

Agronomic performance, nutritional quality and cooking traits of common bean genotypes grown under terminal drought conditions

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ABSTRACT

Drought stress significantly impacts the agronomic and nutritional properties of common bean (*Phaseolus vulgaris* L.), affecting agronomic traits, content of bioactive compounds and their antioxidant activity. This study evaluated the effect of two water regimes—no drought (ND) and terminal drought stress (DS)—on 20 bean genotypes and commercial cultivars over two growing seasons. Productive and quality traits were assessed, including grain yield (GY), number of grains per pod (NGP), hundred-grain weight (HGW), hydration capacity (HC), cooking time, crude protein content, total phenolic content, and DPPH-based antioxidant activity. Results showed a significant reduction ($p < 0.001$) in GY (-22.3%) and NGP (-61.3%) under DS, while HC increased for most genotypes (+1.9%). Some genotypes, such as 464, 483, and 478, maintained high GY ($> 3600\text{kg ha}^{-1}$) despite reduced NGP. A positive correlation was observed between seed weight and protein content ($r = 0.4$) under ND and DS conditions. Under DS, most genotypes exhibited increased phenolic compounds and antioxidant capacity, highlighting their potential for stress resilience. The study highlights the intricate relationship between productivity, grain quality, and drought resistance in common beans. These findings provide valuable information that could contribute to improving the genotype selection process and development of common bean cultivars, highlighting the importance of selecting genotypes for both high yield and grain quality under water-limited conditions, while enhancing the sustainability and resilience to climate variability in this important crop.

Key words: Antioxidant, common bean, drought stress, grain yield, hydration capacity, *Phaseolus vulgaris*, phenolic content.

INTRODUCTION

Common beans (*Phaseolus vulgaris* L.) are an important component of human diets worldwide, particularly in regions where they serve as a primary source of plant-based protein (Lisciani et al., 2024). Their high nutritional value, affordability, and adaptability to various agroecological conditions make them a key crop for ensuring food security and improving human health (Didinger and Thompson, 2022). However, climate change has increasingly threatened the cultivation of common beans, mainly due to rising temperatures and decreasing

water availability. These environmental changes can result in yield losses of up to 70%, posing a significant threat to food security in regions where beans are a staple food (Farrow and Muthoni-Andriatsitohaina, 2020). By 2040, Chile is projected to be among the 30 nations facing the most severe water scarcity (Luo et al., 2015). Environmental stresses such as temperature and drought can impact bean crop productivity in agronomic and phenological traits (Campos et al., 2021) but also influence the nutritional and technological characteristics of the beans, including the concentration of phenolic and antioxidant compounds, cooking time, hydration capacity, and crude protein content—parameters that determine both acceptability and nutritional value (Wang et al., 2016). Beans are rich in bioactive compounds, such as phenolics, which exhibit strong antioxidant properties associated with health benefits (Messina, 2014). The concentrations of these compounds vary depending on genotype and environmental conditions (Smith et al., 2022). Water restriction during cultivation can induce metabolic changes, leading to variations in bioactive compounds concentrations and a reduction in overall protein content (Sica et al., 2021). To better understand these changes, the antioxidant capacity of beans can be quantitatively evaluated using assays such as the 2,2-diphenyl-1-picrylhydrazyl (DPPH) method, which is widely used for measuring free radical scavenging activity in legumes (Mojica et al., 2017). This analysis, therefore, provides critical insights into how environmental stresses influence the health-promoting properties of beans, bridging the gap between agronomic conditions and nutritional outcomes (Zhao et al., 2007). Other studies suggest that bean genotypes are resilient in maintaining nutritional content in the seed across environmental conditions (Smith et al., 2022). This nutritional stability becomes particularly relevant when evaluating technological traits such as hydration and cooking time, which are closely related to seed structure and composition (Wang et al., 2016). In this context, hydration describes the rate and extent of water uptake during soaking—and serves as a valuable tool to assess water absorption kinetics and their relationship to seed coat permeability and internal texture (Katuuramu et al., 2020). Bean genotypes that exhibit rapid and extensive water uptake during soaking are likely to require less cooking time because the water has already penetrated the seed coat and softened the texture. This can help preserve more of the bean's nutritional content, as prolonged cooking can cause heat-sensitive vitamins and minerals to be lost (Brito et al., 2013). Therefore, understanding the hydration characteristics of bean genotypes is essential for developing cultivars that are not only high yielding but also optimized for consumer preferences and nutritional value.

This research aimed to evaluate the effects of two contrasting water regimes on a set of bean genotypes and commercial cultivars, focusing on their agronomic and phenological performance and how these factors relate to grain quality traits.

MATERIALS AND METHODS

Experimental site conditions and plant material

The experiment was conducted at the Santa Rosa Experimental Field of the Instituto de Investigaciones Agropecuarias (INIA), INIA Quilamapu, Chillán (36°31' S, 71°54' W, 196 m a.s.l.), Chile. The soil at the experimental site is volcanic, Melanoxerand, according to the USDA classification system (USDA, 2014) and has a loamy texture. The climate is temperate Mediterranean type, featuring a hot, dry summer and a cold, wet winter. Field trials were conducted during the 2021-2022 and 2022-2023 growing seasons. Sowing was carried out on 5 November 2021 and 3 November 2022. Meteorological data, including precipitation, evapotranspiration, and temperature, were obtained from an automated weather station at the research site (Table 1). The trials received only 11 and 8 mm precipitation between flowering and harvest during the 2021-2022 and 2022-2023 seasons, respectively.

The germplasm consisted of 20 common bean (*Phaseolus vulgaris* L.) genotypes (Table 2). Fifteen genotypes were selected from the US dry bean breeding drought nursery at the University of Nebraska, Lincoln, USA. Additionally, five cultivars from the Chilean race and Andean genetic pool were selected from the Bean Breeding Program at INIA.

