International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2025): 5.29
IJABR 2025; SP-9(9): 352-354
www.biochemjournal.com
Received: 09-06-2025
Accepted: 14-07-2025

Shivashankaragouda Patil
Ph.D. Scholar, Department of Genetics and Plant Breeding, College of Agriculture, UAS, Raichur, Karnataka, India

SA Desai
Professor, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, India

Suma S Biradar
Professor, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, India

JR Diwan
Professor, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, India

Krishnaraj PU
Professor, Department of Microbiology, College of Agriculture, Dharwad, UAS, Dharwad, Karnataka, India

Basvaraja B Bagewadi
Associate Professor, Department of Biotechnology, College of Agriculture, Dharwad, UAS, Dharwad, Karnataka, India

Corresponding Author:
Shivashankaragouda Patil
Ph.D. Scholar, Department of Genetics and Plant Breeding, College of Agriculture, UAS, Raichur, Karnataka, India

Exploitation of genetic variability in agro-morphological and physiological traits for breeding drought-tolerant wheat genotypes

Shivashankaragouda Patil, SA Desai, Suma S Biradar, JR Diwan, Krishnaraj PU and Basvaraja B Bagewadi

DOI: https://www.doi.org/10.33545/26174693.2025.v9.i9Se.5517

Abstract

The present investigation was carried out to assess the extent of genetic variability and the potential of various agro-morphological and physiological traits in twenty wheat genotypes under moisture stress conditions. The study revealed considerable variation among genotypes for all traits studied, including phenological, yield-contributing, and physiological parameters. High heritability coupled with moderate to high genetic advance was observed for traits such as spike length, thousand grain weight, grain yield per hectare, and leaf waxiness, indicating the predominance of additive gene action and the effectiveness of direct selection for these traits. Physiological indicators like SPAD chlorophyll content and relative water content also exhibited high heritability, confirming their reliability as screening tools for drought tolerance. Conversely, traits such as NDVI I and II showed moderate heritability with low genetic advance, suggesting polygenic control influenced by the environment. The findings underscore the significance of exploiting genetic variability in traits with high heritability and genetic gain for enhancing drought resilience in wheat. The identified genotypes and traits may be effectively utilized in breeding programs aimed at developing drought-tolerant wheat cultivars.

Keywords: Genetic variability, drought tolerance, wheat, agro-morphological traits, physiological traits, heritability, genetic advance, selection indices

Introduction

Wheat (*Triticum aestivum* L.) is one of the most widely cultivated staple food crops globally and plays a crucial role in the food and nutritional security of millions, especially in South Asia. In India, wheat occupies a significant share of the total cropped area and is a key component of the rabi cropping system. However, wheat productivity is increasingly threatened by abiotic stresses, among which moisture stress has emerged as a major constraint in rainfed and limited-irrigation areas. The erratic distribution and delayed onset of rainfall, coupled with rising temperatures, often lead to terminal drought stress that adversely affects growth, development, and grain yield in wheat (Sharma *et al.*, 2023; Bansal and Tiwari, 2023) [16, 4].

Moisture stress affects several physiological and biochemical processes such as leaf expansion, chlorophyll stability, reproductive success, and assimilate partitioning, thereby reducing yield potential. Identifying and selecting genotypes with inherent tolerance to drought is therefore crucial. A key prerequisite for genetic improvement under stress conditions is the presence of sufficient heritable variation in the breeding material. Genetic variability for important traits can be quantified using parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability, and genetic advance as percent of mean (Rani *et al.*, 2022; Gupta *et al.*, 2024; Patil *et al.*, 2024; Supreetha *et al.*, 2023) [14, 6, 1, 19]. Traits exhibiting high heritability coupled with high genetic advance are largely governed by additive gene effects and are thus more amenable to selection in early generations.

In this context, the present study was undertaken to estimate the magnitude of genetic variability among twenty diverse wheat genotypes evaluated under moisture stress. The analysis focused on key agro-morphological and physiological traits including days to 50% flowering, maturity duration, plant height, productive tillers, spike and grain characteristics, physiological indices such as SPAD chlorophyll content, NDVI, relative water content, and ultimately, grain yield per hectare. The findings are expected to guide the selection of drought-resilient genotypes for use in future wheat improvement programs targeting stress-prone regions.

