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RESEARCH ARTICLE

Promising segregants for enhanced grain yield under moisture stress in bread wheat (*Triticum aestivum* L.)

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Abstract

This study aimed to identify transgressive segregants with enhanced yield under moisture stress condition. A population of UAS 375 × HTWYT_66 was developed by hybridizing UAS 375 (a rainfed variety) with HTWYT_66 (NDVI > 0.74 under stress). A total of 125 $F_{3:4}$ progeny lines were evaluated under restricted irrigation during the *rabi* 2023-24 season, revealing significant genetic variation. Traits such as peduncle length, flag leaf length, grains per spike, and grain yield exhibited high heritability coupled with high genetic advance, indicating the predominance of additive gene action, which makes them ideal for selection. Grain yield was positively correlated with plant height, peduncle length, flag leaf length, tillers per plant, and thousand-grain weight. Conversely, early maturity showed a negative correlation with grain yield, suggesting that early-maturing varieties perform better under moisture stress conditions. Path coefficient analysis revealed strong direct effects of thousand-grain weight (0.409), peduncle length (0.253), and plant height (0.129) on grain yield, emphasizing these traits as key targets for selection. Principal component analysis indicated that three components collectively explained 61.5% of the observed variation in the UAS 375 × HTWYT_66 population. Selection indices incorporating traits such as plant height, thousand-grain weight, and grain yield demonstrated high genetic gains with a minimal number of characters involved. Promising segregants, including F_4:23-24 (11) and F_4:23-24 (71), exhibited high yields under moisture stress, making them potential donor lines for breeding programs aimed at enhancing yield in such challenging conditions.

Keywords

moisture stress; principal components; restricted irrigation; selection indices; transgressive segregants

Introduction

While nearly 3,00,000 plant species are potentially edible for humans, only about 100 of them are primarily cultivated (1). Remarkably, just three crops—maize, rice, and wheat—account for nearly 60% of the global human caloric intake. Among these, wheat serves as a primary nutritional source for 36% of the global population and is grown in approximately 70% of the world's agricultural regions (2). It contributes around 20% of total calorie and protein intake (3). Beyond its caloric value, wheat provides essential carbohydrates (71%), protein (13%), dietary fiber (12%), fat (2%), vitamins, and minerals that are vital for a balanced diet.

As a major staple crop, wheat plays a critical role in ensuring global food and nutritional security. It not only provides substantial calories but also contributes significantly to dietary protein, offering higher nutritional value compared to other staple cereals like rice and maize (4). Thus, enhancing wheat productivity is imperative to meet the needs of a growing population. However, the ability to sustain wheat production is increasingly challenged by moisture stress, which is becoming more frequent and severe due to climate change and human activities. Wheat crops require between 300 and 500 mm of water, a significantly higher amount than crops such as maize (5). Under moisture stress, wheat experiences a 9.4% decline in germination percentage, accompanied by a delay of 1.91 to 2.05 days in germination (6,7). In developing countries, water scarcity limits wheat yields to only 50-90% of their irrigation potential.

To meet the rising demand for wheat and address the challenges posed by climate change, it is essential to develop new varieties capable of achieving high yields under moisture stress conditions. The success of breeding efforts to improve moisture stress tolerance in wheat depends on the genetic variability available. Utilizing genetically diverse parents validated for moisture stress responsiveness allows researchers to better understand the variability within populations, facilitating the selection of superior genotypes with enhanced stress tolerance. This study aimed to gather foundational data on the variability of grain yield under restricted irrigation by examining 125 F3:4 progeny lines derived from the cross UAS 375 × HTWYT_66. Morphological traits, yield, and yield-contributing characteristics were assessed under moisture stress conditions to identify high-performing lines (segregants) suited for such environments.

Materials and Methods

The field experiment was conducted during the *rabi* season of 2023-24 at the All India Coordinated Research Project on Wheat, Main Agricultural Research Station, University of Agricultural Sciences, Dharwad. This is situated at 150 29’ north latitude and 740 59’ East longitude, at an altitude of 689 m above mean sea level. Dharwad falls under the Northern Transitional Zone (Zone-8) of the Karnataka’s agro-climatic zones and is characterized by black soil type (Vertisol).

The experiment material comprised 125 $F_{3:4}$ progeny lines derived from the cross UAS 375 × HTWYT _66 of bread wheat. These lines were evaluated alongside seven standard checks (UAS 347, UAS 375, CWYT_609, HTWYT_66, HTWYT_67, UAS 446, UAS 466) known for their suitability to moisture stress conditions and their popularly in the Central and Peninsular zone of India. An Augmented Block Design (ABD) was used to evaluate the genotypes under restricted irrigation conditions, with irrigation provided only twice during the entire crop season, once at 25 days after sowing (DAS) during the Crown Root Initiation (CRI stage) and again at 45 DAS during the heading stage. Each entry was grown with a line spacing of 20 cm, and the plot size consisted of six rows, each measuring 3 meters in length. The genotypes were grown following recommended agronomic practices, and all plots were protected against weeds, pests, and diseases using agrochemical applications as necessary. Sprinkler irrigation, with an average discharge rate of 300 litres per hour, was applied at the specified intervals during the crop’s growth period.