Table 1. Monthly maximum (T Max), minimum (T Min), average (T Ave), evapotranspiration (ET₀), rainfall (Rf), and applied irrigation (Irr) at Chillán, Chile, during the 2021-2022 and 2022-2023 seasons. Regular irrigation (ND) and terminal drought stress (DS). The bold values refer to irrigations applied only in the ND water regime after flowering to physiological maturity.

Season	Month	T° Max	T° Min	T° Ave	ET ₀	Rf	Irr	ND	DS
		°C			mm				
2021/2022	Nov	25.2	6.7	16.0	119.5	6.0	60	66.0	66.0
	Dec	29.3	9.3	19.3	147.0	13.0	100	113.0	113.0
	Jan	29.2	9.0	19.1	143.2	1.6	120	121.6	1.6
	Feb	29.7	8.3	19.0	130.4	9.5	90	99.5	9.5
2022/2023	Nov	26.5	9.3	17.9	123.1	25.7	60	85.7	85.7
	Dec	29.0	9.7	19.4	142.2	0.0	100	100.0	100.0
	Jan	30.3	9.9	20.1	159.5	7.4	140	147.4	7.4
	Feb	31.1	8.6	19.8	128.8	0.0	90	90.0	0.0

Table 2. Genotypes from the University of Nebraska (NE), USA, and the Institute of Agricultural Research (INIA), Chile, were evaluated at Chillán, Chile, from 2021 to 2023. The common bean's growth habit classification standards are Type I: Determinate bush, characterized by a reproductive phase with terminal flowering and pod set; Type II: Indeterminate bush, exhibiting prolonged vegetative growth with upright architecture and continuous pod production; and Type III: Indeterminate vining, with prostrate or climbing growth.

Code	Genotype	Market class	Growth habit	Origen
442	GN16-7	Great Northern	II	NE
452	SB2-171	Cream	II	NE
456	NE1-09-19	Great Northern	II	NE
457	NE2-17-6	Pinto	II	NE
458	NE14-17-2	Black	II	NE
463	Matterhorn	Great Northern	II	NE
464	Marquis	Great Northern	II	NE
467	NE1-18-9	Great Northern	II	NE
473	NE1-18-42	Great Northern	II	NE
475	NE3-18-3	Great Northern	II	NE
478	NE3-18-9	Great Northern	II	NE
479	NE3-18-22	Great Northern	II	NE
483	NE3-18-40	Great Northern	II	NE
485	NE3-18-58	Great Northern	II	NE
487	NE3-18-99	Great Northern	II	NE
Curi	Curi	Black	I	INIA
Lpci	Lpci	Coscorrón	III	INIA
Zorzal	Zorzal	Tórtola	III	INIA
Sel 6	Sel 6	Tórtola	III	INIA
Blanco Español	Blanco Español	Great Northern	III	INIA

Crop management and experimental design

Genotypes were assigned to experimental units using a randomized complete block design with four replicates. Each plot consisted of four 5.0 m rows spaced 0.6 m apart, targeting a plant density of 250 000 plants ha⁻¹. Furrow irrigation systems were used throughout the trial. Before sowing, the soil was fertilized with 60 kg ha⁻¹ N, 90 kg ha⁻¹ P₂O₅, 60 kg ha⁻¹ K₂O, 15 kg ha⁻¹ S, and 30 kg ha⁻¹ MgO. Seeds were treated with fludioxonil (0.35 g ai kg⁻¹ seed) and thiamethoxam (0.35 g ai kg⁻¹ seed). Chemical weed control was applied with the sodium salt of fomesafen (375 g ai ha⁻¹), and weed management also included manual labor.

The genotypes were evaluated under two water regimes: Regular irrigation or no drought (ND) and terminal drought stress (DS). Trials were irrigated from sowing until flowering to ensure proper plant establishment and early growth. Irrigation volumes applied are shown in Table 1. In DS plots, irrigation was discontinued on day 56 after sowing, coinciding with the period when all genotypes were in full flowering. A 20 m buffer zone was maintained between adjacent trials to minimize water movement from the non-stressed to the drought-stressed plots.

Agronomic and phenological evaluations

Grain yield, number of grains per pod, and hundred-grain weight were evaluated. The grain yield (GY) was determined by harvesting seeds at a uniform moisture content (14%) from two central rows of each plot, excluding 50 cm end plants, for both the ND and DS plots. Then, data were extrapolated to a per-hectare basis. For the hundred-grain weight (HGW) at harvest, a random sample was taken to determine the weight of 100 seeds. The values were expressed in grams. The number of grains per pod (NGP) was extrapolated to the number of grains per area (m²). Days to flowering (DF) is the number of days after sowing until 50% of the plants have at least one open flower. Days to physiological maturity (DM) are the days after sowing until 50% of plants have at least one pod losing its green pigmentation.

Grain quality traits and crude protein content

The determination of anthocyanins, total phenolics, and antioxidant capacity of whole bean seeds was ground using a benchtop mill (IKA A10; IKA-Werke GmbH & Co., Staufen im Breisgau, Germany). Chemical extraction was performed according to the method described by López et al. (2022). A total of 0.5 g homogenized bean powder (particle size 430 nm) was extracted with 5 mL solvent mixture composed of methanol, water, and formic acid in a ratio of 24:25:1 (v/v/v). The mixture was placed in an ultrasonic bath for 1 h and then stored in sealed tubes for 24 h. Afterward, the samples were subjected to ultrasound for 1 h, then centrifuged at 3500 rpm for 15 min, and the supernatant was collected.

Total protein content (PC) was determined using the macro-Kjeldahl method, following the Association of Official Analytical Chemists protocol (Method 991.20) (AOAC, 1996).

