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Genetic Behavior of Yield and Component Traits in Bread Wheat (*Triticum aestivum* L.)

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Authors' contributions

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

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ABSTRACT

The present investigation was undertaken to assess the extent of genetic variability, heritability, and genetic advance among early-sown wheat genotypes for yield and related traits. The experiment was laid out in a Randomized Block Design (RBD) with three replications, comprising 65 genotypes including 15 parents (5 males and 10 females) and 50 hybrids derived from a Line × Tester mating design. The study was conducted at the Zonal Agricultural Research Station,

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Powarkheda, Hoshangabad (Madhya Pradesh), India, during the *rabi* seasons of 2019–20 and 2020–21. All genotypes were evaluated for sixteen agronomic and physiological traits. Analysis of variance (ANOVA) was performed to assess genetic variability, while genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability (H^2), and genetic advance (GA) were estimated to determine the nature and extent of genetic control. ANOVA revealed highly significant differences among genotypes for all traits, confirming the presence of substantial genetic variability. A close correspondence between GCV and PCV across most traits indicated minimal environmental influence and strong genetic control. Broad-sense heritability estimates were notably high, ranging from 83.10% (peduncle length) to 99.90% (biological yield). Traits such as grain yield per plant (H^2 = 99.40%), biological yield (99.90%), harvest index (98.90%), number of effective tillers per plant (94.30%), and number of spikes per plant (96.60%) exhibited high heritability coupled with high genetic advance (GA% = 58.66%, 68.18%, 51.82%, 50.50%, and 38.27%, respectively), indicating the predominance of additive gene action. In contrast, traits like peduncle length, canopy temperature, and 1000-grain weight showed high heritability but moderate genetic advance, suggesting a combination of additive and non-additive gene effects. The study highlights the predominance of additive genetic variance in most traits, indicating that direct phenotypic selection would be effective for yield improvement. For traits governed by both additive and non-additive gene effects, hybridization strategies could be more suitable. These findings provide a strong genetic foundation for developing high-yielding, early-sown, and climate-resilient wheat cultivars under Central Indian conditions.

Keywords: GCV; genetics; genetic advance; genetic variability; heritability; PCV; plant breeding and quantitative traits.