Data were recorded for the traits *viz.*, days to 50% flowering, days to maturity, plant height, peduncle length, flag leaf length, spike length, grains per spike, tillers per plant thousand-grain weight, and grain yield, all other observations were taken from ten randomly selected, tagged, and competitive plants per $F_{3:4}$ germplasm lines.

Statistical analysis

The statistical analyses for genetic variability, correlation, path analysis, and selection indices were performed using various packages such as augmented RCBD, metan, lavaan, and selection index from R studio version 4.4.0. Principal component analysis was performed using GRAPES version 1.0.0.

Results and Discussion

The analysis of variance showed significant differences among treatments, indicating substantial genetic variation, which is crucial for population evolution and adaptation. This variation allows breeders to select individuals with desirable traits. Minimal block-to-block variation, as evidenced by block-eliminating treatments, suggests a homogenous experimental condition (Table 1). These findings align with prior studies (8,9).

Genetic variability studies

Moderate to high values of GCV and PCV were observed for traits such as plant height, peduncle length, flag leaf length, spike length, grains per spike, thousand-grain weight, and grain yield, indicating a broad range of variation and potential for genetic improvement (Table 2). Similar results were reported for tillers per plant in previous studies (10, 11), while other studies (12, 13) reported high GCV values for grain yield. Additionally, low GCV and PCV for days to 50% flowering and maturity align with findings from study (14).

Heritability and genetic advance

High heritability combined with high genetic advance was observed for traits like plant height, peduncle length, flag leaf length, grains per spike, thousand-grain weight, and grain yield, indicating strong additive gene action (Table 2). These traits are highly valuable for selection and improvement programs. Similar findings were reported for grain yield in other studies (8,15).

Correlation coefficients

At the phenotypic level, traits such as thousand-grain weight (0.58), peduncle length (0.44), spike length (0.44), plant height (0.37) number of tillers per plant (0.34), grains per spike (0.31), and flag leaf length (0.25) exhibited

Table 1. Analysis of variance for morphological and grain yield related traits in the $F_{3:4}$ population of cross UAS 375 × HTWYT_66

Source	df	PH	PL	FLL	SL	NTP	TGW	GS	DTF	DTM	GY
Treatment (ignoring Blocks)	131	107.65**	8.15**	13.03**	2.49**	0.42**	56.36**	61.71**	29.28**	30.04**	3.72**
Treatment: Check	6	373.82**	64.22**	115.71**	12.53**	2.59**	166.66**	56.59**	136.83**	294.92**	5.20**
Treatment: Test	124	93.37**	4.84**	5.16**	2.03*	0.29*	51.41**	55.07**	24.29**	17.21**	3.64**
Treatment: Test vs. Check	1	281.42**	82.26**	372.33**	0.01ns	3.28**	8.02ns	915.50**	3.15ns	31.76*	5.27**
Block (eliminating Treatments)	4	27.42^{ns}	0.99^{ns}	0.83^{ns}	1.95^{ns}	0.13^{ns}	9.73^{ns}	15.79^{ns}	6.46^{ns}	3.36^{ns}	1.55^{ns}
Residuals	24	23.21	1.34	0.94	1.06	0.13	8.45	7.02	5.76	6.92	0.62

PH: Plant height, PL: Peduncle length, FLL: Flag leaf length, SL: Spike length, NTP: number of tillers per plant, TGW: 1000 grain weight, DTF: days to fifty per cent flowering, DTM: days to maturity, GY: grain yield(t/ha)

** = significant at 5% level of probability, * = significant at 1% level of probability, ^{ns} =Nonsignificant

Table 2. Genetic variability parameters for morphological and grain yield traits in $F_{3:4}$ population of cross UAS 375 × HTWYT_66

Trait	Mean	Min	Max	GCV	PCV	h_{bs}(%)	GA	GAM (%)
Days to fifty per cent flowering	55	42	67	7.81	8.94	76.29	7.76	14.06
Days to maturity	94	80	106	3.4	4.4	59.78	5.12	5.43
Plant height (cm)	71.24	50.64	89.92	11.67	13.46	75.14	14.98	20.87
Peduncle length (cm)	12.01	6.04	17.07	15.95	18.77	72.25	3.28	27.97
Flag leaf length (cm)	14.32	8.84	21.43	14.99	16.56	81.85	3.84	27.97
Spike length (cm)	8.55	5.27	13.14	11.48	16.64	47.6	1.4	16.34
No. of tillers/plant	3	2	5	15.03	20.2	55.37	0.62	23.08
Grains per spike	42	28	64	16.41	17.57	87.25	13.36	31.63
1000 grain wt. (gm)	42.023	26.636	60.774	15.63	17.1	83.55	12.36	29.47
Grain yield (t/ha)	2.05	0.58	3.55	34.88	38.32	82.84	3.26	65.5

GCV = Genotypic coefficient of variation, PCV = Phenotypic Coefficient of Variation, GA = Genetic advance, GAM = Genetic advance as percent mean, h_{bs}= Heritability in broad sense

significant positive correlation with grain yield (Fig.1). Conversely, negative correlations were noted between grain yield with both days to 50% flowering and days to maturity, emphasizing earliness as a critical strategy for moisture stress tolerance, which is consistent with earlier findings (16,17).