Total phenolic content and antioxidant activity

Total phenolic content (TPC) was determined using the Folin-Ciocalteu assay, adapted to a microscale format as described by Brunet-Loredo et al. (2023), with slight modifications. An amount of 25 µL 0.5 N Folin-Ciocalteu reagent, 25 µL sample, blank or standard, and 200 µL distilled water were added to each well of a 96-well microplate. The plate was shaken for 30 s and incubated in the dark for 5 min at 25 °C. Subsequently, 25 µL 10% Na₂CO₃ was added to each well, and the absorbance was measured at 765 nm using a Synergy H1 multimode microplate reader (Biotek, Winooski, Vermont, USA). Results were expressed as mg gallic acid equivalents per 100 g sample (mg GAE·100 g⁻¹ sample).

The antioxidant capacity of the extracts was evaluated using the 2,2-diphenyl-1-picrylhydrazyl (DPPH) assay (Bondet et al., 1997). This method assesses the extract's capacity to scavenge DPPH radicals. For that, 25 µL extract was mixed with 200 µL DPPH solution and incubated in the dark for 1 h. Then, absorbance was measured at 515 nm. Results were expressed as µmol Trolox equivalents per 100 g bean powder (µmol TE 100 g⁻¹).

Hydration capacity and cooking time

A total of 30 seeds from each experimental unit was weighed and then soaked in 100 mL distilled water for 4 h at room temperature (Silva et al., 2019). The initial and final weights of the seeds, before and after soaking, were meticulously recorded. Hydration capacity (HC) was then calculated on a dry weight basis using the following equation (Hamabwe et al., 2024):

$$\text{HC (\%)} = \left(\frac{\text{Seed weight after soaking} - \text{Seed weight before soaking}}{\text{Seed weight before soaking}} \right) \times 100$$

The cooking time (CT) was assessed using 25 seeds samples previously hydrated in 100 mL distilled water for 12 h (Katuramu et al., 2020). After hydration, beans were cooked in a 2 L beaker of boiling distilled water using a Mattson cooker with 25 plungers (Customized Machining and Hydraulics Co., Winnipeg, Canada). The cooking process was considered complete when the plungers fully pierced 80% of the 25 seeds, and the corresponding time was recorded.

Statistical analysis

The study was conducted as a factorial experiment involving two water regimes, no drought (ND) and drought stress (DS), and 20 genotypes, evaluated across four environments: ND1, no drought during the 2021-2022 growing season; DS1, drought stress during the 2021-2022 growing season; ND2, no drought during the 2022-2023 growing season; and DS2, drought stress during the 2022-2023 growing season. Each water regime included a total sample size of 160 observations, derived from two growing seasons \times 20 genotypes \times 4 replicates. Because the effects of year and its interactions with water regime and genotype were nonsignificant, data from the two growing seasons were pooled and analyzed as a 2 \times 20 factorial experiment. A combined two-way ANOVA was then performed using the general linear model (GLM) procedure to assess the effects of water regime (WR), genotype (G), and their interaction (G \times WR). Mean comparisons between water regimes (ND vs. DS) were carried out using the independent samples t-test ($P \leq 0.05$), while differences among genotypes were evaluated using Duncan's multiple range test.

Pearson correlation analysis was performed in Rstudio version 4.2.1 (R Core Team, Vienna, Austria, 2022). All evaluated trait values were normalized to a 0-1 scale for heatmap generation. Hierarchical clustering was conducted using the Euclidean distance method. The analysis was carried out using the Morpheus tool (<https://software.broadinstitute.org/morpheus/>) (Morpheus Software, Broad Institute, Cambridge, Massachusetts, USA).

RESULTS

Agronomic and phenological traits

Significant variation was observed among the 20 bean genotypes evaluated under ND and DS water regimes for GY, NGP, and HGW (Tables 3 and 4).

Under DS conditions, average GY was 3023 kg ha⁻¹, ranging from 2148 to 4071 kg ha⁻¹. Genotype 464 achieved the highest yield, while 'Blanco Español' exhibited the lowest value. Within the DS regime, differences were observed among genotypes ($p < 0.05$), with the genotypes 'Blanco Español', 'Curi', 'LPCI', 'Sel 6', and 'Zorzal' having the lowest yields. Under ND conditions, the mean GY increased to 3890 kg ha⁻¹ a 19.3% gain over DS and ranged from 3223 to 4379 kg ha⁻¹. Genotype 483 displayed the highest yield, while genotype 452 recorded the lowest; both significantly differed ($p < 0.05$). Similarly, the NGP was affected by water availability. Under DS conditions, the average NGP was 821 grains m⁻², ranging from 674 to 895 grains m⁻². Genotype 463 had the highest NGP (895 grains m⁻²), while 'Lpci' registered the lowest (674 grains m⁻²), with significant differences observed among genotypes ($p < 0.05$). Under ND conditions, the mean NGP was substantially higher, averaging 2136 grains m⁻², ranging from 1586 to 2657 grains m⁻². Genotype 464 again stood out with the highest value (2657 grains m⁻²), while genotypes 'Curi', 'Lpci', and 'Blanco Español' had significantly lower NGP values (1586, 1624 and 1611 grains m⁻², respectively).

Table 3. Effect of water regime, genotypes, and their interaction on agronomic traits and biochemical compounds evaluated in 20 bean genotypes during two seasons under terminal drought stress (DS) and no stress (ND). The data show the mean of the 20 genotypes studied for each water condition. GY: Grain yield; NGP: number of grains per pod; HGW: hundred-grain weight; DF: days to flowering; DM: days to physiological maturity; CT: cooking time; DPPH: antioxidant capacity (2,2-diphenyl-1-picrylhydrazyl); TPC: total phenolic content; HC: hydration capacity; PC: total protein content; G: genotypes; WR: water regime; G × WR: genotype by water regime interaction. Means followed by different letters were significantly different by the independent samples t-test * $p \leq 0.05$, *** $p \leq 0.001$.

