

GENOTYPIC VARIATION IN PHYSIOLOGICAL TRAITS CONTRIBUTING TO DROUGHT AVOIDANCE AND ITS CONSEQUENCES FOR GROWTH AND YIELD IN WHEAT (*TRITICUM AESTIVUM* L.)

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ABSTRACT

Drought is the single most important abiotic constraint limiting wheat (*Triticum aestivum* L.) productivity, and identifying physiological traits that confer drought avoidance remains central to breeding resilient cultivars. In this study, thirty diverse bread wheat genotypes were screened under well-watered (control) and restricted-irrigation (drought, imposed by withholding irrigation from 30 days after sowing) conditions in a randomised complete block design with three replications at the Crop Research Farm, RPCAU, Pusa, Bihar, during the 2021-22 rabi season. Six physiological traits associated with drought avoidance – canopy temperature (CT), tissue temperature (TT), normalised difference vegetation index (NDVI), relative water content (RWC), specific leaf weight (SLW) and SPAD-based greenness index – were recorded at the reproductive stage, and a cumulative response index (CRI) integrating all six traits was used to rank genotypes for drought responsiveness. Genotype, treatment and genotype × treatment interaction effects were highly significant ($P < 0.001$) for all traits. Canopy and tissue temperature increased under drought while RWC, SLW, SPAD and NDVI declined in most genotypes, though the magnitude of change varied widely across the panel, indicating substantial exploitable genetic diversity. Based on CRI ranking, five genotypes (RAUW105 P10, HD2968, 11HPYT405, 41ESWYT102 P2 and SSN3) that maintained comparatively stable canopy temperature, tissue temperature, water content and greenness under drought were advanced for evaluation of growth and yield. In these genotypes, drought reduced plant height, spike length, grains per spike, test weight, grain yield and total biomass relative to the control, but the decline was consistently smaller in genotypes that had shown a favourable physiological response at the vegetative/reproductive screening stage, confirming a physiological basis for yield stability under water deficit. These results identify canopy temperature, tissue temperature, RWC, SLW and SPAD value as low-cost, high-throughput indicator traits for large-scale screening of drought avoidance in wheat, and RAUW105 P10, HD2968, 11HPYT405, 41ESWYT102 P2 and SSN3 as promising donors for incorporation into drought-tolerance breeding programmes.

KEYWORDS: Wheat · Drought avoidance · Canopy temperature · Relative water content · Cumulative response index · Genotypic screening

INTRODUCTION

Wheat is the staple food for more than half of the world's population and, together with rice and maize, supplies over half of the calories and protein consumed globally (Awika 2011; McKeivith 2004). India is the world's second largest wheat producer, yet productivity in eastern states such as Bihar (2.6 t ha^{-1}) remains well below the national average (3.42 t ha^{-1}), reflecting the impact of recurrent terminal drought and heat stress in this agro-ecology.

Water deficit is the most widespread environmental constraint on crop production, and its impact on wheat is most severe at the reproductive and grain-filling stages, when a short episode of stress can trigger pollen sterility, poor seed set and reduced grain weight (Nezhadahmadi et al. 2013). Frequent, severe drought events in rainfed tracts – which supply roughly 70% of the world's staple food – can depress yields by 20–40% (Kadam et al. 2014), and this risk is projected to intensify under climate change. Because modern wheat cultivars carry limited within-species variability for drought tolerance, systematic screening of breeding germplasm for component physiological traits, followed by their deployment in crossing programmes, offers a faster route to resilience than reliance on yield selection alone.

Plant strategies for coping with water deficit are broadly grouped into drought avoidance, in which plants restrict water loss from aerial tissues or enhance water capture by the root system, and dehydration tolerance, achieved through osmotic adjustment, reactive-oxygen-species management and protein-stabilising mechanisms (Levitt 1980). Avoidance traits are particularly attractive for large-scale screening because several of them can be measured rapidly and non-destructively in the field. Canopy temperature, for instance, integrates stomatal

conductance and transpirational cooling into a single infrared measurement and has been used extensively to rank wheat lines for drought and heat tolerance (Mason and Singh 2014; Maes and Steppe 2012). Relative water content reflects the balance between water supply and transpirational demand at the cell level and is widely regarded as an indicator of drought resistance (Ritchie et al. 1990), while chlorophyll content (SPAD) and canopy reflectance indices (NDVI) capture stress-induced senescence and loss of photosynthetic area (Tian et al. 2013; Yang et al. 2001).

