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Correlation studies among yield and its components in bread wheat (*Triticum aestivum* L.)

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Abstract

The present research work was conducted at Crop Research Farm, Nawabganj, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.) India. The experimental material for present investigation comprised of 45 F₁s developed by crossing 10 lines viz., HD3086, DBW88, HD2733, DBW39, K0307, HD2967, K0402, K1601, K 8962 and K1314 followed by half diallel mating design. A total of 100 treatments with 10 parents (45 F₁s and 45 F₂s) were grown in Randomized Block Design for the study of correlation coefficient for twelve characters such as days to 75% heading, days to maturity, plant height (cm), number of productive tillers per plant, spike length (cm), number of spikelets per spike, number of grains per spike, 1000-grain weight (g), grain yield per plant (g), biological yield (g), harvest index (%), and protein content(%) in bread wheat. The correlation analysis revealed that at phenotypic level, grain yield per plant was significantly and positively correlated with days to maturity, spike length, number of grains per spike, 1000-grain weight, biological yield and harvest index in both the generations.

Keywords: Correlation coefficient, phenotypic, diallel mating design

Introduction

Wheat (*Triticum aestivum* L.) is the principal food grain of the world population. It constitutes the major food for billions people of the world. Among the cereals, wheat has the pride place because of vast acreage covered under cultivation, and nutritional value which supplies about 20% of the calories for the world growing population. It is the most important staple food of about two billions people (36% of the world population). The importance of the wheat is evident from the dependency of more than half of the world's population on wheat as a basic food.

Wheat ranks first among the world food crops, in terms of cultivated area 221.18 mha and production 774.74mmt with productivity of 35 qha⁻¹ (USDA 2021). In India, wheat is the second most important cereal crop next only to rice, India stands second among wheat producing countries after China. During the crop year 2020-2021, wheat was grown over an area of 31.47 million hectares with the production of 109.52million metric tones and during 2019-2020 was 32.72 million hectares with the production of 101.20 million tones and average productivity was 34.24 q/ha. (Project Director's Report, IIW&BR 2018-19). The demand of wheat in India by 2022 has been projected to be between 101-115 million tonnes as against 109.50 million tonnes production of present day.

Uttar Pradesh state ranks first in both area and production among states, Uttar Pradesh produces a significant level of wheat record production of 35.47mt (34%) with 36.04 mt productivity in the area of 9.84 mh, followed by Punjab (19.78 mt: 18%), Madhya Pradesh (18.35 mt: 17%), Haryana (12.65 mt: 12%), Rajasthan (9.60 mt: 9%) and Bihar (6.02 mt: 6%). Therefore mentioned six states hold a share of about 93 per cent in total wheat production. With the exception of Bihar, Gujarat, Himachal Pradesh, Jharkhand, Karnataka, Maharashtra, Odisha, Punjab and Uttarakhand, the rest of the states registered an increase in production during 2018-19 in comparison to 2017-18. Overall production from all these states has declined by 1.67 mt owing to the fall in yield levels and/or acreage. The highest fall was noticed in Maharashtra (-0.97mt: -57.24%). The increase in wheat production was maximum in the case of Madhya Pradesh (+1.44 mt: +9.04%), followed by Haryana (+0.89 mt: +8.25%) and Uttar Pradesh (+0.33 mt: 1.03%).

Therefore, for attaining high yield potential level, the breeders need is to simplify this complex situation through handling of yields components. There is need to improve the quality of wheat grains by increasing protein percentage and to develop high yielding potential varieties with high quality of seeds as well as high degree of resistance for different agroclimatic conditions.

Materials and Methods

Ten genotypes of wheat (*Triticum aestivum* L. Em. Thell) namely HD3086, DBW88, HD2733, DBW39, K0307, HD2967, K0402, K1601, K8962 and K1314 as basic material which had been taken on the basis of their differences in origin, adaptability and morphological characters from the germplasm maintained at Section of Economic Botanist (Rabi Cereals), C.S. Azad University of Agriculture and Technology, Kanpur. All these parents have genetic variability for yield level as well as for various good yield components. In the present investigation all possible crosses among the selected parents were made in one direction only, i.e. direct crosses. Here each parent was used either as male or as female in the mating. The number of single crosses attempted was equal to $[n(n-1)/2]$, where n is the number of parents used. Half diallel design was used in the present study because reciprocal differences are not significant in wheat crops.

All possible single crosses were made during the year 2018-19 to complete a 10x10 half diallel set without reciprocal due to absence of extra nuclear inheritance in wheat (Whitehouse, at al.1958) The experiment was conducted in randomized block design (RBD) with 45 F₁, 45 F₂ with ten diversified parents during the year 2019-2020) at Crop Research Farm, Nawabganj, Kanpur. The experimental material was sown in each replication, parents and F₁s were sown in single row while F₂s were sown in two rows. The length of each row was 3.0m with inter and intra-row distance of 25 and 10cm respectively. Recommended doses of fertilizers @ 120 kg N + 60 kg P₂O₅ + 40 kg K₂O per hectare were applied in the experimental area along with four irrigations at all critical stages.