Materials and Methods

The experiment was carried out in AICRP on wheat MARS and experimental consists of 20 genotypes (Table 1). The experiment was laid out split plot based on RCBD design with two replications. The individual plot was 3 m × 1 m in size. The distance maintained between row to row and between plants to plant were 20 cm and 5 cm, respectively. Recommended agronomic package and practices were applied to raise a healthy crop. Data were recorded on various parameters, *viz*., days to 50% flowering (DFF), days to maturity (DM), plant height (PH), number of productive tillers per meter (NPTM), peduncle length (PDL), spike length (SL), number of grains per spike (NGP), thousand grain weight (TW), harvest index (HI), NDVI I, NDVI II, SPAD chlorophyll content (SPAD II), relative water content (RWC), leaf waxiness (LW), and grain yield per hectare (YLD). Data from five plants of each genotype were averaged replication wise and mean data was used for statistical analysis. Mean, range and coefficient of variation (CV) were also estimated. Genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were estimated according to Burton (1953) [5]; heritability in broad sense (h^2b_s) was estimated according to Burton and Devane (1953) [5]; genetic advance (GA) and genetic advance as per cent of mean (GAPM) were calculated by Johnson *et al.* (1955) [10].

Results and Discussion

The analysis of twenty wheat genotypes under moisture stress revealed substantial genetic variability for all traits (Table 2), which is vital for drought-resilient breeding. Days to 50% flowering ranged from 50.00 to 63.00 days, showing low GCV (5.77%) and PCV (6.59%). High heritability (76.48%) and moderate genetic advance (10.39%) indicate the presence of additive genetic control and potential for selection. These findings align with those of Bano *et al.* (2023), who reported similar variability in flowering under drought. Days to maturity exhibited a narrow range (80.00 days to 89.50 days) with high heritability (81.94%) and low genetic advance (8.50%), suggesting limited scope for improvement a pattern consistent with observations by Rathi *et al.* (2022) [15]. Plant height displayed moderate variability (GCV 8.61%, PCV 10.64%) with high heritability (65.54%) and moderate genetic advance (14.37%), indicating a fair response to selection, as also supported by Sharma and Gill (2023) [16]. Productive tillers per meter exhibited genetic variation (GCV 9.52%) with high heritability (68.43%) and moderate genetic advance (16.22%), reinforcing the trait's relevance for yield improvement under water stress (Patel *et al*., 2024) [13]. Peduncle length showed similar moderate variability (GCV 9.40%) and high heritability (63.11%), affirming the results of Khokhar *et al.* (2023) [11], who emphasized its role in assimilate translocation under drought. Spike length ranged from 5.20 to 9.52 cm with high GCV (19.84%) and heritability (82.11%), accompanied by a high genetic advance (37.03%), suggesting strong additive gene action. These results are comparable to those reported by Yousaf *et al.* (2023) [21]. Number of grains per spike revealed moderate variability (GCV 15.03%), high heritability (78.06%), and good genetic gain (27.36%), confirming the findings of Singh and Sheoran (2022) [18]. Thousand grain weight showed GCV of 14.36%, heritability of 81.65%, and high genetic advance (26.73%), suggesting this trait is governed by fixable genetic variation, corroborated by findings of Zafar *et al.* (2023) [22]. Grain yield per hectare, a key economic trait, showed high variability (GCV 20.13%) and heritability (80.44%) along with a high genetic advance (37.20%), indicating excellent prospects for direct selection similar to the results of Hussain *et al.* (2024) [7]. Physiological traits such as SPAD chlorophyll content and relative water content (RWC) demonstrated high heritability (84.55% and 85.86%, respectively) and moderate genetic advance, affirming their utility in drought tolerance screening (Ali *et al*., 2023; Verma *et al*., 2024) [2, 20]. Leaf waxiness recorded very high GCV (36.93%), heritability (80.26%), and genetic advance (68.16%), identifying it as a key selection trait for drought resilience as reported by Jahan *et al.* (2023) [9]. In contrast, NDVI I and II showed moderate heritability but low genetic advance (6.04% and 8.29%, respectively), indicating polygenic control with environmental influence, similar to conclusions drawn by Iqbal *et al.* (2022) [8]. Overall, the observed variability and genetic parameters suggest that traits such as spike length, grain yield, TGW, and waxiness can be prioritized for improvement in wheat breeding under moisture stress (Table 3).

