)/2n]\hat{E}$$

$$Wr = (1/2)\hat{D} - (1/4)\hat{F} + (1/n)\hat{E}$$

$$Vm = (1/4)\hat{D} + (1/4)\hat{H}_1 - (1/4)\hat{H}_2 - (1/4)\hat{F} + (1/2\,n)\hat{E}$$

Jinks (1956) and Hayman (1958) gave expectations for F_2 diallel crosses. The expected statistics for F_2 generation are the same of that of F_1 except the contribution of h which is halved by one generation of inbreeding. Hence, the coefficient of H_1 and H_2 are (1/4) of those F_1 statistics while the coefficient of F is halved being second and first degree statistics h^2, respectively (**Jinks, 1956; Hayman 1958; Mather and Jinks, 1971.**

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Heritability

Heritability (in narrow sense) in F_1 generation was calculated by the formula proposed by **Crumpacker and Allard, (1962)**, which is as follows:

$$\text{Heritability} \quad (\hat{h}^2) = (1/4)\hat{D} / [(1/4)\hat{D} + (1/4)\hat{H}_1 - (1/4)\hat{F} + \hat{E}]$$

Heritability in F_2 generation was calculated according to the methodology proposed by **Verhalen and Murray (1969)**.

$$(\hat{h}^2) = (1/4)\hat{D} / [(1/4)\hat{D} + (1/16)\hat{H}_1 - (1/8)\hat{F} + \hat{E}]$$

or

1/2D/VP

Where,

$\hat{h}^2$ = Estimates of heritability coefficient and $\hat{D}$, $\hat{H}_1$, $\hat{F}$ and $\hat{E}$ are the same as explained earlier.

D = additive genetic variance

VP = phenotypic variance

The estimates of heritability and genetic advance were arbitrarily categorized in three classes by **Robinson in 1966** as:

(i) High- above 30%

(ii) Moderate- below (30-10)%

(iii) Low below- 10%

Heritability (%) = Heritability coefficient X 100

Genetic Advance:

The genetic advance was calculated by the formula given by **Robinson *et al.* (1949)** as:

Genetic advance (GA) = (k)x($\hat{h}^2$)x(σph), and

Genetic advance over mean of the character

$$[GA(\%)] = \frac{GA}{\bar{x}} \times 100$$

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Where

GA	=	Estimate of genetic advance
K	=	Selection differential at 5% selection intensity, i.e. 2.06
σph	=	Phenotypic standard deviation
$\hat{h}^2$	=	Heritability coefficient in narrow sense
$\overline{X}$	=	Mean of the character concerned

Genotypic and Environmental variances:

Computed from the respective mean squares following the procedures suggested by Singh and Chaundhary (1979) and Allard (1960), thus

Genotypic variance

$$\sigma^2_g = \frac{MSg - MSgI}{rl}$$

Genotypic by environment interaction variance

$$\sigma^2_{gl} = \frac{MSgl - MSe}{rl}$$

Phenotypic variance

$$\sigma^2_p = \sigma^2_g + (\frac{\sigma 2e}{rl}) + (\frac{\sigma 2gi}{l})$$

where,

MS_g = mean square of genotype;

MS_{gl} = meansquare due to genotype by environment interaction;

MS_e = error mean square (mean square of environment);

l = number of locations;

r = number of replications.

Genotypic (GCV), Phenotypic (PCV) and Environment (ECV) coefficients of variation (%) estimated according to the procedure outlined by Johnson *et.al.,* (1955).

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RESULTS AND DISCUSSIONS

HERITABILITY AND GENETIC ADVANCE:

The understanding of genetic variability present in a given crop species for the traits under improvement was imperative for the success of any plant breeding program **(Sankar *et al,* 2006).** The parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV) are useful in detecting the amount of variability present in a given characteristic. The efficiency with which genotypic variability can be exploited by selection depends upon heritability and the genetic advance (GA) of individual trait **(Bilgin *et al,* 2010).** Genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an efficient breeding program **(Akinwale *et al,* 2011).** Heritability provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations (**Bello *et al,* 2012**).

HERITABILITY:

Accordingly, the high magnitude of heritability (over 30%) were observed for the characters, days to 75% flowering (84.53), plant height (93.05), number of tillers per plant (94.35), number of spikelets per spike (91.48), spike length (87.27), number of grain per spike (95.14), days to maturity (80.42), 1000 grain weight (97.20), ear density (68.54), duration of reproductive phase (75.32), protein content (98.70), and grain yield per plant (99.14) in F_1 generation. In F_2 generation high heritability (over 30%) were observed for the characters, days to 75% flowering (77.32), plant height (90.87), number of tillers per plant (92.87), number of spikelets per spike (89.37), spike length (86.23), number of grain per spike (94.45), days to maturity (47.44), 1000 grain weight (96.94), ear density (58.60), duration of reproductive phase (53.26), protein content (98.35), and grain yield per plant (99.08) (Figure 1).