Path coefficient analysis

Path analysis indicated positive direct effects of plant height, peduncle length, flag leaf length, spike length, tillers per plant, thousand-grain weight, and grains per spike on grain yield. Thousand-grain weight (0.409) had the highest direct effects, followed by peduncle length (0.253) and plant height (0.129), as shown in (Table 3). This highlights thousand-grain weight as a key trait under moisture stress, as it reflects the genotype's ability to produce higher yields by accumulating photosynthates through various drought tolerance mechanisms. Consequently, this trait should be prioritized in selection programs for improved grain yield. The residual effect of 0.259 suggests that approximately 70% of the variability in grain yield was explained by the traits analysed.

Principal component analysis (PCA)

10 principal components were identifiedwith the first three explaining 61.59% of the total variation in the UAS 375 × HTWYT_66 cross.PC1, accounting for 34.81% of the variance, was influenced primarily by grain yield (0.457), spike length (0.387), and grains per spike (0.345). PC2 explained 15.25% of the variance, driven by days to 50% flowering (0.582) and maturity (0.512), while PC3 accounted for 11.51% of the variance, with contributions from grains per spike (0.438), flag leaf length (0.26), and

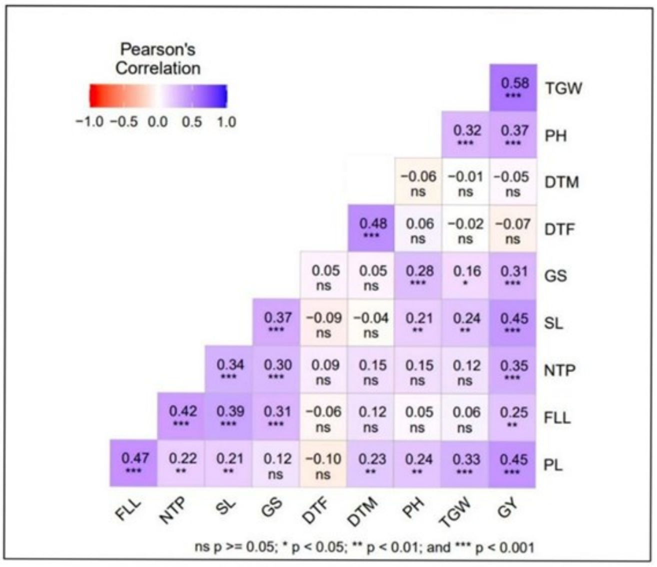

Fig. 1 Heat map depicting correlation of grain yield and its attributing traits in population UAS 375 × HTWYT_66.

Table 3. Direct and indirect effects of yield attributing characters on grain yield per plot in the cross UAS 375 × HTWYT_66

	PH	PL	FLL	SL	NTP	TGW	GS	DTF	DTM	r
PH	**0.129**	0.062	0.004	0.033	0.029	0.108	0.047	-0.0001	0.0004	0.3744***
PL	0.031	**0.253**	0.010	0.030	0.020	0.137	0.014	0.006	-0.0005	0.4467***
FLL	0.018	0.077	**0.033**	0.044	0.036	0.036	0.046	-0.001	-0.0003	0.2514***
SL	0.037	0.067	0.013	**0.115**	0.040	0.128	0.060	-0.003	-0.0005	0.4455***
NTP	0.031	0.043	0.010	0.038	**0.119**	0.098	0.049	-0.005	-0.0005	0.3453***
TGW	0.034	0.084	0.002	0.036	0.028	**0.409**	0.019	-0.0006	-0.0001	0.5839**
GS	0.048	0.029	0.012	0.054	0.046	0.063	**0.127**	-0.004	-0.0004	0.3115***
DTF	0.0004	-0.04	0.001	0.008	0.015	0.006	0.014	-**0.042**	-0.0014	-0.0718^{ns}
DTM	-0.014	0.038	0.003	0.017	0.019	0.012	0.014	-0.017	-**0.0035**	-0.0457^{ns}

plant height (0.211) (Table 4). These findings align with (18,19).

The G-T (Genotype × trait) biplot, which plots PC1 against PC2, highlights genotypes based on their genetic variation and trait importance as shown in Fig.2. Longer vectors indicate greater trait variability, while genotype placement along vectors highlights trait relevance. For example, genotypes such as 79, 33, 6, 56, 5, and 86, which are farther from the axis of differentiation, exhibit distinct or extreme trait values, making them promising candidates for breeding programs. Conversely, genotypes like 69, 27, 102, 82, and 75, positioned near the origin, display moderate and consistent trait performance without significant variation.

Selection indices

Selection indices assign weights to traits to identify desirable genotypes. Discriminant function analysis was used to select genotypes based on combinations of traits. A total of sixty-three selection indices were constructed using traits with positive direct effects and significant correlations. Among these traits, thousand- grain weight, plant height, and grain yield were identified as key traits due to their strong positive correlations and high direct effects. Plant height (X1) exhibited a genetic gain of 14.99%, surpassing grain yield (3.26%).

