*SKUAST Journal of Research* 25(1): 67-77; (2023)
(*10.5958/2349-297X.2023.00007.7*); NASS rating: 4.17

**Research Paper**

# Genetic variability for agro-morphological traits in wheat (*Triticum aestivum* L.) under temperate rainfed conditions of Kashmir valley

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(Received December 10, 2022; accepted January 02, 2023)

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ABSTRACT

**The present study was undertaken to estimate the extent of genetic variability for different agro-morphological traits in an $F_2$ bi-parental mapping population derived from the cross between CW-5018 and SW-3. High GCV% (genotypic coefficient of variation) and PCV% (phenotypic coefficient of variation) was observed for the traits viz., number of tillers per plant, spikelets per spike, grains per spike, 1000 grain weight and grain yield per plant, indicating that there is an ample scope for the selection of promising plants for yield and its component traits from the population. At the same time, low GCV% and PCV% was recorded for traits viz., days to flowering and days to maturity, suggesting that selection for such traits in segregating populations like $F_2$ may not be effective. High heritability coupled with high genetic advance as percent of mean was recorded for traits viz., number of tillers per plant, plant height, spike length, number of spikelets per spike, grains per spike, 1000 grain weight and grain yield per plant, indicating better scope for selecting superior transgressive segregants out of the population. It is concluded that the selection of superior plants on the basis of desirable yield parameters in segregating generations like $F_2$ could be effective for developing high yielding wheat genotypes as direct selection for yield is difficult considering its complex nature being governed by many small effect genes/QTLs.**

**Key words:** GCV, genetic advance, grain yield, heritability, PCV, segregating $F_2$ population, wheat.

Bread wheat (*Triticum aestivum* L.; Genome: AABBDD) is one of the most important and widely grown cereal crops in the world (Gupta *et al*., 2021). It is a self-pollinating, annual crop belonging to the family *Poaceae* (grasses), with diploid chromosome number of 42 (2n=6x=42) and a large genome size of 16 GB. Wheat is the second-most-produced cereal grain after maize. The global trade of wheat is greater than all other crops combined (*https://worldpopulationreview.com/country-rankings/wheat-production-by-country*). Wheat is consumed by more than 40 per cent of the world population as a staple food and provides about 20 per cent of daily dietary energy and protein. It is a major source of essential micronutrients such as grain Fe and grain Zn (Velu *et al*., 2017; Tahir *et al*., 2021). Wheat is cultivated as a cash crop, as it produces good yield per unit area, grows well in temperate climate with a moderately short growing season and yields a versatile, high-quality flour. The majority of wheat flour is used to make products including bread, pasta, pastries, cookies, crackers, muffins, tortillas, and pitas. Wheat has acquired a premier place among cereals due to its vast acreage and adaptability in different agro-climatic conditions. Globally, wheat is cultivated on an area of 219.06 million hectares with a production of 760.9 million metric tonnes. India is the second largest producer of wheat after

China, growing the crop over an area of about 31.6 million hectares with a production of 107.6 million metric tonnes (*https://en.wikipedia.org/wiki/International_wheat_production_statistics*). Although it is a tremendous accomplishment, India still continues to face formidable problem of ever-increasing population. If the population growth goes up to expected 9.7 billion by 2050, the need for wheat crop is predicted to rise by 60% (Molotoks *et al*., 2020. Therefore, breeding for enhanced yield has always remained a major objective for wheat breeders. However, improving yield is one of the most difficult tasks for breeders as yield is a complex physiological trait controlled by several small effect genes/QTLs (Mir *et al*., 2021). Grain yield response in wheat is influenced by several agronomic and physiological traits (Liu *et al*., 2015). Agronomic traits such as plant height, harvest index, total biomass, number of productive tillers, grain number per spike, spike length, number of kernels per spike, thousand grain weight and grain weight per spike contribute to grain yield improvement in wheat (Chen and Hao, 2015). Due to their high heritability and correlation with grain yield, agronomic traits can be used as indirect selection criteria during breeding and cultivar development (Gao *et al*., 2017). Moreover, it has been suggested that genetic progress in yield can be achieved if several traits conferring better agronomic and physiological performance with biotic and abiotic stress tolerance are simultaneously selected and introgressed in a single variety (Lopes *et al*., 2012). Therefore, there is a need for trait-based breeding using high performing and genetically complementary genotypes to accelerate further grain yield improvement in wheat (Reynolds *et al*., 2017).