Despite the mechanistic understanding of these individual traits, few studies have combined them into a single index to rank a large, diverse panel of wheat genotypes and then verified whether the physiological ranking translates into yield stability under field drought. The present study was therefore designed (i) to explore genetic diversity for six drought-avoidance-related physiological traits among 30 promising wheat genotypes at the reproductive stage, and (ii) to quantify the consequences of contrasting physiological performance for growth and yield in a subset of genotypes carried through to harvest under control and restricted-irrigation conditions.

MATERIALS AND METHODS

Experimental site and weather conditions

The study was conducted during the 2021-22 rabi season at the Crop Research Farm, Dr Rajendra Prasad Central Agricultural University (RPCAU), Pusa, Bihar (25.98°N, 85.67°E; 52.0 m above mean sea level), located in the Middle Gangetic Plains on the southern bank of the river Burhi Gandak. The soil was alluvial, calcareous, medium-to-hard textured (Khadar type) with pH 8.43, EC 0.46 dS m⁻¹, organic carbon 0.47%, and available N, P and K of 241, 12.18 and 135.62 kg ha⁻¹, respectively. The site experiences a subtropical climate with hot, humid summers and cool winters; daily minimum and maximum temperature, relative humidity, rainfall, evaporation and bright sunshine hours were recorded throughout the crop season from the meteorological observatory at the Centre for Advanced Studies on Climate Change (CASCC), RPCAU.

Plant material, treatments and experimental design

Thirty diverse bread wheat genotypes, obtained from the Department of Genetics and Plant Breeding, RPCAU, Pusa, were sown on 27 November 2021 in a randomised complete block design (RCBD) with three replications and a row-to-row spacing of 17 cm. Two water regimes were imposed: an irrigated control, and a drought treatment in which irrigation was withheld from 30 days after sowing (DAS) onward, giving 180 plots in total (30 genotypes × 2 treatments × 3 replicates) for the initial screening. Based on their physiological response (see below), five contrasting genotypes were subsequently carried forward under the same design and water regimes for evaluation of growth and yield components through to harvest.

Physiological trait measurements

Canopy temperature (CT) and tissue temperature (TT) were recorded at the reproductive stage using an infrared thermometer (Apogee, USA, model MI-210), held at 45° to the canopy for CT and inserted directly into leaf tissue for TT, between 11:30 and 14:30 h on clear days, following Bahuguna et al. (2015). Canopy cover/greenness of the crop stand was assessed as the normalised difference vegetation index (NDVI) using a hand-held Green Seeker sensor (Trimble, USA) held 50–60 cm above the canopy. Relative water content (RWC) was determined on flag-leaf samples using the standard fresh weight–turgid weight–dry weight method: $RWC (\%) = [(fresh\ weight - dry\ weight) / (turgid\ weight - dry\ weight)] \times 100$, with leaf pieces rehydrated for 4 h before recording turgid weight and oven-dried at 70°C for 72 h for dry weight. Specific leaf weight (SLW) was calculated as leaf dry weight per unit leaf area (mg cm⁻²) on flag-leaf discs of known area. Leaf greenness (SPAD index) was measured on the youngest fully expanded (flag) leaf using a SPAD-502 chlorophyll meter (Konica Minolta, Japan) between 09:00 and 11:30 h, following Bahuguna et al. (2022). Each trait was recorded on three plants per replicate per genotype and averaged.

Cumulative Response Index (CRI)

To integrate the six physiological traits into a single measure of drought responsiveness, a response index (RI) was calculated for each trait and genotype as:

$$RI = (1 - YT/YC) / (1 - XT/XC)$$

where YT and YC are the trait values of a given genotype under drought and control conditions, respectively, and XT and XC are the corresponding mean trait values across all genotypes. The cumulative response index (CRI) for each genotype was obtained by summing its RI values across the six traits; genotypes with the lowest (most stable) CRI were considered the most drought-avoidant and were advanced to the growth and yield evaluation.