Traits	WR	G	WR × G	DS	ND
GY	0.000***	0.000***	0.098	3022.84 ± 70.84 ^a	3890.84 ± 62.55 ^b
NGP	0.000***	0.000***	0.000***	815.00 ± 6.29 ^a	2105.12 ± 29.08 ^b
HGW	0.000***	0.000***	0.183	33.89 ± 0.70 ^a	37.74 ± 0.69 ^b
DF	0.835	0.000***	0.291	48.19 ± 0.32 ^a	47.92 ± 0.24 ^a
DM	0.000***	0.000***	0.000***	83.63 ± 0.19 ^a	91.23 ± 0.46 ^b
CT	0.358	0.000***	0.628	44.63 ± 0.50 ^a	43.02 ± 0.74 ^a
DPPH	0.293	0.000***	0.000***	830.06 ± 107.11 ^a	793.14 ± 101.25 ^a
TPC	0.281	0.000***	0.000***	27.53 ± 1.63 ^a	25.18 ± 1.53 ^a
HC	0.575	0.000***	0.229	37.54 ± 1.61 ^a	36.83 ± 1.52 ^a
PC	0.000***	0.000***	0.779	22.61 ± 0.22 ^b	21.93 ± 0.17 ^a

Table 4. Effect of water regime on agronomic and phenological parameters of 20 common bean genotypes under (ND) and (DS) conditions. GY: Grain yield; NGP: number of grains per pod; HGW: hundred-grain weight; DF: days to flowering; DM: days to physiological maturity; DS: terminal drought stress; ND: no drought stress. Different letters in the column indicate significant differences according to Duncan's multiple range test ($P \leq 0.05$). t: refers to the t independent samples test for each genotype in DS and ND; ^{ns}nonsignificant; * $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq 0.001$.

Genotypes	GY (kg ha ⁻¹)			NGP			HGW (g)			DF (d)			DM (d)		
	DS	ND	t	DS	ND	t	DS	ND	t	DS	ND	t	DS	ND	t
442	2953.3 ^{abcd}	4191.9 ^{bc}	***	855.6 ^{de}	2148.0 ^b	***	31.3 ^{bcd}	31.4 ^c	ns	47.2 ^{ab}	47.5 ^{abcd}	ns	83.2 ^a	87.5 ^{abc}	***
452	3623.5 ^{cde}	3226.9 ^a	ns	821.0 ^d	2210.8 ^b	***	20.6 ^a	25.6 ^b	***	46.6 ^{ab}	46.3 ^{ab}	ns	83.0 ^a	87.5 ^{abc}	***
456	3588.0 ^{cde}	3538.5 ^{abc}	ns	784.8 ^{bcd}	2356.5 ^{bc}	***	30.2 ^{bc}	33.9 ^{cde}	**	46.0 ^{ab}	47.0 ^{abc}	ns	83.0 ^a	87.2 ^{abc}	***
457	3443.3 ^{bcde}	3430.0 ^{ab}	ns	857.1 ^{de}	2205.8 ^b	***	33.8 ^{cde}	36.9 ^{ef}	ns	47.2 ^{ab}	48.5 ^{abcd}	ns	83.3 ^a	88.0 ^{abc}	***
458	3065.0 ^{abcde}	3711.3 ^{abc}	*	823.8 ^{de}	2278.6 ^b	***	19.1 ^a	22.0 ^a	***	45.3 ^{ab}	45.8 ^{ab}	ns	83.5 ^a	88.0 ^{abc}	***
463	3396.9 ^{bcde}	3657.0 ^{abc}	ns	900.0 ^e	2223.9 ^b	***	33.2 ^{bcd}	37.6 ^f	***	44.3 ^a	47.0 ^{abc}	ns	82.8 ^a	88.6 ^{abc}	***
464	4071.3 ^c	4244.4 ^{bc}	ns	847.6 ^{de}	2660.9 ^c	***	29.2 ^b	33.4 ^{cd}	***	46.0 ^{ab}	47.0 ^{abc}	ns	83.5 ^a	88.0 ^{abc}	***
467	3465.0 ^{bcde}	3965.0 ^{abc}	ns	809.5 ^d	2144.6 ^b	***	32.9 ^{bcd}	36.0 ^{def}	*	47.4 ^{ab}	48.8 ^{bcd}	ns	83.0 ^a	87.8 ^{abc}	***
473	3574.2 ^{cde}	3562.5 ^{abc}	ns	857.1 ^{de}	2330.6 ^b	***	34.8 ^{de}	42.4 ^g	***	46.8 ^{ab}	46.2 ^{ab}	ns	82.7 ^a	88.4 ^{abc}	***
475	2775.8 ^{abcd}	3345.4 ^{ab}	*	825.4 ^{de}	2395.2 ^{bc}	***	34.7 ^{cde}	38.5 ^f	**	45.8 ^{ab}	46.7 ^{ab}	ns	82.7 ^a	88.7 ^{abc}	***
478	3693.0 ^{de}	4370.0 ^c	*	845.7 ^{de}	2172.5 ^b	***	34.0 ^{cde}	38.5 ^f	***	46.6 ^{ab}	47.0 ^{abc}	ns	82.8 ^a	89.8 ^{bc}	***
479	3353.0 ^{bcde}	4192.1 ^{bc}	*	857.1 ^{de}	2343.2 ^{bc}	***	32.1 ^{bcd}	37.2 ^f	*	46.4 ^{ab}	45.8 ^{ab}	ns	82.8 ^a	88.3 ^{abc}	***
483	4066.7 ^e	4379.2 ^c	ns	860.3 ^{de}	2339.2 ^{bc}	***	34.2 ^{cde}	42.2 ^g	ns	47.7 ^{ab}	45.0 ^a	ns	83.0 ^a	90.0 ^c	***
485	3186.0 ^{abcde}	3236.7 ^a	ns	801.9 ^{cd}	2236.8 ^b	***	35.3 ^{de}	35.4 ^{def}	ns	45.6 ^{ab}	49.0 ^{bcd}	ns	83.0 ^a	87.7 ^{abc}	***
487	2558.8 ^{abc}	3355.0 ^{ab}	**	850.8 ^{de}	2218.6 ^b	***	36.4 ^e	42.3 ^g	**	48.0 ^{abc}	47.8 ^{abcd}	ns	83.0 ^a	87.4 ^{ab}	***
Blanco Español	2148.4 ^a	3674.6 ^{abc}	***	733.3 ^{abc}	1610.9 ^a	***	48.1 ^f	50.8 ^h	ns	49.4 ^{bc}	48.8 ^{bcd}	ns	83.8 ^a	95.5 ^d	***
Curi	2273.4 ^a	3485.6 ^{abc}	***	676.2 ^a	1584.2 ^a	***	19.2 ^a	22.5 ^a	**	47.4 ^{ab}	46.0 ^{ab}	ns	83.0 ^a	89.5 ^{abc}	***
Lpci	2280.6 ^a	3245.5 ^a	*	711.9 ^{ab}	1625.1 ^a	***	46.6 ^{ef}	49.8 ^h	*	55.5 ^e	50.8 ^{de}	ns	87.3 ^b	104.4 ^e	***
Sel.6	2968.0 ^{abcd}	3993.1 ^{abc}	***	733.3 ^{abc}	1613.9 ^a	***	41.6 ^f	49.4 ^h	**	51.6 ^{cd}	50.3 ^{cde}	ns	86.4 ^b	104.5 ^e	***
Zorzal	2483.3 ^{ab}	3905.5 ^{abc}	**	720.6 ^{ab}	1648.0 ^a	***	47.7 ^{ef}	49.8 ^h	ns	54.5 ^{de}	53.0 ^e	ns	87.5 ^b	104.8 ^e	***