The greatest genetic gain (26.78%) was achieved by selecting for plant height (X1) and thousand-grain weight (X5). Incorporating three traits—plant height (X1), thousand-grain weight (X5), and grain yield (X6)—increased genetic advance to 29.44%.The highest genetic gain of 32.50% was observed when six traits were considered: plant height (X1), thousand-grain weight (X5), grain yield (X6), peduncle length (X2), flag leaf length (X3), and spike length (X4) (Table 5a and Table 5b). These findings align with earlier studies (20), which reported that selection effectiveness improves as the number of traits considered increases.

Table 4. Factors loading for eigenvalues representing phenotypic diversity under cross UAS 375 × HTWYT_66

Factors	PC1	PC2	PC3
Plant height	0.313	-0.094	0.211
Peduncle length	0.315	-0.221	-0.361
Flag leaf length	0.299	0.07	0.26
Spike length	0.387	0.085	0.14
Number of tillers plant^{-1}	0.326	0.249	0.181
Thousand grain weight	0.327	-0.18	-0.41
Grains per spike	0.345	0.196	0.438
Days to 50% flowering	0.037	0.582	-0.234
Days to maturity	0.103	0.512	-0.484
Grain yield	0.457	-0.17	-0.193
Eigen value	2.747	1.575	1.211
Percentage of variance	27.465	15.748	12.113
Cumulative percentage of variance	27.465	43.213	55.326

PC = Principal components

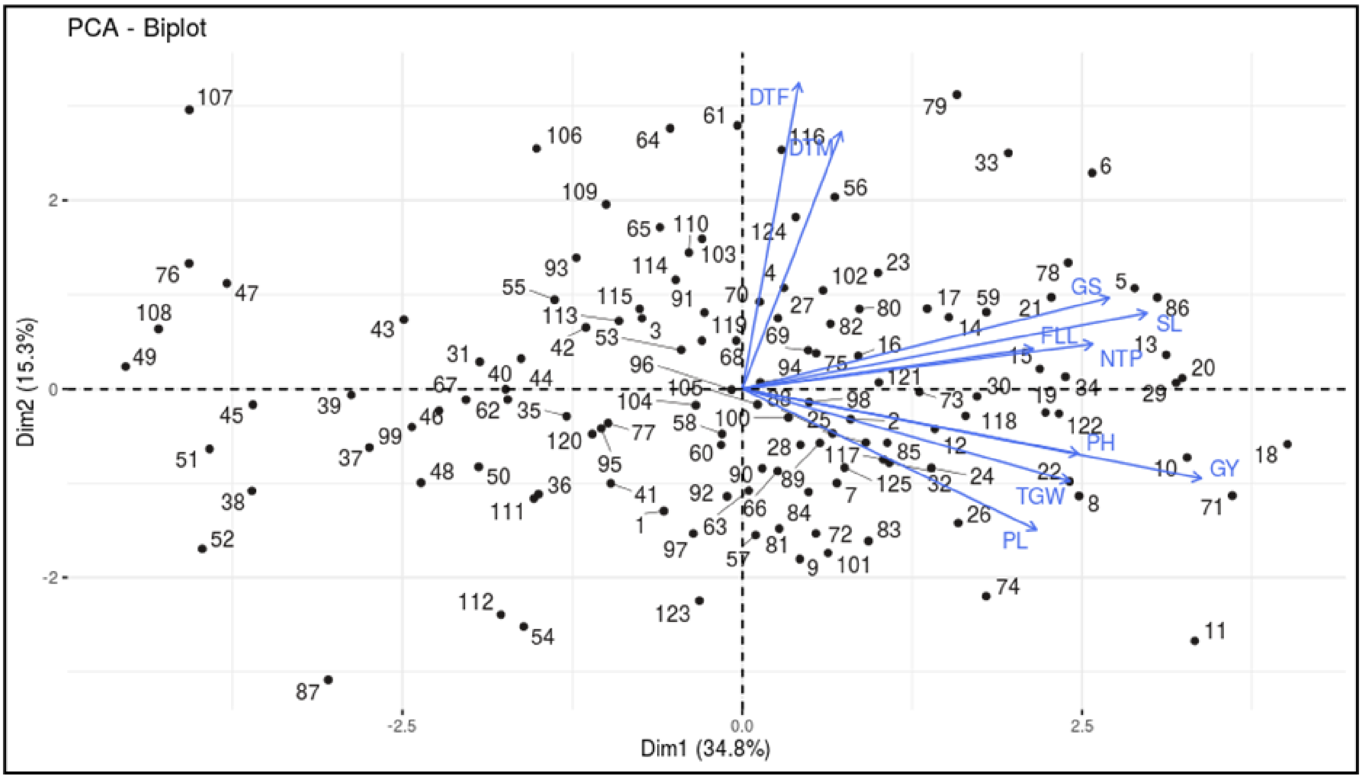

Fig. 2 PCA Biplot and distribution of genotypes under moisture stress conditions in cross UAS 375 × HTWYT_66.