Growth and yield component traits

In the five genotypes carried through to harvest, plant height was measured from the root–shoot junction to the tip of the longest tiller's spike; spike length was measured on the main tiller spike; grains per spike were counted manually; test weight (1000-grain weight) and grain yield per plot were recorded using an electronic balance after harvest at physiological maturity; and total above-ground biomass per plant was recorded after oven-drying. Five plants per replicate were sampled for morphological traits and averaged.

Statistical analysis

Data were analysed as a two-factor (genotype × treatment) randomised block design using GENSTAT 15th Edition (Rothamsted Experimental Station, UK). Significance of genotype (G), treatment (T) and G × T

interaction effects was assessed by two-way ANOVA, and mean separation used Fisher's least significant difference (LSD) at $P<0.05$; significance levels are indicated as * $P<0.05$, ** $P<0.01$ and *** $P<0.001$.

Statement on human and animal rights

This study did not involve human participants, human data or animal subjects; it was conducted entirely on field-grown wheat plants.

RESULTS

Physiological screening of 30 genotypes under control and drought

Genotype, treatment and genotype $\times$ treatment ($G \times T$) effects were highly significant ($P<0.001$) for all six physiological traits recorded at the reproductive stage (Tables 1–6). Drought increased both canopy temperature (mean rise from 27.9 to 29.6°C) and tissue temperature (24.6 to 25.7°C) relative to the control, although the response varied widely: canopy temperature rose by less than 0.5°C in genotypes such as RAUW105 P10 and 41ESWYT102 P2, but by more than 3°C in genotypes such as 38SAWSN3253 and 38SAWSN, indicating markedly better stomatal/transpirational regulation in the former group under water deficit (Table 1). Tissue temperature showed a broadly similar pattern, with the smallest drought-induced rise in RAUW105 P10 and 11HPYT405 (Table 2).

Canopy cover (NDVI, Table 3), relative water content (Table 4), specific leaf weight (Table 5) and SPAD greenness index (Table 6) all declined, on average, under drought, but genotypes again differed strongly in the magnitude of decline. Relative water content fell by less than 1 percentage point in 41ESWYT102 P2 (80.8% to 80.1%) but by more than 6 points in 38SAWSN3224 (60.9% to 54.0%). Likewise, SPAD value was essentially unchanged in 41ESWYT114 (42.3 to 42.2) and 11HPYT433 (37.0 to 37.6) but fell by 11–12 units in 38SAWSN3253 and 11HPYT413. These patterns are consistent with the operation of drought-avoidance mechanisms – principally maintenance of leaf water status and canopy cooling through regulated transpiration – in a subset of the panel.

Ranking genotypes by the cumulative response index (CRI), which integrates the response of all six traits relative to the panel mean, identified RAUW105 P10, HD2968, 11HPYT405, 41ESWYT102 P2, 41ESWYT114 and SSN3 as the most drought-avoidant genotypes, on the basis of their comparatively stable canopy/tissue temperature, water content and greenness under restricted irrigation. These genotypes were carried forward for evaluation of growth and yield component traits.

Table 1 Canopy temperature (°C) of 30 wheat genotypes at the reproductive stage under control and drought (restricted irrigation) conditions.

Genotype	Control (°C)	Drought (°C)
NEST20-30 P33	27.54±0.28	30.77±0.09
11HPYT431	28.33±0.08	31.41±0.22
11HPYT408	26.44±0.22	29.86±0.94
11HPYT449	29.40±0.08	30.74±0.09
11HPYT425	27.19±0.10	29.95±0.53
41ESWYT114	28.43±0.08	28.65±0.19
9HPYT432	28.95±0.06	29.80±0.08
NEST2039 P42	26.63±0.07	28.55±0.28
NEST20-3 P3	26.68±0.16	29.43±0.08
SSW20-21157 P82	28.39±0.21	31.30±0.17
38SAWSN 3174	26.41±0.30	30.30±0.08
41ESWYT108	28.60±0.08	30.37±0.08
11HPYT433	28.11±0.06	28.29±0.08
38SAWSN3253	28.59±0.20	31.67±0.09
41ESWYT102 P2	27.70±0.08	27.83±0.08
38SAWSN	28.31±0.16	31.27±0.09
11HPYT417	29.67±0.08	28.53±0.08
9HPYT424	28.30±0.17	30.03±0.08
SSN20-21106	28.43±0.08	30.57±0.09