Quantitative data were collected on five plants in each row. Days to 75% heading, days to maturity, plant height, number of productive tillers, spike length, number of spikelets per spike, number of grains per spike, 1000-grain weight, and grain yield per plant, biological yield per plant, Harvest index, and protein content. Regarding statistical analysis data recorded on parents with forty five F₁ and forty five F₂ were analyzed together.

Correlation coefficients

The estimates of phenotypic and genotypic correlation were worked out as given under:

(a) Genotypic correlation

$$r_{xy}(g) = \text{Cov}_{.xy}(g) / [\text{V}_x(g) \cdot \text{V}_y(g)]^{0.5}$$

Where

Cov_{.xy}(g) = genotypic covariance between character X and y was obtained as follows:

$$\text{Cov}_{.xy}(g) = [\text{Cov}_{.xy}(p) - \text{Cov}_{.xy}(e)]/r$$

V_x(g) and V_y(g) = Genotypic variance for the characters x and y respectively

r = number of replications.

(b) Phenotypic correlation

$$r_{xy}(p) = \text{Cov}_{.xy}(p) / [\text{V}_x(p) \cdot \text{V}_y(p)]^{0.5}$$

Where

Cov_{.xy}(p) = Phenotypic correlation between the character x and y and this was obtained as follows:

$$\text{Cov}_{.xy}(p) = \text{Cov}_{.xy}(g) + \text{Cov}_{.xy}(e)$$

V_x(p) and V_y(p) = Phenotypic variance for the characters x and y, respectively.

xy(e) = the error variance obtained from the ANNOVA of x and y characters.

Test of significance of correlation coefficients

The significance of phenotypic coefficient was tested against 'r' values from 'r' Table of Fisher and Yates (1938) [3] for (n-2) degree of freedom where 'n' is number of treatments.

Results and Discussion

Indirect selection is more effective than direct selection procedure when the attribute in question has low heritability and/or is not easily and precisely measured. The aim of correlation studies is primarily to know the suitability of various characters for indirect selection because selection for one or more traits results in correlated response for several other traits (Searle, 1965) [6], and the pattern of variation will also be changed (Waddington and Robertson, 1966). Therefore, knowledge of genetic correlation existing between yield and its components is essential.

All possible phenotypic and genotypic correlations were worked out for 12 characters in ten parents, 45 F₁s, 45F₂s, though, the significance of genotypic correlations could not be tested as no suitable statistical test is available yet their magnitude is considered in relation to the corresponding phenotypic estimates (Fisher, 1918) [3]. The magnitudes of genotypic correlations were greater than phenotypic correlation coefficients in parents, F₁s and F₂s for all the traits except in few combinations. The similar has also been reported by Khan *et al* (2010 a, b). in bread wheat. Hence, the significant phenotypic associations between characters were primarily due to genetic causes, which might be due to pleiotropic effect rather than linkage between genes affecting different characters. The self-pollination mechanism is a prelude to the fixation of blocks of genes as well as due to limited chances for breaking linkage compared with the random mating system prevailing in open-pollinated crops. Such reports have also been made by Weber and Murthy (1952), Johnson *et al.* (1955) and Anand and Torrie (1963) in soybean and Kempthorne (1955) and Kheder (1971) in cereals.

Grain yield per plant had phenotypic positive correlation with days to 75% heading, days to maturity, number of productive tillers, spike length (cm), number of spikelets per spike, number of grains per spike, 1000-grain weight (g), biological yield (g), Harvest index (%), and protein content (%). Therefore, selection for these traits might lead to higher productivity. (Esmail, R.M. 2001). Also support the same result in grain yield which was significantly and positively correlated with days to maturity, 1000-grain weight and Harvest index.

Positive correlation was reported by Khan *et al.* (2010 a, b) [7, 8]. For various traits such as grains per spike have highly significant positive genotypic correlation with spike density and positive non-significant correlation with spike density.

1000-grain weight has significant positive genotypic and phenotypic correlation with spike density.

Grain yield per plant exhibited positive association at phenotypic level with number of ear bearing tillers, days to maturity, duration of reproductive phase per plant, spike length, number of reproductive phase per plant and ear density for F₁ and F₂ generations. Similar results were obtained by Bergale *et al.* (2002)^[15], Lad *et al.* (2003)^[20], for grain yield and number of productive tillers per plant; Bhusan *et al.* (2013)^[16] for grain yield and days to maturity; Baranawal *et al.* (2012)^[14], Kumar *et al.* (2014)^[18] for 1000-grain weight. Emphasis on selection in favour of these characters would help breeders for having desirable correlated response for higher productivity.