However, to optimize breeding efforts, focusing on fewer key traits—such as plant height, thousand-grain weight, and grain yield—can achieve significant genetic gains. For instance, using these traits resulted in a genetic advance of 29.44% with a relative efficiency of 790.38%.

Transgressive segregants

Transgressive segregation is a phenomenon where offspring in the F_2 or later generations exhibit traits that go beyond the range seen in either parent.

In the current study, desirable transgressive segregants were identified, showcasing the accumulation of favourable alleles from the diverse parents involved in hybridization.

Table 6 summarizes the frequency of transgressive segregants across various traits, based on an analysis of 125 lines. For grain yield, 50 segregants (40%) exceeded the better parent, UAS 375 (2.44 t ha^{-1}). Similarly, a study (21) reported 9 to 9.52% transgressive segregants for grain yield. Regarding plant height, 30 lines (24%) surpassed the better parent, HTWYT_66 (74.43 cm), highlighting their superior root architecture under moisture stress. For peduncle length, 47 lines (37.6%) were identified as transgressive segregants compared to UAS 375 (12.38 cm).

In terms of flag leaf length, only 6 lines (4.8%) exceeded UAS 375 (17.94 cm). For spike length, 48 individuals (38.4%) surpassed UAS 375 (8.81 cm). Regarding the number of tillers per plant, 54 lines (43.2%) exceeded the better parent, while 31 lines (24.8%) showed higher thousand-grain weight than the better parent, HTWYT_66 (45.908 g). Regarding the number of grains per spike, 6 lines (4.8%) surpassed HTWYT_66 (50 grains). Furthermore, 55 lines (44%) reached 50% flowering in 53 days or less, while 31 lines (24.8%) matured within 92 days or fewer, both outperforming their respective better parent (HTWYT_66)

These findings suggests that UAS 375 contributed favourable alleles for traits such as peduncle length, flag leaf length, spike length, number of tillers per plant, and grain yield. Meanwhile HTWYT_66 provided desirable alleles for plant height, thousand-grain weight, grains per spike, days to 50% flowering, and days to maturity.

Table 7 highlights promising segregants, such as F_4:23-24 (11) and F_4:23-24 (71), which exhibited a combination of seven favourable traits alongside high grain yield. PCA analysis further highlighted F_4:23-24 (71) as the most promising segregants (Fig.3), showing significant contributions to trait variation. Additionally, traits such as spike length, thousand-grain weight, and peduncle length showed a strong correlation with grain yield based on cosine angles.

Table 8 showcased the mean performance of the identified segregants, comparing them with seven standard checks across all yield-related and yield-contributing characters.

Conclusion

Our findings demonstrated that progeny from diverse crosses displayed a wide range of heterogeneity, thereby increasing the potential to isolate high-yielding segregants in subsequent generations. In this context, promising segregants were successfully identified within the $F_{3:4}$ populations, benefiting from the accumulation of favourable genes contributed by the diverse parents involved in the UAS 375 × HTWYT_66 hybridization.

Genotypes such as F_4: 23-24 (11) and F_4: 23-24 (71) demonstrated early maturing, taller plant stature, and