The HGW also showed significant genotypic differences under both water regimes ($p < 0.05$). In ND, the highest HGW was observed in genotypes 'Blanco Español' (50.82 g), 'Lpci' (49.96 g), 'Zorzal' (49.44 g), and 'Sel 6' (48.36 g). Conversely, genotypes 458 (21.85 g) and 'Curi' (22.32 g) displayed the lowest HGW. Under DS conditions, 'Blanco Español' (48.12 g), 'Zorzal' (47.68 g), 'Lpci' (46.53 g), and 'Sel 6' (41.53 g) maintained relatively high seed weight values with nonsignificant differences among them, suggesting stability in seed size despite water limitation. Meanwhile, 458 (19.12 g) and 'Curi' (19.20 g) consistently showed the lowest HGW across both environments ($p < 0.05$).

Crude protein, total phenolics, and antioxidant capacity

The stress moderately affected the protein content; only a few genotypes showed significant differences between water regimes (Figure 1a). Genotypes 467, 475, 487, BE, and 'Lpci' showed significant increases ($p < 0.001$) in protein content in DS. Genotype 467 increased from 20.76% in ND to 22.55% under DS, and 475 showed a similar rise from 24.10% to 25.98%. The commercial 'Blanco Español' also exhibited a notable increase in protein under DS (23.13% in ND to 25.43% in DS), indicating a potentially beneficial physiological response to water deficit. Most of the genotype's protein levels remained stable across treatments, suggesting that PC accumulation is relatively conserved and less sensitive to terminal drought.

The TPC varied significantly among genotypes under both DS and ND, with several genotypes exhibiting marked changes between the two water conditions (Figure 1b). Significant increases ($p < 0.05$) in phenolic concentration due to DS were observed in genotypes 452, 457, 458, 464, 467, 483, 487, and 'Blanco Español'. For instance, genotype 452 rose from 57.32 to 69.92 mg 100 g⁻¹, and 457 nearly doubled from 34.88 to 67.93 mg 100 g⁻¹. Genotype 458 exhibited a significant increase from 46.77 in ND to 57.02 mg 100 g⁻¹ in DS. Conversely, 'Curi' had the highest phenolic content under ND (85.84 mg 100 g⁻¹) and a significant decrease ($p < 0.05$) under DS (65.72 mg 100 g⁻¹). These findings suggest that drought stress induces phenolic compounds accumulation in several genotypes, likely as part of an antioxidant defense mechanism.

The DPPH antioxidant activity showed marked differences among genotypes under both irrigation (ND) and drought stress (DS) conditions (Figure 1c). Under ND, the highest antioxidant activity was recorded in Curi (3632.92 $\mu\text{mol TE g}^{-1}$), followed by genotypes 452 and 457 (3340.71 and 3269.73 $\mu\text{mol TE g}^{-1}$, respectively), which are significantly different from all other genotypes. Nonsignificant differences were observed among the remaining genotypes. In DS treatment, 'Curi' again exhibited the highest antioxidant activity (4825.46 $\mu\text{mol TE g}^{-1}$) ($p < 0.05$), followed by 458 (3536.22 $\mu\text{mol TE g}^{-1}$), 457 and 452. Most genotypes remained in the same statistical group with values below 400 $\mu\text{mol TE g}^{-1}$, except for 'Lpci' and 'Sel 6', which, although still in the same group, showed a notable increase in antioxidant capacity under DS. The mean separation letters indicate that most genotypes did not significantly shift groups under DS. Genotypes 'Lpci' and 'Sel 6' showed substantial increases in the DPPH antioxidant activity under DS compared to their ND values. In contrast, genotypes like 'Curi' and 458 consistently maintained superior antioxidant power under both conditions.