Genetic manipulation is the best way to boost up wheat production (Nimbal and Naik, 2021). To start successful wheat breeding programmes, it is required to evaluate and research genetic variation and mode of inheritance for yield and its related features (Wani *et al*., 2020). Understanding the genetic effects of hybridization requires the study of genetic factors from segregating populations (Nimbal and Naik, 2021). Heritability which is a measure of phenotypic variance provides an estimate of the genetic advancement a breeder could expect from selection being applied to a population in a specific environment. High heritability associated with high genetic advance for yield and its component traits offer a better scope for selecting high yielding genotypes (Mangi *et al*., 2007). Genetic variability studies in bread wheat genotypes have been attempted by several workers including Ali *et al*. (2008), Abinasa *et al*. (2011), Singh *et al*. (2012), Bharat *et al*. (2013), Kumar *et al*. (2013), Said (2014), Naik *et al*. (2015), Deepak (2016), Uzma *et al*. (2017), Arya *et al*. (2017), Jamil *et al*. (2017), Nelwadker *et al*. (2019), Bartaula *et al*. (2019), Mofokeng *et al*. (2020), Roy *et al*. (2021) and Hasan *et al*. (2021). Genetic variability studies in segregating populations of wheat have also been carried out by several researchers like Mangi *et al*. (2007), Hokrani *et al*. (2013), Veeresha (2016), Swathykrishna (2018) and Nimbal and Naik (2021). However, to the best of our knowledge, genetic variability studies for phenological and yield/yield related traits in segregating populations have not been carried out so far in the temperate hill ecologies of Kashmir valley of the UT of Jammu and Kashmir. Therefore, the present study was carried out to assess the extent of genetic variability, heritability and magnitude of genetic gain expected to occur during the selection for yield parameters in $F_2$ population of the cross CW-5018 × SW-3 under temperate conditions of Kashmir Valley. Such studies in future will enable breeders to make predictions regarding possible progress that can be achieved through selection in segregating populations.

## MATERIALS AND METHODS

The present study was carried out at the Division of Genetics and Plant Breeding (GPB), Faculty of Agriculture (FoA), SKUAST-K, Wadura Campus, Sopore. The experimental material used during the present study consisted of $F_2$ segregating population derived from the cross CW-5018 × SW-3. The female parent 'CW-5018' was one among the advanced breeding lines obtained from Borlaug Institute for South Asia (BISA), CIMMYT, Ludhiana while the male parent 'SW-3' a recently released early maturing variety by SKUAST-K, was already available with us at FoA, Wadura, Sopore.

Crossing was attempted in the research field of Division of GPB, during the main cropping season of rabi 2020-21 (Fig. 1) and $F_1$ seed was harvested in June, 2021. The $F_1$ seed obtained was sown in polyhouse as an off-season crop in July, 2021 to obtain $F_2$ seed in October, 2021 which was sown in the main cropping season of rabi 2021-22 in the field. The seeds of $F_2$ population along with the two parents were space planted in rows of length 2.5 m, maintaining plant to plant distance of 20 cm and row to row distance of 25 cm (Fig. 2).

**Trait data recorded:** During the present study, data on each individual $F_2$ plant were recorded for nine agro-morphological traits viz., days to 50 percent flowering (DTF), days to maturity (DTM), number of tillers per plant (TPP), plant height (PH), spike length (SL), number of spikelets per spike (SPS), grains per spike (GPS), 1000 grain weight (TGW) and grain yield per plant (GYPP) as per the descriptors of PPV & FRA (2007).

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**Fig.1: Image showing two parents crossed at FoA, Wadura during the present study to develop $F_1$ seed**




**Fig. 2: $F_2$ population of cross CW 5018 × SW 3 along with the two parents in field**

**Statistical analysis:** The data recorded in $F_2$ population were subjected to statistical analyses. The statistical methods adopted and the genetic parameters estimated are as follows:

**General mean ($\bar{x}$)** = sum of observations in a trait /number of observations in a trait

**Range** = the minimum and maximum values for a given trait

**Estimation of genetic parameters**:

Phenotypic variance ($\sigma^2p$) = Var $F_2$; where, Var $F_2$ = variance of $F_2$ population

Environmental variance ($\sigma^2e$) = (Var $P_1$ + Var $P_2$) / 2

where, Var '$P_1$' = variance of parent '$P_1$' and Var '$P_2$' = variance of parent '$P_2$'

Genotypic variance ($\sigma^2g$) = $\sigma^2p$ - $\sigma^2e$

where, $\sigma^2p$ = phenotypic variance and $\sigma^2e$ = environmental variance

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Genotypic coefficient of variability (GCV)

$GCV\ (\%) = \sqrt{(\sigma^2 g)} / \bar{x} * 100$

Phenotypic co-efficient of variability (PCV)

$PCV\ (\%) = \sqrt{(\sigma^2 p)} / \bar{x} * 100$

where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

$\bar{x}$ = Grand mean of the character

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

**Heritability (Broad Sense):** Heritability in broad sense was estimated as the ratio of genotypic to the phenotypic variance and was expressed in percentage as suggested by Hanson (1956).

$$h^2_{bs} = \sigma^2 g / \sigma^2 p * 100$$

where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

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

**Genetic advance (GA):** The extent of genetic advance to be expected from selecting 5% of the superior progeny was calculated by using the following formula.