Table 5a. Selection indices for the population UAS375 × HTWYT_66

S. No.	Selection index	Discriminant function	Expected genetic advance	Relative efficiency
1.	X1	0.9669X1	14.99	506.79
2.	X2	0.8684X2	3.28	109.06
3.	X3	0.4658X3	1.40	31.35
4.	X4	0.7673X4	0.62	28.58
5.	X5	0.9929X5	12.36	392.24
6.	X6	0.962X6	3.26	100.15
7.	X1.X2	0.9719 + 0.8024	20.13	540.28
8.	X1.X3	0.9826 + 0.5557	19.59	525.91
9.	X1.X4	0.9707 + 0.7844	19.29	517.79
10.	X1.X5	0.9655 + 1.0034	26.78	718.98
11.	X1.X6	0.9632 + 1.0499	20.83	559.23
12.	X2.X3	0.9056 + 0.4582	4.57	122.64
13.	X2.X4	0.8765 + 0.849	4.40	118.09
14.	X2.X5	0.8738 + 1.0044	16.34	438.72
15.	X2.X6	0.8535 + 1.0376	6.80	182.50
16.	X3.X4	0.4803 + 1.0825	2.14	57.56
17.	X3.X5	0.5018 + 1.0161	15.32	411.22
18.	X3.X6	0.4185 + 1.1106	4.80	128.88
19.	X4.X5	0.7187 + 0.9969	14.87	399.21
20.	X4.X6	0.7597 + 0.9889	4.31	115.68
21.	X5.X6	1.0005 + 0.9505	17.30	464.50
22.	X1.X2.X3	0.9864 + 0.8169 + 0.5676	20.87	560.16
23.	X1.X2.X4	0.9735 + 0.8079 + 0.8827	20.55	551.73
24.	X1.X2.X5	0.9673 + 0.7985 + 1.0206	28.34	760.77
25.	X1.X2.X6	0.9596 + 0.7426 + 1.1917	22.33	599.54
26.	X1.X3.X4	0.9809 + 0.583 + 1.0136	20.04	537.95
27.	X1.X3.X5	0.9767 + 0.5999 + 1.0185	27.65	742.29
28.	X1.X3.X6	0.9715 + 0.5014 + 1.161	21.66	581.54
29.	X1.X4.X5	0.9701 + 0.7225 + 1.0058	27.19	730.00
30.	X1.X4.X6	0.9663 + 0.7113 + 1.0762	21.29	571.48
31.	X1.X5.X6	0.9633 + 0.9947 + 1.0523	29.44	790.38
32.	X2.X3.X4	0.9024 + 0.4629 + 1.1616	5.09	136.66
33.	X2.X3.X5	0.8901 + 0.4827 + 1.027	17.07	458.22
34.	X2.X3.X6	0.8371 + 0.377 + 1.205	7.66	205.58
35.	X2.X4.X5	0.8825 + 0.7805 + 1.0067	16.63	446.35
36.	X2.X4.X6	0.8556 + 0.7814 + 1.0608	7.25	194.73
37.	X2.X5.X6	0.8695 + 1.0015 + 1.0152	19.20	515.51
38.	X3.X4.X5	0.5326 + 0.9789 + 1.0146	15.63	419.64
39.	X3.X4.X6	0.4516 + 0.9795 + 1.1027	5.46	146.48
40.	X3.X5.X6	0.4949 +1.0033 +1.0737	18.12	486.34
41.	X5.X5.X6	0.7085 + 0.9981 +0.9893	17.62	473.09
42.	X1.X2.X3.X4	0.9831 + 0.8173 +0.5849 + 1.1093	21.33	572.60
43.	X1.X2.X3.X5	0.9786 + 0.801 +0.5952 + 1.0357	29.21	784.24
44.	X1.X2.X3.X6	0.9687 + 0.7247 +0.4624 + 1.3201	23.18	622.32
45.	X1.X2.X4.X5	0.9702 + 0.8047 +0.8038 + 1.0217	28.76	771.99
46.	X1.X2.X4.X6	0.9625 + 0.7437 +0.7286 +1.2159	22.80	612.01
47.	X1.X2.X5.X6	0.9595 + 0.7583 + 0.9948 + 1.1859	31.12	835.51
48.	X1.X3.X4.X5	0.9767 + 0.6378 + 0.92 + 1.0176	28.09	753.98
49.	X1.X3.X4.X6	0.9717 + 0.5405 + 0.8975 + 1.1611	22.15	594.58
50.	X1.X3.X5.X6	0.9703 + 0.5794 + 0.9972 + 1.1407	30.36	815.09
51.	X1.X4.X5.X6	0.9671 + 0.6549 + 0.992 + 1.0906	29.88	802.03
52.	X2.X3.X4.X5	0.8912 + 0.5049 + 1.049 + 1.0247	17.40	467.16
53.	X2.X3.X4.X6	0.8418 + 0.4078 + 1.0102 + 1.1914	8.19	219.93
54.	X2.X3.X5.X6	0.8533 + 0.4533 + 1.0043 + 1.157	20.02	537.46
55.	X2.X4.X5.X6	0.871 + 0.7327 + 0.9994 + 1.0499	19.54	524.47
56.	X3.X4.X5.X6	0.5333 + 0.9109 + 1.0023 + 1.0752	18.48	496.05
57.	X1.X2.X3.X4.X5	0.9772 + 0.8036 + 0.6245 + 1.0055 + 1.0341	29.66	796.11
58.	X1.X2.X3.X4.X6	0.9686 + 0.7284 + 0.5 + 0.9212 + 1.3164	23.67	635.51
59.	X1.X2.X3.X5.X6	0.9674 + 0.7407 + 0.5405 + 0.9974 + 1.2914	32.05	860.30
60.	X1.X2.X4.X5.X6	0.9631 + 0.7584 + 0.6744 + 0.9922 + 1.2219	31.56	847.28
61.	X1.X3.X4.X5.X6	0.9714 + 0.6234 + 0.8256 + 0.9956 + 1.1507	30.82	827.30
62.	X2.X3.X4.X5.X6	0.8572 + 0.4892 + 0.9443 + 1.0037 + 1.1523	20.39	547.41
63.	X1.X2.X3.X4.X5.X6	0.9681 + 0.7434 + 0.5828 + 0.8517 +0.996 + 1.2973	32.50	872.59

Table 5b. Highest selection efficiencies with the characters combinations in cross UAS375 × HTWYT_66

Characters in the index	Relative efficiency (%)
Plant height	**506.79**
Plant height + Thousand grain weight	**718.98**
Plant height + Thousand grain weight + Grain yield	**790.38**
Plant height + Thousand grain weight + Grain yield + Peduncle length	**835.51**
Plant height + Thousand grain weight + Grain yield + Peduncle length + Spike length	**860.30**
Plant height + Thousand grain weight + Grain yield + Peduncle length + Spike length + tillers plant^{-1}	**872.59**

