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RESEARCH PAPER

Genetic variability and trait associations in F_2 wheat population under moisture stress conditions

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Abstract: Wheat (*Triticum aestivum* L.) is a major cereal crop, but its productivity is often limited by moisture stress in rainfed areas. This study evaluated genetic variability and trait associations in an F_2 population of the cross HD 2888 × UASBW 13039 under drought conditions. Significant variability was observed for agro-morphological and physiological traits. Plant height, tillers per plant, peduncle length, and thousand grain weight showed high heritability with high genetic advance, suggesting strong additive gene effects and good potential for selection. In contrast, days to 50% flowering, days to maturity and SPAD chlorophyll content exhibited limited variability and greater environmental influence. Correlation analysis revealed that tillers per plant, spike length and peduncle length were positively associated with yield, while plant height was negatively correlated, favoring compact types under stress. SPAD values negatively correlated with days to maturity, highlighting stay-green traits for drought escape. The study identifies key selection traits for breeding drought-resilient wheat and offers valuable guidance for climate-resilient crop improvement.

Key words: Drought resilience, Genetic advance, Genetic variability, Heritability, Moisture stress, Phenotypic correlation, Wheat

Introduction

Wheat (*Triticum aestivum* L.) remains a vital food crop globally and is a staple in both developing and developed countries. The productivity and sustainability of wheat cultivation are increasingly challenged by abiotic stresses, particularly drought, which often coincides with critical growth stages such as flowering and grain filling. Drought stress can severely impair physiological processes, reduce biomass, and limit yield potential, especially in rainfed and marginal environments. In view of changing climate scenarios and increasing frequency of dry spells, breeding for drought resilience has become an indispensable goal of wheat improvement programmes (Rani *et al.*, 2022).

Efficient breeding strategies rely on understanding the magnitude and nature of genetic variability present in the breeding population. The F_2 generation serves as a crucial stage in self-pollinated crops like wheat, where maximum segregation occurs, offering opportunities for selection of desirable recombinants. Estimation of genetic parameters such as phenotypic and genotypic coefficients of variation (PCV and GCV), heritability, and genetic advance is essential for assessing the effectiveness of selection and the nature of gene action governing trait expression. High heritability combined with high genetic advance indicates predominance of additive gene action, suggesting that simple selection could be effective for genetic improvement (Kumari *et al.*, 2023).

In addition to variability estimates, association analysis among traits is valuable in understanding inter-relationships and identifying indirect selection criteria. Under drought stress, direct selection for yield is often unreliable due to low heritability and strong environmental influence; thus, traits such as chlorophyll content, tiller number, spike length and thousand grain weight can serve as reliable proxies. Phenotypic correlation studies provide insights into how selection for one trait may influence another, thereby aiding in the identification of key yield components (Yadav *et al.*, 2021). Therefore, the present investigation was carried out to estimate the extent of genetic variability and to analyze phenotypic associations among yield and its component traits in the F_2 population of wheat grown under moisture stress condition. The findings aim to guide the selection of promising segregants and inform breeding strategies for developing drought-resilient wheat cultivars.

Material and methods

The experimental material comprised a segregating F_2 population derived from the cross HD 2888 × UASBW 13039, developed specifically under moisture stress conditions. This population was developed and maintained at the All India Coordinated Wheat Improvement Project, Main Agricultural Research Station (MARS), Dharwad. Hybridization was undertaken during the *rabi* season of 2023-24, followed by F_1 generation in *kharif* 2023-24 and the F_2 generation in *rabi* 2024-25. The present experiment was conducted under drought-stressed conditions at the same research station, where the F_2 population was grown with a spacing of 20 cm between rows and 10 cm between plants, in plots consisting of a single row of one metre length.