1. INTRODUCTION

“Wheat (*Triticum aestivum* L.) is a self-pollinated crop belongs to family Gramineae. It is widely grown all over the world as food crop. Wheat is third most produced cereal in the world after rice and maize. China is the world’s largest producer of wheat which produces more than 2.4 billion tonnes of wheat in the last 20 years, around 17% of the total wheat production. Russia is the largest exporter of wheat in the world, which exported more than 7.30 billion tonnes of wheat in 2021 (Anonymous (a) 2022-23). The top 10 wheat producing countries in the world are China, India, Russia, United States, France, Canada, Germany, Pakistan, Australia and Ukraine (Anonymous (b) 2022-23). Every month of the year wheat is harvested somewhere in the world as food crop. In India, wheat is extensively cultivated in North West India, Eastern part, Central plain to some extent Southern peninsular zone. The top wheat producing states in the India are Uttar Pradesh, Punjab, Madhya Pradesh, Haryana, Rajasthan, Bihar, Gujarat, Maharashtra, West Bengal and Uttarakhand. Genus *Triticum* includes many wild species namely *T. monococcum, T. speltoides, T. comosum, T. umbellulatum, T. tauschii, T. dichasian, T. dicoccoides, T. araraticum, T. ovatum, T. kotschyi, T. cylindricum, T. juvenile* etc. some of these species may be found in cultivation today at Lebanan, Syria, northern Israel, Iraq and eastern Turkey. In early agriculture several species of wheat were in cultivation, but in modern agriculture only *T. aestivum* L. (common wheat) and *T. turgidum* L. (durum wheat) are important” (Gupta, 2010). “In India only three species of wheat *viz*., *Triticum aestivum* (Bread wheat), *Triticum turgidum* var. Durum (Durum wheat) and *Triticum dicocum* (emmer wheat) are of economic importance. *Triticum aestivum* and *T. durum* covers 90% and 9% of the total area of wheat respectively. *T. Dicoccum* and *T. monococcum* are collectively covers only less than 1% of the total area of wheat. All the known species of wheat are grouped under three major polyploidies *viz*., diploid (2n=2x=14), tetraploid (2n=4x=28) and hexaploid (2n=6x=42). It involves three genomes, A, B and D, out of which genome ‘A’ is derived from einkorn wheat *(T. urartu)*, ’B’ is form *Aegilops speltoides* & genome ‘D’ belong to a weedy grass *Aegilops tauschii*. “Genetics of morphological traits facilitate the breeder to use the efficient breeding bearing inner potential to stabilized the yield productivity in varying environment. The genetic research done for yield improvement in wheat revealed that the grain yield in this crop is mainly determined by component traits, which they are highly complex and variable. Change in maturity duration permits new crop rotations and often extends the crop area. Development of wheat varieties suitable for late planting permitted rice-wheat rotation, thus breeding for early maturity varieties suitable for different dates of planting may be an important objective in many cases. Modifications of agronomical characteristics such as grain yield, plant height, tillering *etc*. is often desirable, for example dwarf-ness in cereals is generally associated with logging resistance and fertilizer responsiveness. Development of higher yield varieties has permitted its cultivation in new areas. Genetic improvement for quantitative traits depends on the nature and amount of variability present in the genetic material and the extent to which the desirable traits are heritable" (Namrata *et al*., 2016). "The knowledge about genetic variability of yield contributing characters, inter relationship among them and their relation with yield are necessary for an effective crop improvement programme (Ali et al., 2008). The genetic variability could be determined with the help of genetical parameters such as Genetic Coefficient of Variation (GCV), heritability estimates and genetic advance (GA). GCV indicates the relative degree of genetic variability existing for different characters in a population of genotypes. Knowledge about heritability helps the breeders to predict the nature of the succeeding generation, to make an appropriate selection and to assess the magnitude of genetic improvement through selection. In addition, high genetic advance coupled with high heritability offers the most effective condition for selection for a particular trait. Heritability estimates provide the information on the proportion of variation that is transmissible to the progenies in subsequent generations. Genetic advance provides information on expected genetic gain resulting from selection of superior individuals".

2. MATERIAL AND METHODS

The present investigation entitled "Evaluation of Genetic Parameters for Yield and Yield Attributes Traits in Bread Wheat (*Triticum aestivum* L.)" was conducted at the Zonal Agricultural Research Station, Powarkheda, Hoshangabad (M.P.) during the rabi seasons of 2019–20 and 2020–21. The study involved 65 bread wheat genotypes in Randomized Block Design (RBD) with three replications, totalling 195 plots. Each plot measured 1.5 m² with a spacing of 5 cm between plants and 20 cm between rows, and sowing was done at a depth of 3-5 cm. Hoshangabad, now known as Narmadapuram, is located in Madhya Pradesh at 22.75°N and 77.72°E, with an elevation of 278 meters. The district experiences a typical central Indian climate hot and dry summers with temperatures reaching 40-42°C, followed by a monsoon season and mild winters. The average annual rainfall is around 134 cm. Statistical analysis included analysis of variance (ANOVA) as per Panse and Sukhatme (1967) to test the significance of variation among genotypes.