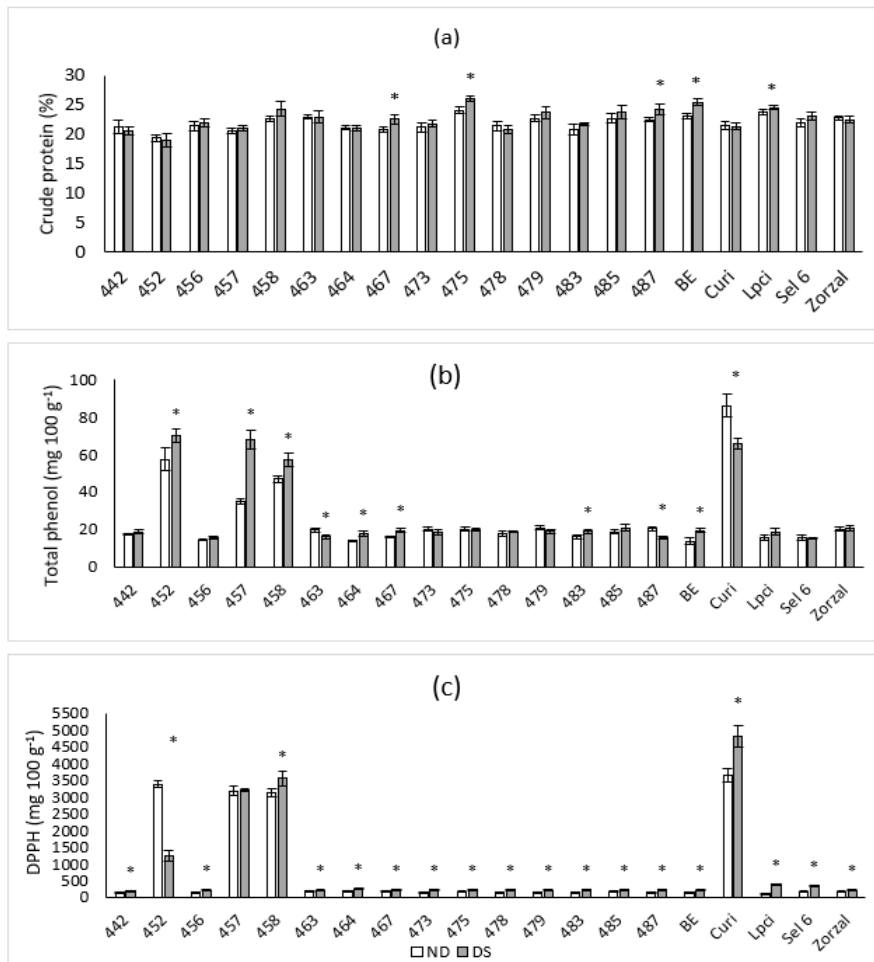


Figure 1. Crude protein content (a), total phenolic content (b), and antioxidant capacity (DPPH) (c) evaluated in 20 bean genotypes during two seasons under no stress (ND) and terminal drought stress (DS). Error bars represent the standard error of the mean. Means marked by asterisks indicate the significant difference between ND and DS for the same genotype using the independent-samples t-test ($p \leq 0.05$). DPPH: 2,2-diphenyl-1-picrylhydrazyl.

Hydration capacity and cooking time

Significant differences ($p < 0.05$) in HC were observed between ND and DS irrigation treatments in several genotypes (Figure 2a). Most genotypes exhibited increased HC under DS conditions ($p < 0.05$), including 442, 452, 458, 464, 475, 478, 479, 483, 487, 'Curi', and 'Zorzal'. Genotype 458 exhibited one of the highest hydration levels under both treatments, increasing from 61.63% in ND to 72.41% in DS, while 'Curi' reached the highest absolute hydration under DS (79.41%). Notably, 478 showed a marked increase, rising from just 9.70% under ND to 28.34% under DS.

Variations in CT between irrigation regimes revealed genotype-dependent responses in several genotypes under DS and ND (Figure 2b). Significant increases in CT under DS were observed in genotypes 442, 452, 467, and 479 ($p < 0.05$); for example, CT in genotype 452 increased from 46.88 min under normal irrigation to 55.83 min under drought stress. In contrast, genotypes 458, 485, and 'Zorzal' under ND irrigation exhibited significant increases in CT ($p < 0.05$), suggesting a genotype-specific reduction in CT under DS. Similarly, 'Zorzal' genotype decreased its CT from 57.58 min in ND to 45.46 min under DS conditions.

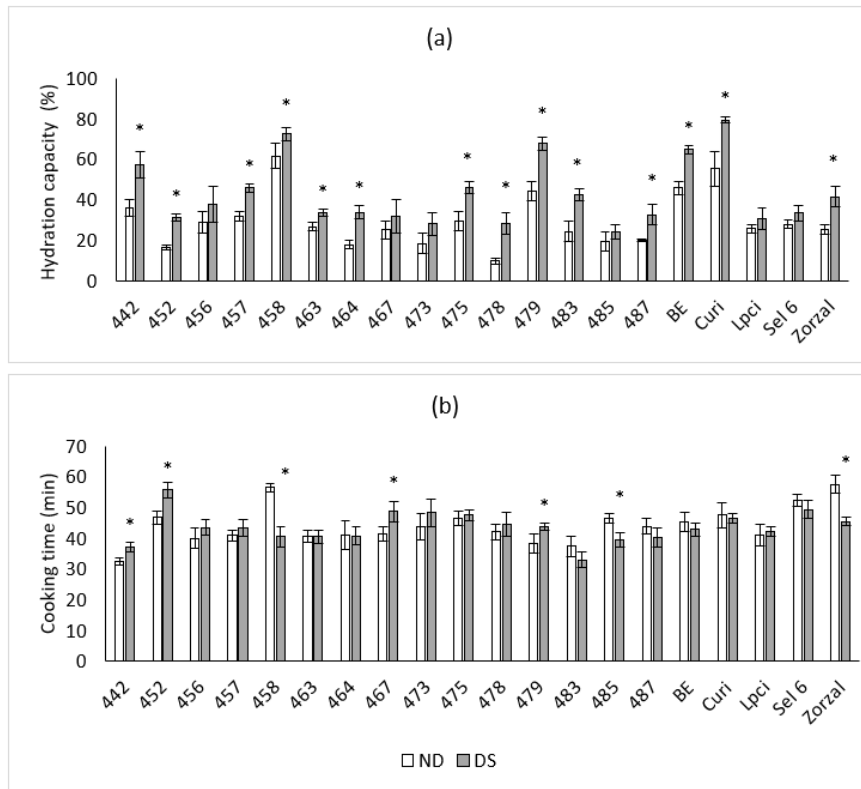


Figure 2. Hydration capacity (a) and cooking time (b) evaluated in 20 bean genotypes during two seasons under no stress (ND) and terminal drought stress (DS). Error bars represent the standard error of the mean. Means marked by asterisks indicate the significant difference between ND and DS for the same genotype using the independent-samples t-test ($p \leq 0.05$).