9HPYT485	29.41±0.21	31.27±0.09
11HPYT405	28.53±0.08	28.39±0.08
11HPYT443	27.38±0.69	30.40±0.08
11HPYT413	28.13±0.08	30.20±0.08
HD2968	28.26±0.13	29.97±0.08
DBW187	29.53±0.08	29.93±0.08
11HPYT414	29.37±0.20	29.57±0.08
RAUW105 P10	25.53±0.07	25.63±0.07
11HPYT 439	27.28±0.16	29.57±0.08
SSN3	26.28±0.14	31.17±0.09
38SAWSN3224	28.41±0.30	28.73±0.08
G	0.41***	
T	0.11***	
G × T	0.59***	

*Values are mean ± SEM of three replicates. G, genotype; T, treatment; G × T, genotype × treatment interaction; ns, not significant; *P<0.05; **P<0.01; ***P<0.001 (LSD).*

Table 2 Tissue temperature (°C) of 30 wheat genotypes at the reproductive stage under control and drought conditions.

Genotype	Control (°C)	Drought (°C)
NEST20-30 P33	24.36±0.07	25.13±0.07
11HPYT431	24.96±0.07	26.40±0.07
11HPYT408	25.23±0.07	26.80±0.07
11HPYT449	23.29±0.15	25.36±0.07
11HPYT425	24.53±0.07	25.73±0.07
41ESWYT114	25.00±0.07	25.49±0.07
9HPYT432	24.90±0.07	26.46±0.07
NEST2039 P42	26.19±0.41	26.60±0.07
NEST20-3 P3	24.86±0.07	27.37±0.08
SSW20-21157 P82	25.33±0.17	25.96±0.07
38SAWSN 3174	24.60±0.07	26.40±0.07
41ESWYT108	25.50±0.07	27.37±0.08
11HPYT433	25.93±0.07	26.36±0.07
38SAWSN3253	25.23±0.07	26.46±0.07
41ESWYT102 P2	25.08±0.46	23.48±0.07
38SAWSN	23.93±0.07	25.80±0.07
11HPYT417	23.89±0.07	26.43±0.07
9HPYT424	24.09±0.07	27.77±0.08
SSN20-21106	23.79±0.07	25.26±0.07
9HPYT485	24.15±0.08	25.00±0.07
11HPYT405	24.09±0.07	24.04±0.07
11HPYT443	24.19±0.07	24.66±0.07
11HPYT413	23.29±0.07	25.16±0.07

HD2968	22.89±0.44	24.90±0.07
DBW187	23.66±0.07	25.56±0.07
11HPYT414	24.76±0.07	26.80±0.40
RAUW105 P10	24.60±0.07	24.38±0.07
11HPYT 439	25.46±0.23	26.73±0.07
SSN3	24.19±0.07	25.46±0.23
38SAWSN3224	24.16±0.07	26.34±0.33
G	0.29***	
T	0.07***	
G × T	0.41***	

Values are mean ± SEM of three replicates. G, genotype; T, treatment; G × T, genotype × treatment interaction; ns, not significant; *P<0.05; **P<0.01; ***P<0.001 (LSD).

Table 3 Canopy cover / NDVI (Green Seeker) of 30 wheat genotypes at the reproductive stage under control and drought conditions.

Genotype	Control (NDVI)	Drought (NDVI)
NEST20-30 P33	0.80±0.00	0.73±0.00
11HPYT431	0.77±0.00	0.74±0.03
11HPYT408	0.83±0.00	0.73±0.01
11HPYT449	0.75±0.02	0.65±0.00
11HPYT425	0.74±0.00	0.68±0.00
41ESWYT114	0.81±0.01	0.80±0.00
9HPYT432	0.76±0.00	0.63±0.00
NEST2039 P42	0.63±0.00	0.57±0.00
NEST20-3 p3	0.82±0.00	0.74±0.00
SSW20-21157 P82	0.82±0.00	0.68±0.00
38SAWSN 3174	0.64±0.00	0.58±0.00
41ESWYT108	0.82±0.01	0.70±0.00
11HPYT433	0.76±0.02	0.74±0.00
38SAWSN 3253	0.74±0.00	0.57±0.00
41ESWYT102 P2	0.81±0.00	0.83±0.00
38SAWSN	0.76±0.03	0.65±0.00
11HPYT417	0.78±0.00	0.73±0.00
9HPYT424	0.84±0.00	0.73±0.00
SSN20-21106	0.86±0.00	0.65±0.00
9HPYT485	0.78±0.00	0.67±0.00
11HPYT405	0.82±0.00	0.88±0.00
11HPYT443	0.79±0.00	0.68±0.00
11HPYT413	0.82±0.00	0.67±0.00
HD2968	0.83±0.01	0.73±0.00
DBW187	0.68±0.00	0.62±0.00
11HPYT414	0.76±0.00	0.66±0.00
RAUW105 P10	0.73±0.00	0.75±0.00