3. RESULT AND DISCUSSION

The analysis of variance conducted for various agronomic traits demonstrated highly significant differences ($p < 0.01$) among treatments, indicating the presence of considerable genetic variability among the wheat genotypes under study. Specifically, the mean squares due to crosses were highly significant for several key agronomic and physiological traits, which highlights the importance of hybridization in enhancing yield and its components *viz*., days to heading (days), days to maturity (days), plant height (cm), peduncle length (cm), spike length (cm), number of grains/spikes, number of spike/plants, number of spikelets/spike, number of effective tillers/plants, biological yield/ plant (g), harvest index (%), spike weight (g), 1000 grain weight (g), chlorophyll content (flow), canopy temperature (flow) and grain yield/plant (g). Similar findings have been reported by researchers such as Bhutto *et al.* (2016), Saleem *et al.* (2016), Kumar *et al.* (2017), Ghaffar *et al*. (2018), Amin and Towfiq (2019), Elahi *et al*. (2020), Prakash *et al.* (2020), Singh *et al*. (2021) and Atsbeha *et al.* (2023).

In a detailed examination of early sowing for sixteen traits, the analysis revealed the following: days to heading averaged at 56.01 days, highlighting an early transition to this critical growth phase, while days to maturity were recorded at 116.79 days, indicating the time taken for the crop to reach full maturity. Plant height was observed at 86.37 cm, showcasing the vertical growth under early sowing conditions, and peduncle length averaged at 34.40 cm, reflecting the length of the stalk holding the spike. Spike length was measured at 8.66 cm, with the number of grains per spike standing at 38.64, illustrating productive spikes. The number of spikes per plant was 8.37, indicating efficient branching, and the number of spikelets per spike was 15.47, showing spike complexity. The number of effective tillers per plant averaged 7.64, highlighting the tillering capacity, and the biological yield per plant was 77.50 g, indicating the total biomass produced. The harvest index was noted at 34.92%, reflecting the efficiency of biomass conversion into grain. Spike weight averaged 2.56 g, 1000 grain weight was measured at 41.56 g, indicating grain bulk weight, and chlorophyll content was 46.72 (flow), suggesting the level of chlorophyll in leaves.

Canopy temperature was recorded at 25.25°c (flow), showing the thermal profile of the crop canopy, and the grain yield per plant was 25.80 g, reflecting the yield of grains per plant. This comprehensive overview emphasizes the growth, development, and yield characteristics of crops under early sowing conditions.

In a comprehensive analysis of early sowing conditions, the data revealed a notable range across sixteen traits. Days to heading varied between 45.00 and 73.00 days, illustrating the variability in reaching the heading stage, while days to maturity spanned from 104.00 to 123.00 days, indicating the maturity period's breadth. Plant height ranged from 71.17 cm to 97.63 cm, showcasing significant variation in growth stature. Peduncle length was observed to vary between 30.27 cm and 38.60 cm, reflecting the diversity in stalk length. Spike length had a range from 7.07 cm to 9.97 cm, and the number of grains per spike showed a fertility range from 31.87 to 47.43 grains. The number of spikes per plant indicated a wide variance from 5.20 to 14.17, while the number of spikelets per spike spanned from 10.23 to 21.51, displaying considerable differences in spikelet formation. The number of effective tillers per plant ranged from 4.17 to 13.30, emphasizing the variability in tillering capacity. Biological yield per plant showed a dramatic range from 42.17 g to 157.87 g, highlighting the potential biomass production variability. The harvest index ranged from 20.36% to 54.97%, indicating efficiency in biomass conversion. Spike weight, 1000 grain weight, chlorophyll content, canopy temperature, and grain yield per plant varied from 1.94 g to 3.31 g, 37.53 g to 47.00 g, 38.55 to 53.80, 23.03°C to 27.31°C, and 14.66 g to 56.34 g, respectively, showcasing a broad range of outcomes in grain weight, chlorophyll levels, canopy temperature, and yield under early sowing conditions. This analysis highlights the diversity and potential adaptability of crops sown early, emphasizing the significant range observed across crucial agricultural traits.