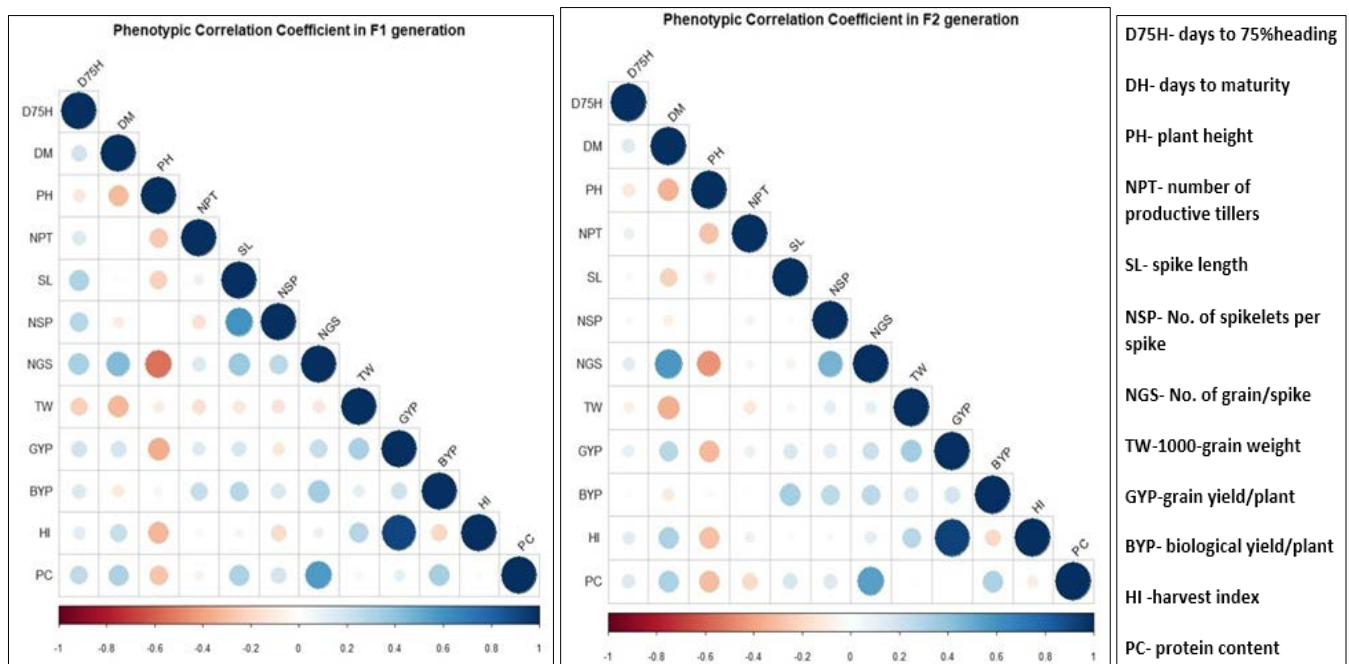
A positive association existed between grain yield per plant with number of ear bearing tillers, spike length, days to maturity, ear density and number of grains per spike, spike length and quality trait like protein content which were indirectly associated with grain yield. In F₂, all qualitative and quantitative traits were positively associated with grain yield except plant height and number of ear bearing tillers as similar result reported by Kashif and Khaliq (2004)^[19] and Led *et al.* (2003)^[20]. Reported that plant height, spike length, spikelets spike-1 and 1000-grain weight were positively and significantly correlated with grain yield at genotypic level.

At genotypic level, positive association of grain yield was observed with plant height and duration of reproductive phase alongwith quality trait i.e., protein content. But in F₂ the significant association of plant height was very clear along

with number of grains per spike and duration of reproductive phase. Quality traits like protein content were also associated with grain yield in F₂ generation.

At genotypic level in generation, the positive correlation of grain yield was due to number of ear bearing tillers, spike length, days to maturity, ear density and number of grains per spike. In F₂, the spike length, days to maturity, duration of reproductive phase, ear density and number of grains per spike, spike length were positively associated with grain yield (Ayudin *et al.* (2018)). Thus, the high order of positive and significant association in both the generations indicated that environmental conditions tended to increase or decrease on variables (Bye *et al.* 2020). Negatively correlated traits with grain yield per plant in parents, F₁ and F₂ were in agreement with the results reported by Bhatia (1978), Loffler (1985), Kerkhi (1983), Mandal and Kour (2004) and Singh (2007) Kamani *et al.* (2017), Bayisa *et al.* (2021) indicating that this relationship might be due to change in proportion of different individuals.