11HPYT 439	0.77±0.04	0.74±0.00
SSN3	0.83±0.00	0.69±0.00
38SAWSN3224	0.81±0.00	0.78±0.00
G	0.018***	
T	0.005***	
G × T	0.025***	

Values are mean ± SEM of three replicates. G, genotype; T, treatment; G × T, genotype × treatment interaction; ns, not significant; *P<0.05; **P<0.01; ***P<0.001 (LSD).

Table 4 Relative water content (%) of 30 wheat genotypes at the reproductive stage under control and drought conditions.

Genotype	Control (%)	Drought (%)
NEST20-30 P33	67.20±0.19	63.91±0.18
11HPYT431	69.30±0.19	65.54±0.18
11HPYT408	74.34±0.21	68.90±0.19
11HPYT449	73.10±0.08	70.53±0.20
11HPYT425	68.45±0.19	65.48±0.18
41ESWYT114	73.29±0.20	74.54±0.21
9HPYT432	71.47±0.20	64.33±0.18
NEST2039 P42	77.54±1.27	73.92±0.21
NEST20-3 p3	68.85±0.19	64.39±0.18
SSW20-21157 P82	78.56±0.22	67.58±0.19
38SAWSN 3174	79.31±1.16	75.65±0.21
41ESWYT108	79.59±0.22	72.64±0.20
11HPYT433	78.49±0.22	79.15±0.22
38SAWSN 3253	80.89±0.23	73.49±0.21
41ESWYT102 P2	79.35±0.22	80.08±0.22
38SAWSN	80.64±0.82	72.73±0.20
11HPYT417	65.91±0.18	57.90±0.16
9HPYT424	73.07±0.49	67.48±0.19
SSN20-21106	77.39±0.22	65.44±0.18
9HPYT485	73.85±0.21	64.63±0.18
11HPYT405	75.42±0.21	76.19±0.21
11HPYT443	79.42±1.71	74.60±0.21
11HPYT413	65.64±0.18	54.86±0.15
HD2968	68.21±0.19	65.89±0.18
DBW187	72.31±0.20	65.23±0.18
11HPYT414	72.05±0.20	69.33±0.19
RAUW105 P10	69.95±0.54	70.07±0.20
11HPYT 439	76.22±0.21	67.31±0.19
SSN3	77.71±0.22	73.95±0.21
38SAWSN3224	60.90±2.05	54.06±0.15
G	0.93***	

T	0.24***
G × T	1.32***

Values are mean ± SEM of three replicates. G, genotype; T, treatment; G × T, genotype × treatment interaction; ns, not significant; *P<0.05; **P<0.01; ***P<0.001 (LSD).

Table 5 Specific leaf weight (mg cm⁻²) of 30 wheat genotypes at the reproductive stage under control and drought conditions.

Genotype	Control (mg cm ⁻²)	Drought (mg cm ⁻²)
NEST20-30 P33	4.86±0.01	4.27±0.01
11HPYT431	4.91±0.01	4.61±0.01
11HPYT408	5.51±0.02	5.11±0.01
11HPYT449	5.17±0.01	4.41±0.01
11HPYT425	5.37±0.19	4.78±0.01
41ESWYT114	5.77±0.02	5.90±0.02
9HPYT432	5.57±0.02	4.95±0.01
NEST2039 P42	6.31±0.02	5.36±0.01
NEST20-3 p3	6.01±0.02	5.55±0.02
SSW20-21157 P82	5.47±0.02	5.27±0.01
38SAWSN 3174	5.28±0.14	3.93±0.01
41ESWYT108	6.15±0.07	4.07±0.01
11HPYT433	5.41±0.02	5.49±0.02
38SAWSN 3253	5.50±0.02	5.20±0.01
41ESWYT102 P2	5.27±0.01	5.51±0.02
38SAWSN	6.26±0.13	5.81±0.02
11HPYT417	5.71±0.15	4.27±0.01
9HPYT424	5.30±0.01	4.86±0.01
SSN20-21106	4.86±0.07	4.18±0.01
9HPYT485	5.67±0.02	4.40±0.01
11HPYT405	5.62±0.02	5.81±0.02
11HPYT443	5.57±0.02	5.08±0.01
11HPYT413	5.94±0.02	5.90±0.02
HD2968	5.47±0.02	4.81±0.01
DBW187	5.34±0.33	4.05±0.01
11HPYT414	5.16±0.01	4.96±0.01
RAUW105 P10	5.31±0.01	5.23±0.01
11HPYT 439	5.57±0.22	4.59±0.01
SSN3	5.44±0.02	5.11±0.01
38SAWSN3224	6.15±0.07	5.27±0.01
G	0.77***	
T	0.20***	
G × T	1.09***	