The analysis of genotypic (GCV) and phenotypic (PCV) coefficients of variation revealed that genetic factors predominantly govern the expression of agronomic traits in the studied population, as evidenced by the minimal differences between GCV and PCV values across all traits. In the comprehensive analysis of early sowing conditions, significant insights were derived regarding the genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) across 16 traits. Days to heading displayed a GCV of 10.85% and a PCV of 10.94%, indicating moderate variability in the onset of heading. Days to maturity showed lower variability with a GCV of 4.07% and a PCV of 4.11%. Plant height had a GCV of 8.91% and a PCV of 9.03%, reflecting moderate variation in stature, while peduncle length exhibited a GCV of 5.72% and a PCV of 6.27%. Spike length's GCV was 7.15% with a PCV of 7.35%, and the number of grains per spike had a higher level of variation with a GCV of 12.03% and a PCV of 12.35%. The number of spikes per plant revealed significant variability, with a GCV of 15.42% and a PCV of 15.98%. The number of spikelets per spike, the number of effective tillers per plant, biological yield per plant, and harvest index presented GCV of 8.40%, 11.25%, 18.45%, and 9.67%, respectively, with corresponding PCV indicating moderate to high levels of variation. Spike weight, 1000 grain weight, and chlorophyll content showed moderate variability, with GCV of 7.82%, 6.75%, and 11.22% respectively. Canopy temperature and grain yield per plant had GCV of 4.61% and 17.89%, respectively, highlighting significant variability in yield and lower variability in thermal profiles. This analysis meticulously highlighted the genetic and phenotypic diversity within early sown crops, providing a nuanced understanding of the variability and potential selection within these traits. Overall, the study emphasizes the predominance of additive genetic variance in shaping trait expression, providing a robust framework for designing precision-based breeding initiatives aimed at improving yield and resilience in future crop varieties. Similar findings were also reported by Memon *et al*. (2007), Saleem *et al*. (2016), Rathwa *et al*. (2018) and Kumar *et al*. (2022).

Broad sense heritability, which is ratio of total genotypic variance to total phenotypic variance have been estimated and classified into high (>60%), medium (45-60%) and low (<45%). The heritability analysis for early sowing conditions across 16 traits revealed overwhelmingly high genetic influences, underscoring the significant potential for selective breeding in early sown crops. Both days to heading and days to maturity displayed exceptionally high heritability values at 98.30%, indicating strong genetic control over crop development timings. Plant height also showed substantial genetic determination with a heritability of 97.40%. Peduncle length, with a heritability of 83.10%, and spike length, at 97.90%, further highlighted the genetic influences on plant structure and spike dimensions. The yield components, including the number of grains per spike and number of spikes per plant, exhibited high heritabilities of 97.30% and 96.60%, respectively, indicating significant genetic bases for these traits. Similarly, the number of spikelets per spike and number of effective tillers per plant demonstrated high genetic control with heritabilities of 93.80% and 94.30%. Remarkably, biological yield per plant and harvest index showed near-perfect heritability at 99.90% and 98.90%, respectively, emphasizing almost complete genetic influence over biomass production and its conversion efficiency. Spike weight and 1000 grain weight also indicated strong genetic determinants with heritabilities of 97.30% and 94.50%, respectively. Additionally, chlorophyll content and canopy temperature presented high heritabilities of 94.90% and 86.20%, showcasing significant genetic contributions to physiological traits. Notably, grain yield per plant exhibited an exceptionally high heritability of 99.40%, highlighting the predominant genetic control over grain yield. This comprehensive overview underscores the predominant genetic influence across key agricultural traits in early sown crops, suggesting a robust foundation for enhancing crop performance through genetic improvements. The consistently high h^2 values across all traits imply that phenotypic selection in breeding programs will be highly effective, particularly for traits with $h^2 > 99\%$, where environmental noise is minimal. Even traits with the lowest heritability values retain sufficient genetic determinism to respond favourably to selection, underscoring the potential for accelerated genetic gains in crop improvement efforts. Broad-sense heritability encompasses total genetic variance; partitioning narrow-sense heritability could further clarify the role of additive genetic effects in selection.