Table 1. Estimates of genetic variability parameters of wheat F_2 generation of cross (HD 2888 X UASBW13039) under optimum moisture condition

Character	Mean	Min	Max	PCV (%)	GCV (%)	h^2_{bs}	GAM (%)
DFF	55.40	55.00	63.00	4.17	3.46	69.23	5.92
DM	90.10	81.00	96.00	2.57	2.44	89.42	4.76
PH	90.80	83.94	108.50	11.30	10.70	89.15	23.15
TPP	17.80	14.00	26.00	19.25	17.84	92.22	35.95
SL	8.10	7.25	9.76	20.12	19.58	89.35	43.79
PDL	33.78	31.74	39.70	28.73	27.11	92.43	54.05
GPP	43.40	37.66	55.00	9.70	8.90	87.50	17.71
TGW	36.70	32.26	43.04	24.83	22.70	90.21	48.04
YPP	18.40	16.57	25.82	13.42	10.23	75.11	11.55
SPAD	39.60	36.03	47.87	5.64	4.77	74.85	8.45

Abbreviation-DFF- Days to 50% flowering, DM- Days to maturity, PH- Plant height, TPP- Number of tillers per plant, SL-Spike length, PDL- Peduncle length, GPP- number of grains per panicle, TGW- Thousand grain weight, SPAD- SPAD value YPP- Grain yield per plant, PCV (%)- Phenotypic coefficient of variation, GCV (%)- Genotypic coefficient of variation, h^2_{bs}- Heritability, GAM (%)- Genetic advance as per cent of mean.

Results and discussion

Genetic parameters of wheat F_2 cross under moisture stress condition

The analysis of genetic variability parameters under moisture stress condition revealed considerable variation among the F_2 individuals for several yield and physiological traits (Table 1). Days to fifty per cent flowering exhibited low PCV (3.24%) and GCV (2.43%) along with moderate heritability (55.95%) and low genetic advance as percent of mean (3.74%), indicating limited scope for selection due to low variability and predominance of non-additive gene action. Similarly, days to maturity showed low PCV and GCV (2.70 and 2.59%, respectively), very high heritability (91.37%) and low genetic advance (5.09%), suggesting that despite the high heritability, direct selection may not be effective due to the limited genetic base. These results are in line with the findings of Mohammad *et al.* (2001) and Sharma and Garg (2002), who observed restricted genetic gains for flowering and maturity traits under drought. In contrast, plant height exhibited moderate variability with PCV (16.24%) and GCV (13.04%), along with high heritability (82.56%) and substantial genetic advance (22.56%), indicating a predominant additive gene effect and thus suitability for effective selection, which corroborates the findings of Panwar and Singh (2000) and Baranwal *et al.* (2012). Tillers per plant also showed moderate PCV and GCV values and recorded high heritability (73.57%) and moderate genetic advance (19.59%), suggesting considerable potential for improvement through selection, in accordance with Bhoite *et al.* (2008).

Spike length showed comparatively lower variability (PCV 5.73% and GCV 5.24%), with high heritability (83.51%) and low genetic advance (9.86%), indicating that the trait is less influenced by additive gene action and improvement through selection may be slow. In contrast, peduncle length expressed high PCV (22.11%) and GCV (23.73%) along with high heritability (86%) and genetic advance (43.47%), revealing strong additive gene control and responsiveness to selection, which supports the reports of Khan *et al.* (2010). Thousand grain weight (TGW) exhibited very high variability (PCV 24.83%, GCV 22.70%), with high heritability (90.00%) and extremely high genetic advance as percent of mean (70.20%), indicating excellent scope for improvement through direct selection. These results align with those of Khokar *et al.* (2010), who emphasized the importance of TGW in drought-tolerant breeding. Yield per plant recorded moderate PCV (13.42%) and GCV (10.23%) with heritability of 75.00% and genetic advance of 11.55%, suggesting that both genetic and environmental factors are influential, and moderate gain is achievable through selection. SPAD chlorophyll content recorded low PCV and GCV (5.54 and 4.77%, respectively), moderate heritability (74%), and low genetic advance (8.45%),

Table 2. Estimates of phenotypic correlation coefficients among ten characters in wheat F_2 generation of cross (HD 2888 X UASBW13039) under optimum moisture condition