Table 1: List of twenty durum and bread wheat genotypes used for study

1	UAS 446
2	Amruth
3	DWR-2006
4	AKDW-2997-16
5	Bejaga yellow
6	GDP 40
7	UAS-428
8	UAS-347
9	UAS-375
10	HD-2888
11	UAS-334
12	UAS-3020
13	UASBW 11421
14	UASBW 12982
15	UASBW 13039
16	UASBW 12380
17	UASDW 30805
18	UASDW 31156
19	UASDW 30820
20	UASDW31138

Table 2: ANOVA of randomized block design for yield and yield-related traits under moisture stress condition

Source of Variation	MSS														
	DF	DFF	DM	PH	NPTM	PDL	SL	NGP	TGW	NDVI I	NDVI II	SPAD II	RWC	LW	YLD
Treatment	19	22.86	32.39	101.69	124.49	17.91	4.48	55.46	43.92	13.5	7.27	24.68	0.005	3.59	476916
Replication	1	5.63	4.9	25.6	25.6	10.87	1.9	0.49	0.54	0.23	1.86	8.41	0.0004	0.02	741.51
Error	19	3.05	3.22	21.17	23.34	4.05	0.44	6.83	4.44	3.07	1.45	2.07	0.0004	0.39	51698.3
C.V (%)		3.2	2.14	6.25	6.47	7.18	9.26	7.97	6.81	2.83	3.48	4.14	4.1	18.31	9.93

The abbreviations used for the studied traits are as follows: DFF - Days to 50% Flowering, DM - Days to Maturity, PH - Plant Height, NPTM - Number of Productive Tillers per Meter, PDL - Peduncle Length, SL - Spike Length, NGP - Number of Grains per Spike, TW - Thousand Grain Weight, HI - Harvest Index, NDVI I and NDVI II - Normalized Difference Vegetation Index at two different stages, SPAD II - Chlorophyll Content (SPAD Meter Reading), RWC - Relative Water Content, LW - Leaf Waxiness, and YLD - Grain Yield per Hectare

Table 3: Mean and other genetic parameters for yield and yield-related traits under moisture stress condition

	MEAN	MAX	MIN	GCV	PCV	h^2	GA	GAM
DFF	54.58	63.00	50.00	5.77	6.59	76.48	5.67	10.39
DM	80.28	85.50	72.50	5.36	5.82	84.75	8.16	10.16
PH	73.66	90.65	63.55	8.61	10.64	65.54	10.58	14.37
NPTM	74.70	85.00	63.00	9.52	11.51	68.43	12.12	16.22
PDL	28.01	35.61	23.34	9.40	11.83	63.11	4.31	15.38
SL	7.17	9.52	5.20	19.84	21.89	82.11	2.65	37.03
NGP	32.80	40.83	21.50	15.03	17.01	78.06	8.97	27.36
TW	30.94	38.90	24.00	14.36	15.89	81.65	8.27	26.73
NDVI I	61.78	67.50	57.00	3.70	4.66	62.97	3.73	6.04
NDVI II	34.63	38.00	30.50	4.92	6.03	66.74	2.87	8.29
SPAD II	34.72	43.00	27.75	9.69	10.53	84.55	6.37	18.35
RWC	0.47	0.60	0.41	10.09	10.89	85.86	0.09	19.26
LW	3.43	6.00	1.00	36.93	41.22	80.26	2.33	68.16
YLD	2290.28	2977.78	1058.33	20.13	22.45	80.44	851.91	37.20

The abbreviations used for the studied traits are as follows: DFF - Days to 50% Flowering, DM - Days to Maturity, PH - Plant Height, NPTM - Number of Productive Tillers per Meter, PDL - Peduncle Length, SL - Spike Length, NGP - Number of Grains per Spike, TW - Thousand Grain Weight, HI - Harvest Index, NDVI I and NDVI II - Normalized Difference Vegetation Index at two different stages, SPAD II - Chlorophyll Content (SPAD Meter Reading), RWC - Relative Water Content, LW - Leaf Waxiness, and YLD - Grain Yield per Hectare

Conclusion

The present study revealed substantial genetic variability among twenty wheat genotypes evaluated under moisture stress conditions. The presence of high heritability coupled with moderate to high genetic advance for several traits such as spike length, thousand grain weight, grain yield per hectare, and leaf waxiness suggests the predominance of additive gene action, thereby offering significant scope for improvement through direct selection. Similarly, physiological traits like SPAD chlorophyll content and relative water content exhibited high heritability and moderate genetic gain, indicating their relevance as reliable indicators of drought tolerance. In contrast, traits like NDVI I and II recorded moderate heritability but low genetic advance, suggesting the involvement of non-additive gene action and environmental influence. These findings highlight the importance of utilizing traits with high heritability and genetic advance in breeding programs focused on drought resilience. Consequently, traits such as spike length, thousand grain weight, grain yield, and leaf waxiness can be considered key selection indices for enhancing genetic gain in wheat under moisture-limited environments.

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