$GA = i h^2_{bs} \sigma^2 p$

where, i = intensity of selection, $h^2_{bs}$ = heritability in broad sense, $\sigma^2 p$ = phenotypic variance.

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.

$$GAM = \frac{GA}{Mean} \times 100$$

where, GA = Genetic advance, Mean = general mean of the character ($\bar{x}$). Genetic advance as per cent of mean was categorized as low, moderate and high as per Johnson *et al*. (1955): 0-10% = Low; 10-20% = Moderate; 20% and above = High.

## RESULTS AND DISCUSSION

Wheat is of critical importance for the global food safety providing 18% of consumed calories and 20% of protein intake. Therefore, breeding wheat for higher yield has always remained a major objective for plant breeders. However, grain yield *per se* is a complex quantitative trait governed by many small effect genes/QTLs. Therefore, there has been a great emphasis across all breeding programmes to study the nature of relationship and trait associations between yield and other traits which are relatively less complex and have comparatively better heritability for use as indirect selection criteria. Wheat grain yield is affected by various components like plant height, number of tillers per plant, spike length, spikelets per spike, grains per spike and 1000 grain weight. In this connection, fine knowledge of different variability parameters and their relative significance is very important in order to improve the overall production levels in wheat crop. Parents with

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higher genetic variability will be able to produce higher extent of heterosis in the progeny (Roy *et al*., 2021). Keeping these aspects in view we undertook a study to estimate the extent of genetic variability for different agro-morphological traits in an $F_2$ bi-parental mapping population derived from the cross between CW-5018 and SW-3. The population was evaluated in terms of genetic variability (mean, range, GCV and PCV), heritability and genetic advance for flowering, maturity and grain yield/yield component traits to identify and isolate the segregants which are having higher potential to be either used as potential genetic resources in future or released as new varieties as such after advancing and evaluating through further generations. The results obtained during the present study are discussed below in the light of available literature.

**Range of variation:** The results of genetic variability showed high mean and wider range of values for almost all the traits studied in $F_2$ population, thereby suggesting the existence of sufficient genetic variability in the population (**Table 1**). Analysing the range values critically revealed some significant and insightful data. The wide range and high mean values in yield and yield attributing traits found during the present study could give breeders a chance to select the desired segregants for developing high yielding wheat varieties in future. A wide range of 80-98 cm in plant height can be exploited by the researchers for developing varieties with desirable height (medium stature) in order to avoid lodging in wheat. Our results are in accordance with several earlier studies (Mangi *et al*., 2007; Hokrani *et al*., 2013; Veeresha, 2016; Swathykrishna, 2018; Nimbal and Naik 2021).

**Genetic variability:** Genotypic and phenotypic coefficients of variation are the indicators of variability that exists in a given population. Table 1 presents the estimated genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense ($h^2_{bs}$) and genetic advance as per cent of mean (GAM) of the traits studied. In general, the PCV values were greater than GCV values although the differences were small in most of the traits studied.

**Table 1: Estimates of genetic variability parameters for agro-morphological traits in $F_2$ population of CW-5018 × SW-3**

| Traits | Mean | Min. | Max. | St Dev | SE | CV (%) | GCV (%) | PCV (%) | $h^2_{bs}$ (%) | GAM (%) | Change (%) Vs donor | Change (%) Vs RP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DTF | 189.4 | 184.0 | 204.0 | 3.5 | 0.6 | 1.8 | 2.10 | 2.26 | 86.09 | 17.22 | 6.3 | 3.4 |
| DTM | 246.2 | 239.0 | 256.0 | 7.2 | 1.2 | 2.9 | 1.87 | 1.98 | 89.04 | 17.67 | 4.2 | 1.1 |
| TPP | 14.2 | 10.0 | 20.0 | 3.9 | 0.6 | 29.0 | 18.40 | 21.75 | 71.59 | 99.26 | 3.0 | 15.2 |
| PH (cm) | 87.1 | 80.0 | 98.0 | 7.4 | 1.2 | 8.7 | 4.73 | 5.35 | 78.06 | 40.08 | 5.7 | 3.6 |
| SL (cm) | 10.9 | 7.5 | 12.5 | 1.2 | 0.2 | 10.5 | 9.83 | 10.53 | 87.16 | 21.75 | -7.1 | -11.5 |
| SPS | 21.0 | 14.0 | 26.0 | 2.9 | 0.5 | 13.8 | 11.66 | 13.80 | 71.43 | 58.86 | 4.5 | -16.7 |
| GPS | 50.5 | 36.0 | 59.0 | 8.9 | 1.4 | 17.0 | 12.33 | 12.66 | 94.91 | 158.15 | -2.9 | -24.9 |
| TGW (g) | 51.1 | 42.3 | 64.8 | 7.7 | 1.2 | 15.3 | 12.25 | 12.64 | 93.92 | 158.16 | 5.3 | 12.4 |
| GYPP (g) | 25.6 | 18.0 | 31.6 | 4.8 | 0.8 | 19.1 | 12.57 | 13.40 | 88.10 | 83.37 | 3.0 | -9.6 |