GENETIC ADVANCE:

In order to ascertain relative merit of different attributes, genetic advance in percent of the mean was worked out for all the twelve characters in both generations. Estimates of genetic advance in per cent over mean ranged from 5.24 for days to maturity to 40.51 for grain yield per plant in F_1 generation. High genetic advance was observed for number of tillers per plant (25.64), grain yield per plant (40.51) duration of reproductive phase (22.50) in F_1 generation. In F_2 generation, range of genetic gain was recorded 3.61 for days to maturity to 41.04 for grain yield per plant. High genetic advance was observed for number of tillers per plant (26.25), grain yield per plant (41.04) and protein content (20.01) in F_2 generation (Figure 1).

High genetic advance was observed for number of tillers per plant (25.64), grain yield per plant (40.51) duration of reproductive phase (22.50) in F1 generation. High genetic advance was observed for number of tillers per plant (26.25), grain yield per plant (41.04) and protein content (20.01) in F2 generation. It indicated that manifestation of these traits was primarily governed by additive genetic effects which were fixable, and the desired selection gain could be achieved in early generations. Moderate genetic advance was reported by Kumar *et al.* (1991) and Yadav and Singh (2002), for number of grains per spike and biological yield; Singh *et al.* (1991), Alpay Balkan (2018), Rathwa *et al.* (2018) for biological yield and number of productive tillers per plant.

GENOTYPIC, PHENOTYPIC AND ENVIRONMENT COEFFICIENT OF VARIANCE (%)

Genotypic variation was the heritable portion of phenotypic or total variation. It gives the variation between genotype. Environmental variation was the non-heritable portion of observable variation, suggested by **Subramanian & Menon (1973),** GCV, PCV & ECV arbitrarily categorized into three classes - Low = <10 %, Moderate = 10-20% High= > 20 %. The estimates of GCV, PCV & ECV revealed that the values of PCV % were higher than the GCV % and ECV% for all characters in both generation F_1 and F_2.

GENOTYPIC COEFFICIENT OF VARIATION (GCV %)

Highest value of GCV was observed only in F_2 generation for grain yield per plant (20.01). Moderate value of GCV (%) were observed in both F_1 and F_2 generation for), number of tillers per plant (F_1-12.81, F_2-13.22) and duration of reproductive phase (F_1-12.58, F_2-11.78) while low GCV were observed in both generation for days to 75% flowering (F_1-3.97, F_2-4.35), plant height (F_1-5.91, F_2-6.14) number of spikelets per spike (F_1-5.48, F_2-5.60), spike length (F_1-6.88, F_2-7.13), number of grain per spike (F_1-8.85, F_2-9.01), days to maturity (F_1-2.84, F_2-2.54), grain weight (F_1-7.51, F_2-7.81), ear density (F_1-4.15, F_2-4.07), protein content (F_1-9.60, F_2-9.79), and grain yield per plant (F_1-19.75) (Figure 2).

PHENOTYPIC COEFFICIENT OF VARIATION (PCV %)

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Highest value of GCV was observed only in F_2 generation for grain yield per plant (20.10). Moderate value of GCV (%) were observed in both F_1 and F_2 generation for), number of tillers per plant (F_1-13.19, F_2-13.72) and duration of reproductive phase (F_1-14.50, F_2-16.15) while low GCV were observed in both generation for days to 75% flowering (F_1-4.31, F_2-4.94), plant height (F_1-6.13, F_2-6.45) number of spikelets per spike (F_1-5.73, F_2-5.92), spike length (F_1-7.37, F_2-7.68), number of grain per spike (F_1-9.08, F_2-9.27), days to maturity (F_1-3.16, F_2-3.69), grain weight (F_1-7.61, F_2-7.94), ear density (F_1-5.02, F_2-5.32), protein content (F_1-9.66, F_2-9.87), and grain yield per plant (F_1-19.83).