Table 6. Frequency of transgressive segregants for 10 traits in $F_{3:4}$ population of UAS375 ×HTWYT_66

Trait	$F_{3:4}$ Population			Parents		Transgressive segregants over Better Parent
	Highest	Lowest	population mean	Highest	Lowest	
PH	89.92	50.64	71.95	74.43(HTWYT_66)	59.71(UAS375)	30(24%)
PL	17.07	6.04	11.63	12.38(UAS375)	8.64(HTWYT_66)	47(37.6%)
FLL	21.43	8.84	13.52	17.94(UAS375)	11.01(HTWYT_66)	6(4.8%)
SL	13.13	5.85	8.55	8.81(UAS375)	7.51(HTWYT_66)	48(38.4%)
NTP	4.00	2.00	3.00	3.00(UAS375)	2.00(HTWYT_66)	54(43.2%)
TGW	60.77	26.63	41.90	45.90(HTWYT_66)	37.28(UAS375)	31(24.8%)
GS	64.00	28.00	42.00	50.00(HTWYT_66)	47.00(UAS375)	6(4.8%)
DTF	67.00	42.00	55.00	56.00(UAS375)	53.00(HTWYT_66)	55(44%)
DTM	106.00	80.00	94.00	102.00(UAS375)	92.00(HTWYT_66)	31(24.8%)
GY	3.55	0.58	2.09	2.44(UAS375)	1.24(HTWYT_66)	50(40%)

Table 7. Promising transgressive segregants in $F_{3:4}$ having combination of desirable traits in UAS 375 × HTWYT_66

S.No.	Transgressive segregants	GY in combination with	Combination of desirable traits with GY
1	F_4:23-24 (5)	PL+SL+NTP+TGW	4
2	F_4:23-24 (8)	PL+SL+NTP+TGW+DTF	5
3	F_4:23-24 (10)	PH+PL+SL+NTP+TGW	5
4	F_4:23-24 (11)	PH+PL+SL+NTP+TGW+DTF+DTM	7
5	F_4:23-24 (13)	PH+PL+SL+NTP+TGW	5
6	F_4:23-24 (17)	PL+NTP	2
7	F_4:23-24 (18)	PH+PL+SL+NTP+TGW	5
8	F_4:23-24 (19)	PL+SL+NTP+TGW+DTF	5
9	F_4:23-24 (20)	PH+PL+FLL+SL+NTP	5
10	F_4:23-24 (25)	PH+FLL+NTP+GS+DTF+DTM	6
11	F_4:23-24 (71)	PH+PL+SL+NTP+TGW+DTF+DTM	7
12	F_4:23-24 (74)	PH+PL+TGW+DTF+DTM	5
13	F_4:23-24 (81)	PL+NTP+DTF+DTM	4
14	F_4:23-24 (86)	PL+SL+TGW+GS	4
15	F_4:23-24 (101)	PL+TGW+DTF	3

robust root architecture, traits that are particularly advantageous under moisture stress condition. These genotypes transgressed the better parent for traits *viz.,* peduncle length, spike length, tillers per plant, and high yielding.

Therefore, these genotypes hold significant potential as donor lines for breeding programs aimed at improving moisture stress tolerance. Their integration into breeding strategies can be further enhanced by utilizing trait-specific markers associated with drought tolerance through marker-assisted selection (MAS), thereby facilitating the development of superior drought-resilient varieties.

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Authors' Contributions

BLS participated in drafting the original manuscript, review collection, tables and figures preparation. UG participated in the review collection and correction, tables and figures preparation. KDL carried our review correction and supervised the process. All authors read and approved the final manuscript.

Compliance with Ethical Standards

Conflict of interest: Authors do not have any conflict of

Table 8: Mean performance of the identified transgressive segregants in $F_{3:4}$ population of UAS375 × HTWYT_66

S.No.	Segregants	PH	PL	FLL	SL	NTP	TGW	GS	DTF	DTM	GY
1.	F_4:23-24 (5)	55.02	14.22	13.93	9.35	4	55.331	44	58	103	2.654
2.	F_4:23-24 (8)	52.65	15.54	12.71	12.89	3	56.477	43	48	96	3.416
3.	F_4:23-24 (10)	81.25	13.97	10.34	11.54	4	55.211	41	55	95	3.54
4.	F_4:23-24 (11)	89.34	13.54	17.05	10.54	3	49.211	49	48	84	3.472
5.	F_4:23-24 (13)	89.92	14.14	15.01	10.22	3	48.936	47	57	96	3.501
6.	F_4:23-24 (17)	59.68	13.79	12.73	8.27	4	44.266	44	62	96	3.391
7.	F_4:23-24 (18)	82.62	17.07	15.59	9.78	3	57.121	48	60	94	3.531
8.	F_4:23-24 (19)	72.14	13.57	14.47	9.76	3	46.976	46	54	96	3.456
9.	F_4:23-24 (20)	84.96	14.21	18.13	8.94	4	41.489	47	55	98	3.504
10.	F_4:23-24 (25)	75.81	7.92	17.98	8.2	3	41.054	55	49	90	2.964
11.	F_4:23-24 (71)	85.41	15.64	14.18	9.67	3	58.214	45	53	98	3.557
12.	F_4:23-24 (74)	81.13	14.04	14.87	7.92	2	54.556	44	53	89	3.511
13.	F_4:23-24 (81)	68.47	13.25	13.93	8.11	3	41.692	39	52	89	2.979
14.	F_4:23-24 (86)	71.08	12.46	14.82	11.34	3	57.841	61	56	98	3.261
15.	F_4:23-24 (101)	71.32	15.51	13.82	8.28	2	47.326	42	48	96	3.252
C1	UAS 375	59.71	12.38	17.94	8.81	3	37.281	47	56	102	2.440
C2	CWYT_609	75.82	18.09	23.17	10.62	3	51.873	49	47	88	2.814
C3	UAS 347	60.58	12.68	23.23	10.25	4	34.893	44	53	99	2.321
C4	UAS 446	66.45	14.64	13.45	5.88	4	47.711	43	59	102	1.947
C5	UAS 466	81.25	15.96	17.87	6.84	3	45.514	51	63	105	2.341
C6	HTWYT_66	74.43	8.64	11.01	7.51	2	45.901	50	53	92	1.240
C7	HTWYT_67	61.35	8.72	11.78	8.68	2	41.899	49	53	83	2.016