DTF = days to 50% flowering; DTM = days to maturity; TPP= number of tillers per plant; PH = plant height; SL = spike length; SPS= spikelets per spike; GPS= grains per spike; TGW= 1000 grain weight; GYPP= grain yield per plant; CV = coefficient of variation; GCV = genotypic coefficient of variation; PCV = phenotypic coefficient of variation; $h^2_{bs}$ = heritability in broad sense; GAM = genetic advance as percent of mean

Higher GCV and PCV values were observed for the traits TPP, SPS, GPS, TGW and GYPP; low GCV and high PCV was observed for SL. This indicates that there is an ample scope for selection of promising plants from the present population for yield and its component traits. High genetic variability for grain yield and its component traits in early segregating generations of wheat was also reported by Abinasa *et al*. (2011); Nimbal and Naik (2021). Low GCV and PCV recorded for DTF, DTM and PH suggests that selection for such traits in early segregating generation may not be effective. Such results of low PCV and GCV are in accordance with the findings of Ajmal *et al*. (2009); Subhashchandra *et al*. (2009) and Nimbal and Naik (2021), whereas high PCV and GCV are in accordance with the findings of Manal (2009); Kahrizi *et al*. (2010); Bhushan *et al*. (2013); Arpitha *et al*. (2017) and Nimbal and Naik (2021).

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**Heritability and Genetic Advance:** For selection in any population improvement method, heritability is a very significant parameter. Single plant selection in the early segregating generations may be more effective for a highly heritable trait as compared to the character which has less heritability. High estimates of heritability were observed for all the traits studied during the present investigation with highest recorded in case of GPS (94.91%) followed by TGW (93.92%), DTM (89.04), GYPP (88.10%), SL (87.16), DTF (86.09%), PH (78.06%), TPP (71.59%) and SPS (71.43%). This suggested that heritability for these traits is due to the additive genetic effects and direct selection for these traits in early segregating generations could be effective for improving yield and maturity traits in wheat. Many workers like Singh *et al*. (2006); Ahmed and Kaliq (2007); Rahman (2009); Deepak (2016); Veeresha (2016); Swathykrishna (2018) and Nimbal and Naik (2021) have reported high heritability along with high to moderate genetic advance for grain yield in wheat.

The heritability of the most important trait i.e., grain yield per plant (GYPP) was rather high (above 80%), clearly indicating the higher influence of genetic factors than the environment on the expression of this trait. The findings of our study are in agreement with the findings of Rehaman *et al*. (2016) and Nimbal and Naik (2021). Hence, selection for yield related traits like TPP, SL, SPS, TGW and GYPP could result into the improvement of yield in wheat crop. Furthermore, heritability estimates combined with genetic advance are typically more effective than heritability estimates alone in predicting genetic gain under selection (Johnson *et al*. 1955). High heritability coupled with high genetic advance as percent of mean was recorded for TPP, PH, SL, SPS, GPS, TGW and GYPP (Table 1), suggesting predominance of additive gene action in the expression of these traits. Therefore, selection will be effective in the improvement of these traits. High heritability coupled with moderate genetic advance over mean was noticed for DTF and DTM suggesting predominance of additive and non-additive gene action in the expression of these traits. Therefore, these traits can be improved by mass selection. Nimbal and Naik (2021) found high heritability coupled with high genetic advance as percent of mean for number of productive tillers per plant, number of grains per spike and grain yield per plant while it was low for traits like days to flowering, days to maturity, plant height, spike length, number of spikelets per spike and thousand grain weight. Similar results were also reported by Asif *et al*. (2010).

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## CONCLUSION

The segregating population of the cross CW-5018 ×SW-3 may be regarded as a potential source population for important yield component traits viz., number of tillers per plant, spike length, spikelets per spike, grains per spike, 1000 grain weight and grain yield per plant. These traits could be considered while attempting a breeding strategy for selecting superior and desirable plants to develop high yielding genotypes in wheat. Further, selective inter-population mating involving such type of segregating populations might increase variation for yield, thereby providing better scope for enhancing genetic gain under rainfed conditions.

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