Genetic Appraisal of Wheat Progenies for Grain Yield and Yield Attributing Traits

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

Original Research Article

ABSTRACT

The present investigation was carried out in F_3 and F_4 progenies of wheat to study gene interactions and its attributing traits during the *Rabi* season of 2014-15 and 2015-16. The crop was grown in research area of Wheat and Barley Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. Most of the traits were studied positively skewed and were being governed by several genes indicating quantitative inheritance. Skewness and kurtosis indicated dominance based complementary gene interaction involving large number of genes having decreasing effect in the inheritance of plant height, spike length, number of grains per spike, 1000 grain weight and biological yield per plant in both the progenies However, duplicate interaction was observed for grain length, number of spikelets per spike, grain yield per plant and harvest index in both the progenies, hence, genetic gain will be rapid under mild selection. Grain yield per plant and associated traits showed platykurtic distribution indicated the involvement of few genes in inheritance of these traits. This indicates that selection could be practiced for these component traits to increase grain yield per plant. Hence, as a concluding remark based on measures of shape in both F_3 and F_4, progenies directional selection will effectively enhance the performance of these yield attributing traits.

Keywords: Wheat; skewness; kurtosis; gene interaction; complementary epistasis; duplicate interaction.

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1. INTRODUCTION

Wheat (*Triticum aestivum* L. *em* Thell.) is a self-pollinated crop of the member of *Poaceae* family and one of the most leading cereal of many countries of the world including India. It is the most important food crop of India and is a main source of protein and energy. In India, wheat is the second most important food crop after rice both in terms of area and production. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. It is grown in temperate, irrigated to dry and high-rain-fall areas and in warm, humid to dry, cold environments. Wheat is consumed in a variety of ways such as bread, chapatti, flour, suji etc. Wheat has relatively high content of niacin and thiamin which are principally concerned in providing the special protein called 'Gluten' [1-3]. Wheat proteins are of special significance because gluten provides the framework of spongy cellular texture of bread and baked products. The record production in the country during last few years has enabled India to attain the position of being second largest producer of the wheat in the world. In 2020-21, 765 million metric tonne of global wheat production was reported (Shahbandeh, 2022). In India, wheat production during the period 2020-21 was 109.52 million tons recovered from acreage of 34.6 million hectare (Anonymous, 2020).

However, the demand for wheat is expected to grow and therefore productivity increase is needed. The knowledge about genetic variability, heritability, correlation coefficients and its other parameters help in further improving the grain yield through directed selection of component traits and their interrelationship with yield. Several biotic and abiotic stresses limit the realization of the full genetic potential of modern improved wheat varieties. Among the biotic stresses, late leaf spot rust (*Puccinia striiformis*) are widespread and economically most important [4]. A survey of genetic variability is essentially the first step in crop amelioration [5]. In self-pollinated crop, hybridization stands as one of the methodology by which favorable genes available in different genotypes could be combined into a genotype through genetic recombination. The development of genetic variability with hybridization and selection supplements the spontaneous variability for the crop improvement. An insight into the nature and degree of distribution present in population is of utmost importance as it forms the basis for selection in any crop breeding programme. Skewness and kurtosis reflects the nature of variability existing in a genetic population under study. The frequency distribution was studied for the quantitative traits, under third and fourth order statistics *viz.*, skewness and kurtosis. Skewness, characterizes the degree of asymmetry in the population. A positively skewed distribution indicates that the individuals of the population bunched up towards the lower mean values whereas, negatively skewed distribution exhibits that the individuals are clustered towards higher mean values. Similarly, kurtosis characterizes the relative peak size and flatness of a population distribution compared to normal distribution [6]. Positive kurtosis indicates leptokurtic distribution, negative kurtosis indicates platykurtic distribution and zero value indicates normal or mesokurtic distribution [7]. The most important criteria in any crop improvement program is the selection of progenies with all possible desirable yield attributing traits [8-10]. Skewness, the third degree statistics and kurtosis, the fourth degree statistics were estimated as Snedecor and Cochran (1974) understand to nature of distribution of 12 attributing traits in both the generations. The present investigations was, therefore, undertaken in F_3 and F_4 progenies of wheat with a view to assess the variability produced in respect of grain yield and its twelve attributing traits and frequency distribution pattern based on skewness and kurtosis.