Genetic advance was classified into high (>20%), medium (10-20%) and low (<10%) in order to draw conclusions about these parameters. The genetic advance as a percentage of the mean for early sowing across sixteen traits was meticulously analysed, revealing significant potential for improvement through selective breeding. Days to heading (days) showed a notable genetic advance of 22.16%, indicating a considerable scope for enhancing the timing of heading. Days to maturity (days) had a genetic advance of 8.32%, suggesting moderate potential for selection to improve crop maturation times. Plant height (cm) exhibited a genetic advance of 18.11%, highlighting the possibility for increasing plant stature. Peduncle length (cm), with a genetic advance of 10.74%, and spike length (cm) at 17.00%, both indicated significant opportunities for genetic improvement in these structural traits. Number of grains per spike and number of spikes per plant displayed genetic advances of 23.12% and 38.27%, respectively, underscoring the substantial potential for enhancing yield components. Number of spikelets per spike showed a genetic advance of 21.84%, while number of effective tillers per plant stood out with a remarkable genetic advance of 50.50%, suggesting a high potential for improvement in tillering capacity. Biological yield per plant (g) demonstrated an impressive genetic advance of 68.18%, indicating a significant opportunity for increasing biomass production. Harvest index (%), with a genetic advance of 51.82%, highlighted the potential for enhancing the efficiency of biomass conversion into grain. Spike weight (g) exhibited a genetic advance of 24.52%, suggesting a notable scope for improvement in spike weight. 1000 grain weight (g) had a genetic advance of 10.21%, indicating potential for selective breeding to increase grain size. Chlorophyll content (flow) and canopy temperature (flow) showed genetic advances of 14.61% and 7.73%, respectively, pointing to opportunities for enhancing physiological traits. Lastly, grain yield per plant (g) presented a substantial genetic advance of 58.66%, underscoring the considerable potential for increasing grain yield through genetic selection. This analysis underscores the significant opportunities for genetic improvement across a broad range of agronomic and physiological traits in early sown crops, highlighting the effectiveness of selective breeding in advancing crop performance based on the observed genetic advance percentages.

The heritability estimates in broad sense (H^2) along with genetic advance as a percentage of mean (GA%) for sixteen traits under early sowing conditions revealed substantial genetic control and high potential for improvement through selection. Broad-sense heritability values ranged from 83.10% to 99.90%, indicating that most of the observed phenotypic variability was primarily governed by genetic factors with minimal environmental influence. Both days to heading (98.30%) and days to maturity (98.30%) exhibited very high heritability, signifying strong genetic control over phenological development, with corresponding genetic advances of 22.16% and 8.32%, suggesting moderate to substantial potential for selection to alter crop growth duration. Plant height (97.40%) and peduncle length (83.10%) also showed high heritability,

Table 1. Genetic parameters conducted for various agronomic traits

Trait	Grand Mean	Range		Coefficient of variance		Heritability broad sense (%)	GA at 5%	GA as % of Mean
		Max.	Min.	GCV	PCV			
Days to Heading (Days)	56.01	45.00	73.00	10.85	10.94	98.30	12.41	22.16
Days to Maturity (Days)	116.79	104.00	123.00	4.07	4.11	98.30	9.71	8.32
Plant Height (cm)	86.37	71.17	97.63	8.91	9.03	97.40	15.65	18.11
Peduncle Length (cm)	34.40	30.27	38.60	5.72	6.27	83.10	3.69	10.74
Spike Length (cm)	8.66	7.07	9.97	8.34	8.43	97.90	1.47	17.00
Number of grains/spikes	38.64	31.87	47.43	11.38	11.54	97.30	8.93	23.12
Number of spike/plants	8.37	5.20	14.17	18.90	19.23	96.60	3.21	38.27
Number of spikelets/spike	15.47	10.23	21.51	10.95	11.31	93.80	3.38	21.84
Number of effective tillers/plants	7.64	4.17	13.30	25.25	26.01	94.30	3.86	50.50
Biological yield/ plant (g)	77.50	42.17	157.87	33.12	33.14	99.90	52.84	68.18
Harvest index (%)	34.92	20.36	54.97	25.30	25.44	98.90	18.10	51.82
Spike weight (g)	2.56	1.94	3.31	12.07	12.23	97.30	0.63	24.52
1000 grain weight (g)	41.56	37.53	47.00	5.10	5.25	94.50	4.24	10.21
Chlorophyll content (Flow)	46.72	38.55	53.80	7.28	7.47	94.90	6.83	14.61
Canopy temperature (Flow)	25.25	23.03	27.31	4.04	4.35	86.20	1.95	7.73
Grain yield/ plant (g)	25.80	14.66	56.34	28.57	28.65	99.40	15.14	58.66