ENVIRONMENTAL COEFFICIENT OF VARIATION (ECV %)

The estimates of ECV (%) were observed low to very low in both F_1 and F_2 generation for all twelve characters, namely days to 75% flowering (F_1-1.79, F_2-2.11), plant height (F_1-1.40, F_2-1.44), number of tillers per plant (F_1-2.43, F_2-1.88), number of spikelets per spike (F_1-6.38, F_2-6.96), spike length (F_1-5.39, F_2-5.75), number of grain per spike (F_1-4.73, F_2-6.02), days to maturity (F_1-3.15, F_2-2.71), 1000 grain weight (F_1-2.62, F_2-2.70), ear density (F_1-1.82, F_2-1.56), duration of reproductive phase (F_1-1.56, F_2-1.23), protein content (F_1-2.21, F_2-1.36), and grain yield per plant(F_1-1.09, F_2-0.57) (Figure 2).

CONCLUSION AND RECOMMENDATIONS

High heritability coupled with high genetic advance for protein content and yield per plant which indicate the presence of additive gene action and used for future population improvement these traits could be considered as reliable indices for selection and higher responses of this trait could be expected from selection. The genotypes with specific characters could be utilized for hybridization programme.

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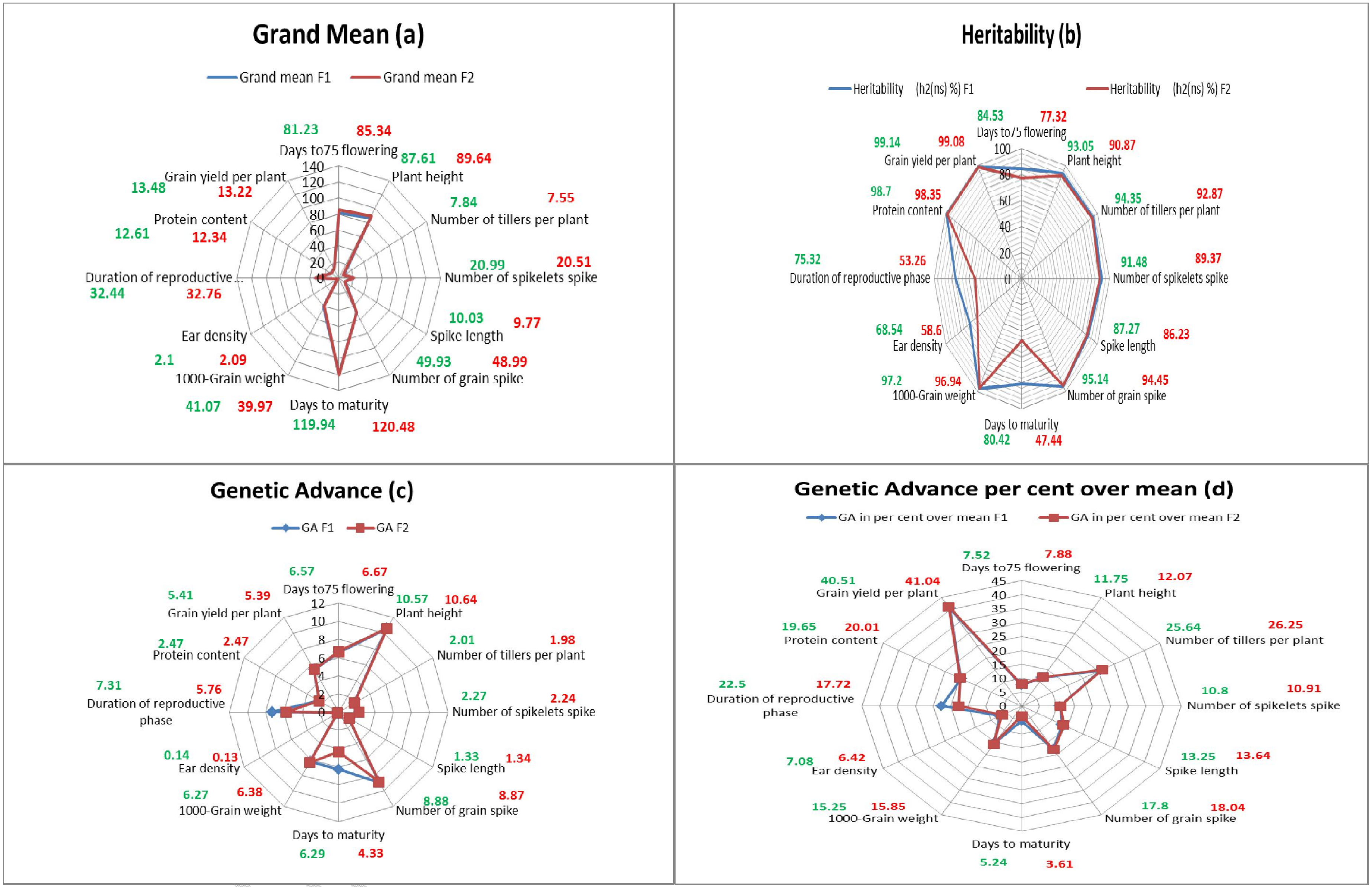

Figure 1: Estimates of grand mean (a), heritability (b), genetic advance(c) and genetic advance in per cent of mean (d) for 12 characters in a 10 parent diallel cress of F_1 and F_2 generation in wheat.