2. RESEARCH METHODOLOGY

2.1 Plant Material

The Genetic material for the present investigation comprised of F_3 and F_4 progenies derived from the cross, WH 711/WH 542. WH 542 is a yellow rust resistant parent, whereas, WH 711 is rust susceptible parent. The experimental material comprised 238 F_3 & F_4 diverse progenies of wheat generated from the cross WH 711 / WH 542. The crop was grown in research area of Wheat and Barley Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, during the *Rabi* season of 2014-15 and 2015-16. Data was recorded on 5 randomly selected plants of segregating generations *viz.*, parents (WH711/ WH542'). Heritability and genetic advance as per cent of mean were estimated following the method of Johnson et al. (1955). Skewness, the third degree statistics and Kurtosis, the fourth degree statistics were estimated as per

Snedecor and Cochran (1974) to understand the nature of distribution of 12 attributing traits in F_3 and F_4 generation of each of the cross.

2.2 Field Experiment and Observations

All progenies were sown during the 2014–15 and 2015–16 growing seasons at experimental fields located at the latitude of 29010"N, longitude of 75046"E and altitude of 215.2 m above sea level in the semi-tropical region of western zone of India. The research work was carried out at Wheat and Barley Section, Department of Genetics and Plant Breeding CCS Haryana Agricultural University, Hisar. Each progenies were sown in the single row of two meter length, keeping row to row distance of 20.5 cm. All the recommended package of practice was followed to raise the crop. Utilizing 5 randomly selected plants, all progenies were characterized as follows: plant height (cm), number of tillers per plant, spike length (cm), spike weight (g), number of spikelets per spike, grain breadth (mm), grain length (mm), number of grains per plant, 1000 grain weight (g), grain yield per plant (g), biological yield per plant (g) and harvest index (%) were measured.

2.3 Statistical Analysis

Skewness, the third degree statistics and Kurtosis, the fourth degree statistics were estimated as per Snedecor and Cochran (1974) to understand the nature of distribution of 12 yield attributing traits in F_3 and F_4 generations. The mean values of yield traits of above cross was used to estimate coefficients of skewness and kurtosis using 'SPSS' software program. Kurtosis indicates the relative number of genes controlling the traits [11]. Three types of kurtosis are recognized based on the kurtosis value which depends on distribution curve. If kurtosis value is 3 it is Mesokurtic. If kurtosis value > 3 it is Leptokurtic, if kurtosis value < 3 it is Platykurtic. Similarly, the lack of symmetry i.e., skewness was recognized based the co-efficient of skewness values which range from -3 to +3. The type of distribution based on the skewness values were as follows. If skewness value is zero then, it is called as symmetrical distribution, if skewness value is negative, it is negatively skewed distribution and if skewness value is positive then it is positively skewed distribution.

2.4 Stepwise Regression

Stepwise regression was used to assess the most significant variables that have contributed significantly to the overall yield variability. Stepwise regression involves adjusting the forward option such that all candidate variables in the model are tested for each step in which a variable is introduced to verify that their significance is reduced below the defined tolerance point. If a variable found non-significant, it is excluded from the model. Stepwise regression eventually requires two levels of information: one for introducing variables and one for removing variables. The cut off probabilities for adding variables should be less than the cutoff probabilities for removing variables so that the procedure does not get into an infinite loop.

3. RESULTS AND DISCUSSION

3.1 Experiments in 2014-2015

In 2014-2015, selected F_3 & F_4 generations were evaluated in augmented designs (Fasoulas 1988). The F_3 & F_4 generations trial was established to evaluate the best 5 plants for the each selected line along with high yielding and yellow rust resistant. The high-yielding and yellow rust resistant progenies were selected from each both year in 2014-2015 & 2015-2016, based on the values of prognostic equations (Fasoula 2006, 2013). In order to introgress yellow rust disease resistance genes from resistant genotype WH542, a marker assisted breeding programme was initiated. The susceptible genotypes *viz.*, WH711 were used as recurrent parents in F_3 and F_4 generations were studied for the nature and degree of population distribution for yield and yield attributing traits using the measures of shape *i.e.* skewness and kurtosis. The results on the estimates of skewness, kurtosis and their distribution across the both generations for yield and yield attributes traits are presented in Table 1. Most of the progenies which were highly resistant in F_3 generation were also found resistant in F_4 generation and there was an association between the results of field evaluation for yellow rust. There were significant differences between the F_3 and F_4 progenies lines selected for high and low values of the traits, grain yield per plant, plant height, the number of productive tillers per plant, spike length, spike breadth, number of grains per spike, grain length, grain breath, number of spikelet per spike, 1000 grain weight, biological yield per plant and harvest index. These results indicated that selections for the characters were effective in early generations.