The undesirable association of grain yield and contributing traits with protein content showed higher values for genotypic correlation coefficient than phenotypic ones. It was accepted that each type of genotypic correlation might be due to the effects of pleiotropy. In case of negative correlation caused by pleiotropy, a new combination of traits would be attained through mutagenesis. On the other hand, if the genotypic correlation was due to linkage, it might be possible to break the linkage by breeding methods such as bi-parental mating or disruptive selection.



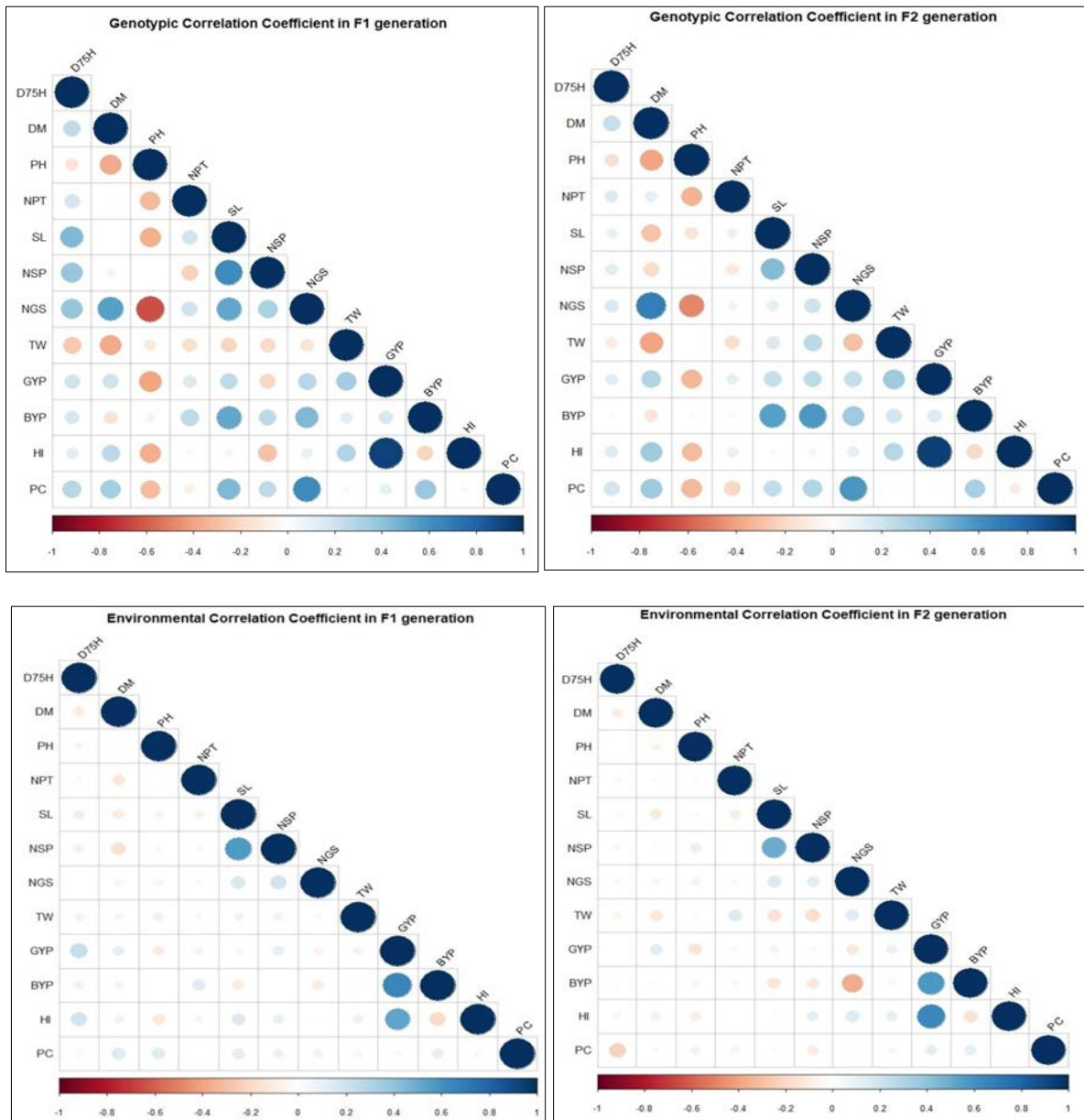


Fig 1: Graphs for correlation coefficient for twelve different characteristics with ten different genotypes

Conclusion

The coefficient of correlation between parental order of dominance and parental measurement was found to be positive for days to maturity, plant height, number of reproductive tillers per plant in both the generation and days to 75% heading, number of spikelets in both F1 generations. The positive values indicated the genes were mostly dominant in the expression of concerned traits and vice-versa for negative values.

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