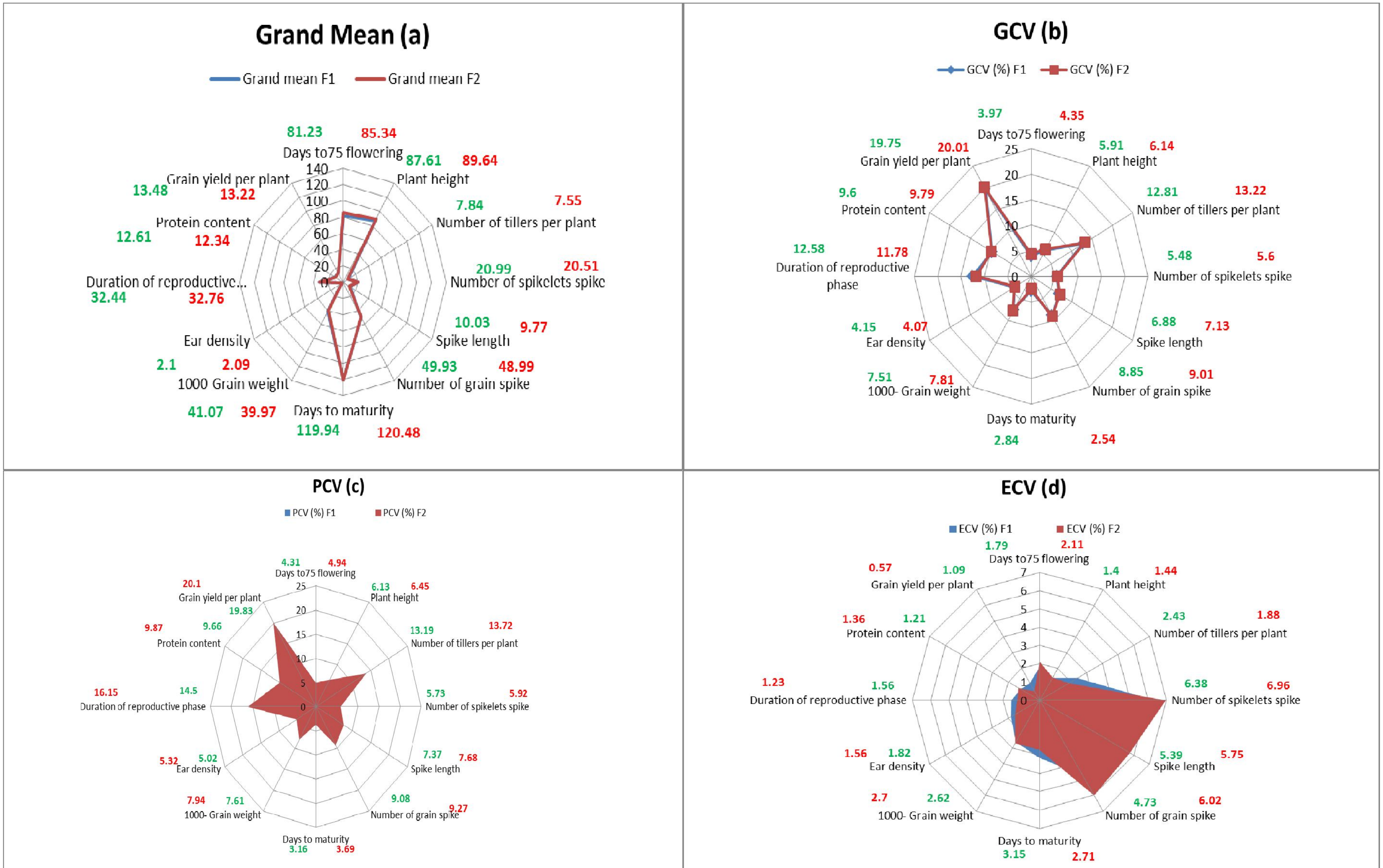

Figure 2: Estimates of Grand mean(a), GCV(b), PCV (c)and ECV(d) for 12 different characters in wheat.