Table 1. Estimates of quantitative trait Skewness and Kurtosis in F_3 and F_4 generations derived from the cross WH711/WH542 in wheat

	Descriptive Statistics

| Trait	Range		Minimum		Maximum		Mean ± SE				Variance		CV(%)		Skewness		Kurtosis	
	F_3	F_4	F_3	F_4	F_3	F_4	F_3		F_4		F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4
Plant height	34.537	30.000	75.197	72.000	109.733	102.000	89.737 ± 0.387		83.553 ± 0.395		36.031	37.509	6.689	7.330	0.266	0.702	0.063	0.698
Number of tillers per plant	10.400	10.400	5.000	4.000	15.400	14.400	7.474± 0.086		8.559 ± 0.071		1.764	1.224	17.773	12.925	0.279	-0.341	-0.383	0.714
Spike length	4.697	3.400	8.200	8.800	12.897	12.200	10.667 ± 0.061		10.597 ± 0.056		0.908	0.756	8.931	8.203	0.016	0.105	-0.444	-0.768
Spike weight	2.173	2.906	1.910	2.036	4.083	4.942	2.959 ± 0.026		3.834 ± 0.041		0.167	0.400	13.817	16.505	-0.262	0.171	-0.456	-0.505
Number of grains per Spike	34.200	41.200	30.800	34.600	65.000	75.800	49.625 ± 0.442		55.179 ± 0.507		46.936	61.659	13.805	14.231	0.208	-0.853	-0.095	0.465
Grain length	2.473	1.256	4.423	5.360	6.897	6.616	5.916 ± 0.023		6.049 ± 0.019		0.132	0.087	6.130	4.884	0.128	0.271	-0.696	-0.347
Grain breadth	1.853	1.378	2.613	2.688	4.467	4.066	3.357 ± 0.017		3.355 ± 0.018		0.071	0.078	7.964	8.315	-0.722	-0.114	1.61	-0.841
No. of spikelets per spike	5.997	4.450	17.400	19.000	23.397	23.450	20.528 ± 0.072		20.724 ± 0.076		1.245	1.401	5.436	5.712	1.137	-0.754	4.29	0.104
1000 grain weight	4.077	3.524	2.533	2.066	6.610	5.590	3.798 ± 0.038		3.304 ± 0.039		0.352	0.356	15.626	18.054	1.728	0.481	4.625	0.695
Grain yield per plant	28.563	27.692	20.840	20.490	49.403	48.182	35.486 ± 0.299		37.456 ± 0.248		21.526	14.813	13.075	10.275	-0.076	-0.185	-0.336	-0.005
Biological yield per plant	67.697	58.347	51.100	51.260	118.797	109.607	91.753 ± 0.667		92.324 ± 0.541		106.635	70.345	11.255	9.084	0.074	-0.162	-0.423	0.167
Harvest index (%)	21.392	13.461	27.103	32.420	48.495	45.880	38.768 ± 0.239		40.603 ± 0.165		13.677	6.505	9.539	6.281	-0.256	-0.11	0.044	-0.228
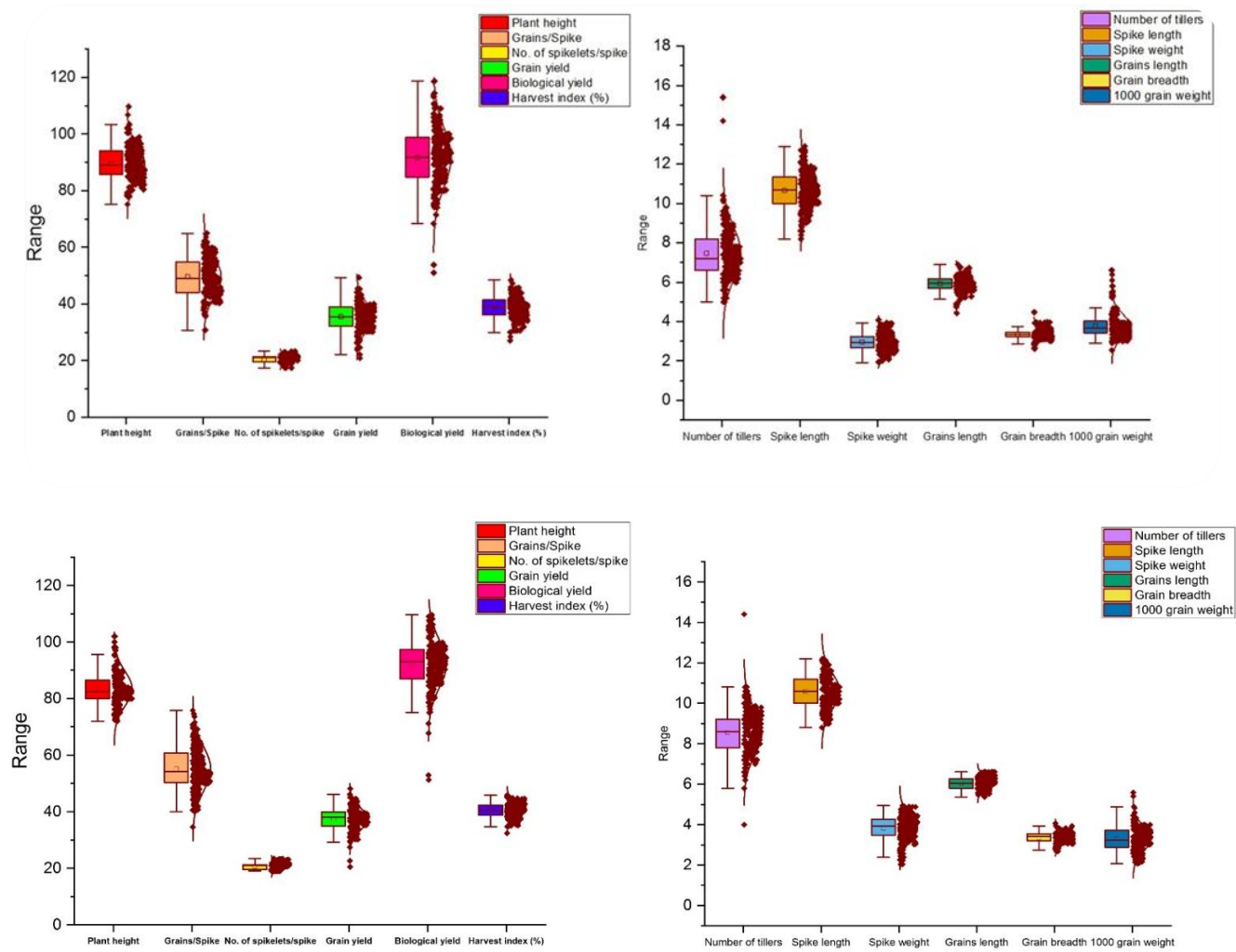
Fig. 1. Box-whisker plot