Values are mean ± SEM of three replicates. G, genotype; T, treatment; G × T, genotype × treatment interaction; ns, not significant; *P<0.05; **P<0.01; ***P<0.001 (LSD).

Table 6 SPAD (greenness index) of 30 wheat genotypes at the reproductive stage under control and drought conditions.

Genotype	Control (SPAD)	Drought (SPAD)
NEST20-30 P33	40.15±0.11	28.47±0.08
11HPYT431	35.14±0.10	27.53±0.08
11HPYT408	40.85±0.11	35.41±0.10
11HPYT449	37.78±0.11	28.77±0.08
11HPYT425	42.67±1.33	35.57±0.10
41ESWYT114	42.25±0.12	42.15±0.12
9HPYT432	34.87±0.10	27.57±0.08
NEST2039 P42	42.33±0.67	35.01±0.10
NEST20-3 p3	34.87±0.10	33.14±0.09
SSW20-21157 P82	41.35±0.12	29.47±0.08
38SAWSN 3174	38.21±0.11	37.54±0.10
41ESWYT108	45.39±0.13	34.57±0.10
11HPYT433	37.01±0.07	37.61±0.10
38SAWSN 3253	38.78±0.11	27.10±0.08
41ESWYT102 P2	40.25±0.11	41.95±0.12
38SAWSN	33.60±0.70	31.54±0.09
11HPYT417	37.04±0.10	34.64±0.10
9HPYT424	39.55±0.11	36.14±0.10
SSN20-21106	42.45±0.72	32.54±0.09
9HPYT485	38.74±0.11	32.84±0.09
11HPYT405	30.66±1.67	30.54±0.09
11HPYT443	33.31±0.09	32.14±0.09
11HPYT413	36.01±0.10	32.04±0.09
HD2968	38.51±0.11	37.54±0.10
DBW187	39.34±1.17	37.54±0.10
11HPYT414	42.78±0.12	40.85±0.11
RAUW105 P10	36.38±0.10	36.54±0.10
11HPYT 439	42.71±0.86	38.04±0.11
SSN3	38.93±0.54	28.30±0.08
38SAWSN3224	42.52±0.12	40.26±0.11
G	0.13***	
T	0.03***	
G × T	0.19***	

Values are mean ± SEM of three replicates. G, genotype; T, treatment; G × T, genotype × treatment interaction; ns, not significant; *P<0.05; **P<0.01; ***P<0.001 (LSD).

Growth and yield of contrasting genotypes under drought

In the five genotypes carried through to harvest, drought significantly reduced plant height (Table 7), spike length (Table 8), grains per spike (Table 9), test weight (Table 10), grain yield (Table 11) and total biomass (Table 12) (P<0.001 for treatment effect in all cases). Grain yield losses under drought ranged from 12% in SSN3 (359 to 308 g plot⁻¹) to 53% in 38SAWSN3253 (416 to 196 g plot⁻¹). SSN3, which had shown the smallest physiological perturbation at the screening stage, also showed the smallest relative decline in grain yield, test weight and biomass under drought, whereas 38SAWSN3253, which had shown a large increase in

canopy temperature and steep declines in RWC and SPAD during screening, suffered the largest yield penalty. This concordance between the physiological ranking obtained at the reproductive screening stage and the eventual yield response under field drought supports the use of canopy temperature, tissue temperature, RWC, SLW and SPAD as early, low-cost indicator traits for drought avoidance in wheat.