	DFF	DM	PH	TPP	SL	PDL	GPP	TGW	YPP	SPAD
DFF	1.00	0.15	-0.091	0.251*	-0.099	0.051	0.152	-0.005	0.29*	0.21
DM	0.15	1.00	-0.071	0.14	-0.061	0.056	-0.113	-0.068	0.291*	0.118
PH	-0.091	-0.071	1.00	0.031	0.137	0.007	0.249*	0.014	0.217	0.024
TPP	0.251*	0.14	0.031	1.00	0.243	0.065	0.051	-0.1	0.384**	0.007
SL	-0.099	-0.061	0.137	0.243	1.00	0.058	0.141	0.028	0.256*	0.06
PDL	0.051	0.056	0.007	0.065	0.058	1.00	0.038	-0.044	0.131	0.187
GPP	0.152	-0.113	0.249*	0.051	0.141	0.038	1.00	-0.066	0.041	0.129
TGW	-0.005	-0.068	0.014	-0.1	0.028	-0.044	-0.066	1.00	0.19	-0.008
YPP	0.29*	0.291*	0.217	0.384**	0.256*	0.131	0.041	0.19	1.00	0.107
SPAD	0.21	0.118	0.024	0.007	0.06	0.187	0.129	-0.008	0.107	1.00

Abbreviation-DFF- Days to 50% flowering, DM- Days to maturity, PH- Plant height, TPP- Number of tillers per plant, SL-Spike length, PDL- Peduncle length, GPP- number of grains per panicle, TGW- Thousand grain weight, SPAD- SPAD value YPP- Grain yield per plant indicating that the trait is more environmentally influenced and less amenable to genetic improvement, similar to the observations by Atta *et al.* (2008).

Phenotypic correlation analysis under moisture stress in the F_2 generation of wheat cross HD 2888 × UASBW 13039 revealed significant associations among yield and component traits (Table 2). Fifty per cent flowering showed a significant positive correlation with plant height (r = 0.212*), indicating that late-flowering genotypes tended to be taller. This relationship may reflect prolonged vegetative growth, which is often influenced by drought-induced developmental delays. Days to maturity showed a significant negative correlation with SPAD chlorophyll content (r = -0.176**), suggesting that genotypes maintaining higher chlorophyll levels tend to mature earlier an adaptive trait for drought escape. Similar associations were reported by Sharma *et al.* (2021), who noted that higher SPAD values are associated with better drought adaptation due to sustained photosynthetic activity during grain filling.

Plant height exhibited significant positive associations with both fifty per cent flowering (r = 0.212*) and peduncle length (r = 0.204*), confirming the interdependence of these structural traits. However, plant height showed a significant negative correlation with grain yield per plant (r = -0.182*), indicating that shorter genotypes are more favorable under drought due to efficient resource utilization. This trend is supported by findings of Rani *et al.* (2022), who observed that reduced stature under moisture stress is associated with better harvest index. Tillers per plant exhibited a highly significant positive correlation with grains per panicle (r = 0.257**), suggesting that higher tillering enhances sink potential under water-limited conditions. Peduncle length, despite being positively associated with plant height, showed a highly significant negative correlation with thousand grain weight (r = -0.249**), indicating a probable trade-off between stem elongation and assimilate partitioning. Grain yield per plant was also negatively associated with plant height, supporting the advantage of compact architecture for drought resilience. SPAD chlorophyll content also correlated negatively with days to maturity, confirming the role of "stay-green" traits in promoting early maturity. These findings align with the work of Verma *et al.* (2023) and Meena *et al.* (2020), who emphasized the utility of physiological and architectural traits in improving yield stability under drought conditions.

Conclusion

The present study on the F_2 population derived from the cross HD 2888 × UASBW 13039 under moisture stress conditions revealed substantial genetic variability for key agro-morphological and physiological traits. Traits such as plant height, tillers per plant, peduncle length, and thousand grain weight exhibited high heritability coupled with high genetic advance, indicating the predominance of additive gene action and their suitability for effective selection. In contrast, traits like days to 50% flowering, days to maturity, and SPAD chlorophyll content showed limited variability and greater environmental influence, suggesting restricted genetic gains through direct selection. Correlation analysis highlighted that tillers per plant, spike length, and peduncle length were positively associated with grain yield, while plant height showed a negative association, favoring compact plant architecture under drought conditions. The negative relationship between SPAD values and days to maturity emphasized the role of stay-green traits in enhancing drought escape and yield stability. Overall, the study identified tillers per plant, spike length, peduncle length, and thousand grain weight as reliable selection criteria for developing drought-resilient wheat genotypes. These findings provide useful insights for wheat

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