3.2 Descriptive Statistics

Descriptive statistical analysis was conducted to obtain statistical summary of data sets. Table 2 includes range, minimum, maximum, average and other statistical properties. Here the mean represents the measure of the central tendency of each variable. The range, SD and the variance is the absolute measure of the variability, which gives statisticians a better understanding of how varied the data set is. Deviations with respect to genotypes are higher for the number of tillers per plant (CV:17.77%) in the F_3 generation, while in the F_4 generation the CV value (18.05%) is higher for the 1000 grain weight across genotypes. Figs. 1, 2 and 3 are a box of variables that is a structured way of presenting data distribution based on a five-number description (minimum, first quartile (Q1), median, third quartile (Q3) and maximum) that gives an idea of data variation or dispersion.

3.3 Skewness and Kurtosis

The study of distribution using skewness and kurtosis provides information about nature of gene action (Fisher, 1932) and number of genes controlling the traits [11] Positive skewness is associated with complementary gene action while negative skewness is associated with duplicate (additive × additive) gene interactions. Genes controlling the traits with skewed distribution tend to be dominant irrespective of whether they have increasing or decreasing effect on the trait. The traits with leptokurtic and platykurtic distribution are controlled by fewer and many genes respectively. Kurtosis is negative or close to zero in absence of gene interaction and positive in presence of gene interaction [12,13].