Table 7 Plant height (cm) of five contrasting wheat genotypes under control and drought conditions, recorded at harvest (115 DAS).

Genotype	Control (cm)	Drought (cm)
41ESWYT108	102.3±0.3	101.3±0.9
SSN20-21106	103.7±0.3	101.0±0.6
38SAWSN3253	104.7±0.3	99.4±0.4
SSN3	101.7±1.0	98.3±1.0
38SAWSN3174	98.0±1.1	93.2±0.6
G	1.35***	
T	0.85***	
G × T	1.90*	

*Values are mean ± SEM of three replicates. G, genotype; T, treatment; G × T, genotype × treatment interaction; ns, not significant; *P<0.05; **P<0.01; ***P<0.001 (LSD).*

Table 8 Spike length (cm) of five contrasting wheat genotypes under control and drought conditions.

Genotype	Control (cm)	Drought (cm)
41ESWYT108	4.6±0.2	4.4±0.3
SSN20-21106	5.7±0.3	3.7±0.1
38SAWSN3253	5.3±0.2	4.3±0.2
SSN3	5.0±0.1	4.8±0.1
38SAWSN3174	5.2±0.1	4.4±0.1
G	0.38 ns	
T	0.23***	
G × T	0.53***	

*Values are mean ± SEM of three replicates. G, genotype; T, treatment; G × T, genotype × treatment interaction; ns, not significant; *P<0.05; **P<0.01; ***P<0.001 (LSD).*

Table 9 Grains per spike of five contrasting wheat genotypes under control and drought conditions.

Genotype	Control	Drought
41ESWYT108	53.3±0.9	46.7±0.9
SSN20-21106	47.8±3.8	42.7±0.9
38SAWSN3253	65.5±1.3	39.0±0.5
SSN3	42.5±0.6	47.5±0.8
38SAWSN3174	51.3±1.2	48.3±1.4
G	3.37**	
T	2.13***	
G × T	4.76***	

*Values are mean ± SEM of three replicates. G, genotype; T, treatment; G × T, genotype × treatment interaction; ns, not significant; *P<0.05; **P<0.01; ***P<0.001 (LSD).*

Table 10 Test weight (1000-grain weight, g) of five contrasting wheat genotypes under control and drought conditions.

Genotype	Control (g)	Drought (g)
41ESWYT108	43.3±0.9	36.0±1.3
SSN20-21106	39.5±0.3	32.0±0.5
38SAWSN3253	45.9±1.1	37.7±0.8
SSN3	42.5±1.1	39.8±0.6
38SAWSN3174	48.9±1.0	36.8±1.4
G	2.03***	
T	1.28***	
G × T	2.86**	

Values are mean ± SEM of three replicates. G, genotype; T, treatment; G × T, genotype × treatment interaction; ns, not significant; *P<0.05; **P<0.01; ***P<0.001 (LSD).

Table 11 Grain yield (g plot⁻¹) of five contrasting wheat genotypes under control and drought conditions.

Genotype	Control (g plot ⁻¹)	Drought (g plot ⁻¹)
41ESWYT108	352±8	274±10
SSN20-21106	398±5	214±9
38SAWSN3253	416±6	196±2
SSN3	359±3	308±4
38SAWSN3174	394±18	255±12
G	17.13*	
T	10.83***	
G × T	24.22***	

Values are mean ± SEM of three replicates. G, genotype; T, treatment; G × T, genotype × treatment interaction; ns, not significant; *P<0.05; **P<0.01; ***P<0.001 (LSD).

Table 12 Total biomass (g plant⁻¹) of five contrasting wheat genotypes under control and drought conditions.

Genotype	Control (g plant ⁻¹)	Drought (g plant ⁻¹)
41ESWYT108	9.7±0.1	7.8±0.2
SSN20-21106	10.7±0.2	8.6±0.5
38SAWSN3253	10.2±0.3	9.1±0.1
SSN3	9.4±0.1	8.1±0.2
38SAWSN3174	9.1±0.2	8.8±0.3
G	0.57**	
T	0.35***	
G × T	0.80*	

Values are mean ± SEM of three replicates. G, genotype; T, treatment; G × T, genotype × treatment interaction; ns, not significant; *P<0.05; **P<0.01; ***P<0.001 (LSD).