with respective genetic advances of 18.11% and 10.74%, indicating that these structural traits could be effectively improved through selection. Among the yield components, spike length (97.90%), number of grains per spike (97.30%), number of spikes per plant (96.60%), and number of spikelets per spike (93.80%) exhibited high heritability coupled with high genetic advance values (17.00%, 23.12%, 38.27%, and 21.84%, respectively), highlighting the strong genetic basis of these traits and the possibility of substantial improvement through phenotypic selection. Number of effective tillers per plant recorded a heritability of 94.30% with the highest genetic advance (50.50%), indicating additive gene action and excellent scope for selection in enhancing tillering ability. Similarly, biological yield per plant (99.90%) and harvest index (98.90%) demonstrated nearly complete genetic determination, along with very high genetic advances (68.18% and 51.82%, respectively), signifying their amenability to direct selection for yield improvement. Spike weight (97.30%) and 1000-grain weight (94.50%) also exhibited high heritability with moderate to high genetic advances (24.52% and 10.21%), suggesting good potential for improvement in yield components related to grain filling and spike development. For physiological traits, chlorophyll content (94.90%) and canopy temperature (86.20%) showed high heritability with genetic advances of 14.61% and 7.73%, respectively, indicating a favourable genetic basis for physiological efficiency under early sown conditions. The most striking observation was the exceptionally high heritability of grain yield per plant (99.40%) accompanied by a genetic advance of 58.66%, confirming that this trait is predominantly under genetic control and can be effectively improved through selection. Overall, the concurrent occurrence of high heritability and high genetic advance for most traits indicates the predominance of additive gene effects, suggesting that simple selection methods would be effective for genetic improvement, while traits exhibiting high heritability but moderate genetic advance may be influenced by both additive and non-additive gene actions, warranting a combination of selection and hybridization strategies. These findings collectively underline the strong genetic potential of early sown wheat genotypes for yield and associated traits under Central Indian conditions. High estimates of heritability were indicated that selection pressure should be exercised in early generations. These findings are also in conformity with Saleem *et al*. (2016), Malbhage *et al*. (2020), and Kumar *et al*. (2022). Moderate genetic advance was reported by Kumar *et al*. (1991) for number of grains per spike and biological yield; Rathwa *et al*. (2018) for biological yield and number of productive tillers per plant. Low genetic advance (below 10%) was observed for physiological maturity, 1000 grain weight and plant height Gaur *et al*., (2012) were in the view of these findings.

4. CONCLUSION

The highly significant differences observed through ANOVA for all agronomic and physiological traits confirm the presence of rich genetic diversity, providing a strong foundation for selection and hybridization in wheat improvement programs. The narrow gap between genotypic and phenotypic coefficients of variation (GCV and PCV) across most traits indicated minimal environmental influence and strong genetic control. High broad-sense heritability estimates coupled with high genetic advance as a percentage of mean (GA%) for traits such as grain yield per plant, biological yield, harvest index, number of effective tillers per plant, and number of spikes per plant suggest the predominance of additive gene action, implying that direct phenotypic selection would be highly effective for genetic improvement. Conversely, traits with high heritability but moderate genetic advance, such as peduncle length, canopy temperature, and 1000-grain weight, may involve both additive and non-additive gene effects, indicating that hybridization followed by selection could enhance genetic gains.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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