Correlation and cluster analysis

Genotypes under ND exhibited strong red intensities in GY and NGP, implying a positive correlation with optimal water availability. Conversely, under DS, a shift towards blue in GY and NGP in several genotypes, indicated a negative correlation with drought stress, consistent with lower yield under water deficit (Figures 3 and 4).

Genotypes 458 and 'Curi' stood out by showing high values (red) for DPPH, TPC, and HC along with lower CT, indicating a high plasticity in grain quality under DS and ND conditions. In contrast, genotypes like DS 'Lpci', DS 'Sel 6', and their irrigated counterparts (ND 'Lpci', ND 'Sel 6') exhibited low values across quality variables, reflecting functional performance.

High values for GY, NGP, and HGW were maintained for the genotypes DS 464 and DS 483, suggesting good agronomic performance under drought stress. The separation between ND and DS conditions within the same genotype, as observed in the clustering pattern, indicates that water regime significantly alters both the functional and productive profiles of the evaluated lines. These results emphasize the importance of integrating nutritional and technological quality parameters with agronomic traits in breeding programs to improve drought tolerance.

The heatmap analysis provided a comprehensive visualization of the integrated responses of common bean genotypes evaluated under ND and DS conditions, the clustering of variables revealed meaningful associations: DPPH and TPC clustered closely, confirming their strong correlation as indicators of antioxidant capacity; GY and NGP were grouped together, indicating that the number of seeds per pod highly influences grain yield and HGW and CP also formed a cluster, suggesting that genotypes with heavier seeds tend to have higher protein content.

Correlation plot from data

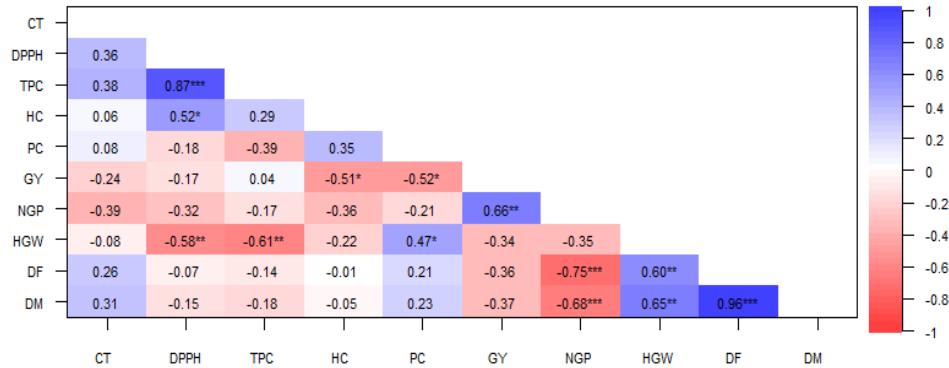


Figure 3. Heat map of Pearson correlations among traits studied under drought stress (DS) in 20 bean genotypes across two seasons. CT: Cooking time; DPPH: antioxidant capacity (2,2-diphenyl-1-picrylhydrazyl); TPC: total phenolic content; HC: hydration capacity; PC: crude protein content; GY: grain yield; NGP: number of grains per pod; HGW: hundred-grain weight; DF: days to flowering; DM: days to physiological maturity. Positively related parameters are highlighted in blue, while negatively related ones are highlighted in red * $p \leq 0.05$, ** $p \leq 0.01$, and *** $p \leq 0.001$.

Correlation plot from data

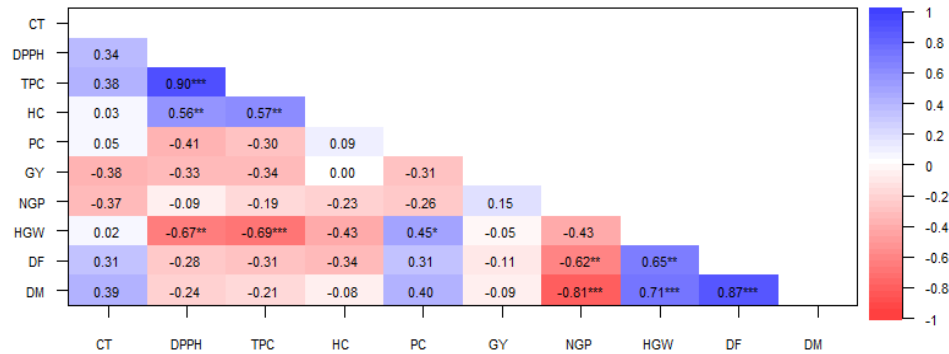


Figure 4. Heat map of Pearson correlations among traits studied under no drought (ND) conditions evaluated across 20 bean genotypes during two seasons. CT: Cooking time; DPPH: antioxidant capacity (2,2-diphenyl-1-picrylhydrazyl); TPC: total phenolic content; HC: hydration capacity; PC: crude protein content; GY: grain yield; NGP: number of grains per pod; HGW: hundred-grain weight; DF: days to flowering; DM: days to physiological maturity. Positively related parameters are highlighted in blue, while negatively related ones are highlighted in red * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$.