DISCUSSION

Drought tolerance in wheat is a complex, polygenic trait, and identifying phenotypes that reliably distinguish avoidant from susceptible genotypes under field conditions remains challenging (Kantar et al. 2011). The wide range of responses recorded here across 30 genotypes for canopy temperature, tissue temperature, RWC, SLW, SPAD and NDVI confirms that substantial exploitable variability for drought-avoidance traits exists within elite and pre-breeding wheat germplasm, consistent with earlier reports of wide genotypic variation for seedling and reproductive-stage drought responses in wheat, maize and triticale (Grzesiak et al. 2012; Tomar and Kumar 2004).

Canopy temperature integrates several underlying physiological processes – stomatal conductance, transpiration and the balance between water supply and evaporative demand – into a single, rapidly measurable trait, and has therefore been widely used to rank breeding lines for drought and heat tolerance (Mason and Singh 2014). The consistent rise in canopy and tissue temperature under drought observed in the present study reflects stomatal closure and reduced transpirational cooling (Maes and Steppe 2012), and genotypes that limited this rise – RAUW105 P10 and 41ESWYT102 P2 in particular – evidently retained greater stomatal conductance or access to soil moisture, or both, relative to genotypes such as 38SAWSN3253 in which canopy temperature rose sharply.

Relative water content is considered a robust indicator of a plant's ability to maintain cellular hydration under water deficit, with higher RWC generally associated with superior osmotic adjustment or reduced cell-wall elasticity (Ritchie et al. 1990). The genotypes that best maintained RWC under drought in this study also showed the smallest declines in SPAD greenness and NDVI, consistent with the well-documented link between water status, chlorophyll retention, and delayed senescence. As leaf water potential falls, nitrogen and carbohydrate remobilisation from vegetative tissue to the developing grain accelerates, hastening leaf senescence and chlorophyll loss (Yang et al. 2001; Tian et al. 2013). SPAD value, therefore, functioned here, as in other cereals, as an accessible surrogate for underlying photosynthetic capacity and stay-green behaviour under stress.

Importantly, the physiological ranking obtained from the cumulative response index at the reproductive screening stage was broadly reflected in the eventual yield performance of the five genotypes carried to harvest. Reduced water availability restricts stomatal conductance and CO₂ assimilation, damages cellular structures through oxidative stress, and ultimately curtails dry matter accumulation and partitioning to grain (Wang et al. 2008); the present results indicate that genotypes able to buffer these downstream effects – evident as smaller declines in plant height, spike length, grains per spike and test weight – were precisely those that had shown the most stable physiological signatures during screening. This concordance supports the practical value of combining several rapidly measured avoidance traits into a single index for large-scale germplasm screening, rather than relying on any one trait in isolation, since the relative importance of individual mechanisms (canopy cooling versus tissue hydration versus stay-green) differed across genotypes.

Modern wheat cultivars carry comparatively narrow genetic diversity for drought tolerance, and wild relatives and diverse breeding lines remain an important reservoir of avoidance-related variation for introgression into elite backgrounds (Zaharieva et al. 2001). The genotypes identified here as the most drought-avoidant – RAUW105 P10, HD2968, 11HPYT405, 41ESWYT102 P2, 41ESWYT114, and SSN3 – combine favourable physiological buffering with comparatively smaller yield penalties under restricted irrigation, and are therefore promising parental material for breeding programmes targeting drought resilience in the eastern Gangetic plains and other similarly drought-prone wheat production environments.

Taken together, these results support canopy temperature, tissue temperature, relative water content, specific leaf weight, and SPAD-based greenness as simple, field-deployable indicator traits for large-scale screening of drought avoidance in wheat, and identify a defined set of genotypes suitable for immediate use in drought-tolerance breeding.

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Author Contributions

JP and RNB conceived and supervised the study. SK conducted the field experiment, recorded observations, and RNB analysed the data. JP and SBG interpreted the results and prepared the manuscript. All the authors reviewed and finalized the manuscript.

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Data Availability

The datasets generated and analysed during the current study are available from the corresponding author on reasonable request.

DECLARATIONS

Conflict of Interest

The authors declare that they have no conflict of interest.

Ethical Approval

This article does not contain any studies with human participants or animals performed by any of the authors.

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