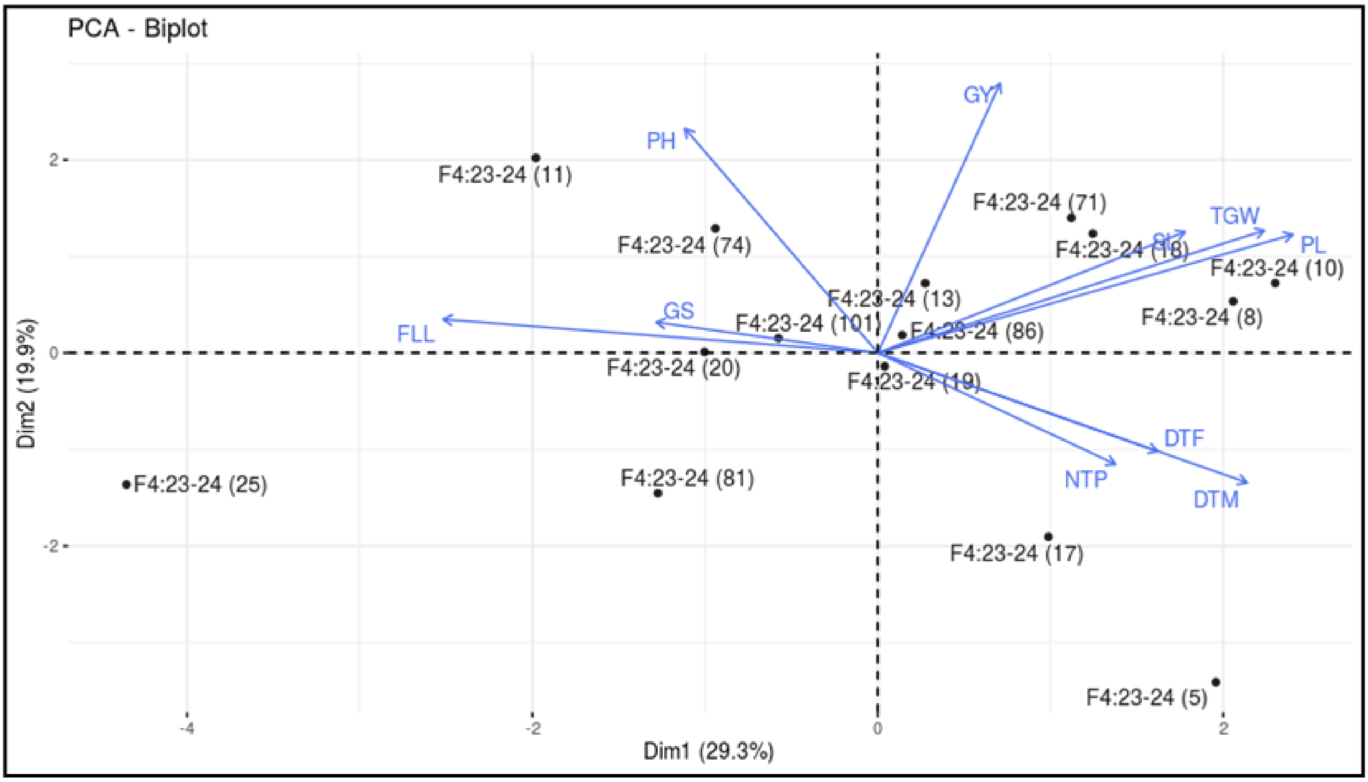

Fig. 3 PCA Biplot and distribution of 15 superior segregants under moisture stress conditions in cross UAS 375 × HTWYT_66.

interests to declare.

Ethical issues: None

Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work the authors used QuillBot in order to improve language and readability, with caution. After using this tool, the authors reviewed and edited the content as needed and takes full responsibility for the content of the publication.

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