3.4 Skewness

The frequency distribution of F_3 progenies(Table 1) was negatively skewed for grain length (-0.72), number of spikelet per spike (-0.262) grain yield per plant (-0.076) and harvest index (-0.256), whereas, positively skewed for plant height (0.266), number of tillers per plant (0.279), spike length (0.016), spike weight (0.208) number of grains per spike (0.128), grain breadth (1.137) 1000 grain weight(1.728), and biological yield per plant (0.74).

In the F_4 generation frequency distribution of progenies was negatively skewed for number of tillers per plant (-0.341), spike weight (-0.853), grain length (-0.114), grain breadth (-0.754), grain yield per plant (-0.185), biological yield per plant (-0.162) and harvest index (-0.11), whereas, positively skewed for plant height (0.702), spike length (0.105), number of grains per spike (0.271), number of spikelet per spike (0.171), and 1000 grain weight (0.481).

3.5 Kurtosis

The frequency distribution of F_3 was platykurtic (Table 1) for plant height (cm), number of tillers per plant, spike length, spike weight, number of grains per spike, grains length, number of spikelets per spike, grain yield per plant, biological yield per plant, harvest index, and grain breadth (Figure), whereas 1000 grain weight was leptokurtic (Figure). In F_4 progenies frequency distribution was platykurtic for all the traits.

In F_3 and F_4 generations negatively skewed platykurtic distribution was observed for grain length, number of spikelet per spike, grain yield per plant and harvest index indicating that these traits were governed by large number of genes and majority of them displaying dominant and dominant based duplicate epistasis, mild selection is expected to result in rapid genetic gain for these traits, whereas, positively skewed platykurtic distribution was observed for plant height, number of tillers per plant, spike length, spike weight, number of grains per spike, grain breadth, 1000 grain weight and biological yield per plant suggesting that these traits were governed by large number of genes and majority of showing dominant and dominant based complementary epistasis. Intense selection is required for rapid genetic gain for these traits. In F_4 generation negatively skewed platykurtic distribution was observed for number of tillers per plant, spike weight, grain breadth, grain yield per plant, biological yield per plant and harvest index indicating that these traits were governed by many genes and majority of them displaying dominant and dominant based duplicate epistasis. Selection will be effective for genetic improvement for these traits, whereas, positive skewed platykurtic distribution was observed for plant height, spike length, number of grains per spike, number of spikelet per spike and 1000 grain weight suggesting that these traits were governed by many number of genes and majority of them displaying dominant and dominant based complementary epistasis. The negatively skewed platykurtic distribution was observed for grain length, grain yield per plant and harvest index in

Table 2. Model summary

Generation	Final selected model	R	R^2	SE of estimate
F3	$GY = -35.68 + 0.38BY + 0.92HI$	0.997	0.994	0.351
F4	$GY = -37.60 + 0.40BY + 0.93HI$	0.999	0.997	0.197
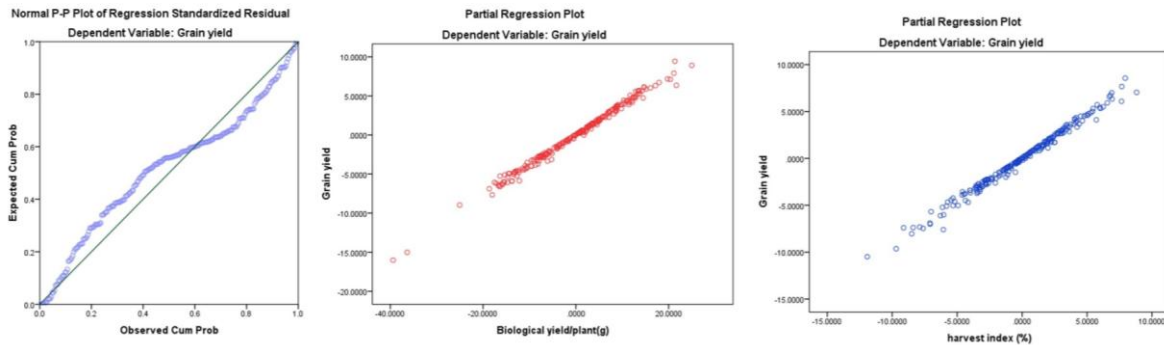
Fig. 2. Regression plot 1
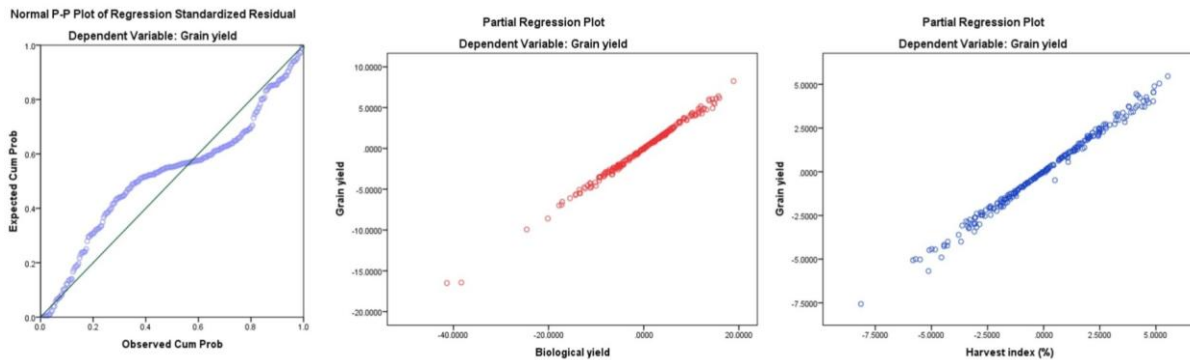
Fig. 3. Regression plot 2

both the generations. Similar finding were also observed by [12,14] studies in F_2 distribution of the cross with respect to reaction to rust disease in wheat and opined that as the distribution is continues, it could be governed by more than two genes. The presence of gene interaction and further it also indicates that these traits are governed by fewer numbers of dominant genes with majority having increasing effect.

In self-pollinated crops germplasm is available in the form of multitude of pure lines. The breeding endeavor revolves around recombining the genes of interest spread over different pure lines in one or few backgrounds, by way of recombination breeding which involves crossing of pure lines followed by selection in segregating generation till the selected lines become homozygous. The present study thus can be rated as integrated approach for wheat improvement using concealed recombination breeding coupled with marker assisted selection.

In this context, the gene constilation governing rust, grain yield, biological yield and 1000 grain weight can be standardized by crossing followed by marker assisted selection. Wheat breeders can use the lines identified in present investigation as parents in wheat improvement programme for developing wheat varieties with desirable yellow rust resistance genes combination. It is also recommended that advance breeding lines should be screened for presence of rust resistance genes with the help of marker assisted selection, so that only desirable gene combination can be carried forward in further wheat varieties.

3.6 Stepwise Regression

Stepwise regression analysis of grain yield with 11 yield attributes traits was performed with a pre-determined cut-off probability of 0.05 and a cut-off probability of 0.10. The model summary of stepwise regression (Table 2) showed that the

biological yield / plant (gms) and harvest index (percent) with a R square of 99.4 per cent, 99.7 *per cent* for the years 2014-2015 &2015-2016 (or F_3 & F_4 crosses) respectively justified the maximum change in yield. Therefore, based on the final step of stepwise regression analyses, the final model of grain yield (Y) were computed for the F_3 and F_4 crosses as follows.

$$GY\ (F3) = -35.68 + 0.38BY + 0.92HI$$

$$GY(F4) = -37.60 + 0.40BY + 0.93HI$$

Where, GY: Grain yield per plant, BY: Biological yield per plant and HI: Harvest index(%).

Existence of significant R square in a successful regression equation indicates the efficacy of these traits in increasing grain yield. Leilah and Al-Khateeb [15], Ahmadizadeh et al, [16] and Zarei et al, [17] reported the importance of the Biological yield per plant and the Harvest Index to the yield of grain. With regard to the positive and significant regression coefficients of the biological yield per plant and harvest index, it could be argued that increasing the amount of these traits will result in an increase in yield. Thus, in this study, two traits, the biological yield per plant and the harvest index had the greatest effect on grain yield.

Normal P P plot Residual standardized and Parial regrsion plots have been shown in Figure (x to xxx) for F_3 and Figure (y to yyy) for F_4 generation. The P-P plot measures up the observed cumulative distribution function (CDF) of the standardized residual to the expected normal distribution CDF. Partial regression plots are most widely used to describe leverage points and influential data points which may not be a leverage points.

4. CONCLUSION

The study indicates that selection could be practiced for these component traits to increase grain yield per plant. Hence, as a concluding remark based on measures of shape in both F3 and F4, progenies directional selection will effectively enhance the performance of these yield attributing traits.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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