DISCUSSION

Grain yield (GY) is the most important and reliable agronomic trait in common bean; it was significantly affected by water regime (WR), genotype (G), and their interaction (WR \times G) ($p < 0.001$) (Table 3). Across all genotypes, the mean GY under non-stress conditions was 3891 kg ha⁻¹, which dropped to 3023 kg ha⁻¹ under drought stress, representing a 22.7% yield reduction. This decline reflects the strong sensitivity of bean productivity to terminal drought. The variation among genotypes and their interaction with water availability suggest differences in

genotype performance under water stress. These findings are consistent with previously reported studies on common beans, showing significant yield reductions ranging from 20% to 76% under water stress compared to well-watered conditions (Androcioli et al., 2020). Some genotypes exhibited high yield stability, performing consistently well under terminal drought stress (DS) and no drought (ND) conditions, indicating drought tolerance (Gonçalves et al., 2019). The GY was positively correlated with hundred-grain weight (HW) under DS conditions ($r = 0.465$, $p < 0.05$), indicating that genotypes can maintain seed size under stress conditions and achieve high productivity. Similar findings were reported by Polania et al. (2017), who observed that seed weight stability under water deficit is a beneficial characteristic in drought-tolerant genotypes.

Water availability also significantly affected the number of grains per pod (NGP) ($p < 0.001$) across genotypes; the mean NGP was 2117 grains m^{-2} , whereas DS reduced this value to 809 grains m^{-2} , a 61% reduction. Furthermore, it was confirmed that interaction (WR \times G) significantly affected NGP ($p < 0.001$) (Table 3), highlighting the substantial influence of both genetic background and drought on this trait (Neto et al., 2022).

The HW, a trait that reflects seed size, exhibited significant differences among genotypes under ND and DS conditions and displayed significant genotypic variation under both water regimes ($p < 0.001$) because of DS (Table 3). On average, HW decreased from 37.74 g under ND to 33.89 g under drought conditions, representing a 10.2% reduction. Despite the overall decline, several genotypes maintained relatively stable HW within DS (Table 4). Genotypes such as 'Blanco Español' (48.1 g), 'Zorzal' (47.7 g), 'Lpci' (46.6 g), and 'Sel.6' (41.6 g) consistently ranked in the top statistical group across both environments (Tables 4 and 5), showing resilience in maintaining seed weight. This stability suggests that these lines possess favorable physiological traits related to seed filling and remobilization of assimilates under terminal drought (Polania et al., 2016). In contrast, drought-sensitive genotypes such as 458 (19.1 g) and 'Curi' (19.2 g) were among the lowest performers in DS and ND conditions. The differential response of HW across genotypes to drought stress can be attributed to adaptive mechanisms, including efficient water use, osmotic adjustment, and resource allocation prioritization for reproductive development (Assefa et al., 2017).

The HW was highly influenced by genotype and water regime. The G \times WR interaction was nonsignificant ($p = 0.183$), indicating that genotypes responded similarly to water stress; this suggests that seed weight is a more genetically stable trait than seed number and less influenced by environmental fluctuations (Mutari et al., 2023). Genotypes 483, 478, and 473 exhibited high HW and above-average GY under drought conditions, indicating efficient assimilation partitioning to the reproductive sink. These findings align with previous studies that emphasize the role of HW in yield maintenance under stress (Elias et al., 2021).

A positive correlation was observed between HW and protein content (PC) under both water regimes, the correlation (ND; $r = 0.454$, DS; $r = 0.465$) (Figures 3 and 4) suggesting that genotypes with heavier seeds tended to maintain higher protein levels despite the water availability and a consistent association between seed size and protein accumulation across environments (Bulyaba et al., 2020).

The hydration capacity (HC) is critical in dry beans because rapid and extensive water uptake shortens cooking time (CT) (Katuramu et al., 2020). Under DS, the HC increased in most genotypes compared with ND, with an average of 29.5 % under ND to 43.7 %. The magnitude of the HC increase was highly genotype-dependent ($p < 0.001$) (Table 3). 'Curi', 458, 479, and 'Blanco Español' displayed the highest absolute values under DS (79.4%, 72.4%, 67.8%, and 64.9%, respectively). This result could be explained by the fact that under DS, plants tend to accumulate high concentrations of soluble sugars, amino acids, and other compatible solutes in their tissues, which could cause a greater absorption capacity (Tapia et al., 2022); conversely, 'Lpci' (30.5%) and 478 (28.3%) remained among the lowest HC even under stress.

The CT and HC in this study were genotype-specific ($p < 0.001$), which indicates that seed hydration alone does not entirely predict thermal softening in faster CT (Barros and Prudêncio, 2016). Genotypes 458 and 'Curi' combined high HC with long CT (46 min), implying that this differential response suggests that water availability during seed development can influence the seed coats' and cotyledons' physicochemical properties, thereby altering cooking behavior. For instance, the observed reduction in CT under DS in some genotypes may be

associated with enhanced seed-coat permeability and accelerated hydration; other factors beyond water uptake, such as cell-wall pectin cross-linking or protein-starch matrix rigidity, also modulate thermal softening (Corrêa et al., 2010). In contrast, 442 and 475 demonstrated increased HC and moderate CT (45 min) under DS.

Table 5. Effect of water regime on the quality and culinary aptitude of 20 common bean genotypes under (ND) and (DS) conditions. PC: Total protein content; DPPH: antioxidant capacity (2,2-diphenyl-1-picrylhydrazyl); TPC: total phenolic content; HC: hydration capacity; CT: cooking time; DS: terminal drought stress; ND: no drought stress. Different letters in the column indicate significant differences according to Duncan's multiple range test ($P \leq 0.05$). t: refers to the t independent samples test for each genotype in DS and ND; ns nonsignificant; * $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq 0.001$.

Genotypes	PC (%)			DPPH (mg 100 g ⁻¹)			TPC (mg 100 g ⁻¹)			HC (%)			CT (min)		
	DS	ND	t	DS	ND	t	DS	ND	t	DS	ND	t	DS	ND	t
442	20.6 ^{ab}	20.8 ^{abc}	ns	185.9 ^a	156.0 ^a	ns	19.3 ^a	17.9 ^a	ns	47.4 ^{de}	47.7 ^e	ns	38.8 ^{abc}	31.3 ^a	**
452	19.3 ^a	19.2 ^a	ns	1192.0 ^b	3338.0 ^c	***	64.8 ^{bc}	61.1 ^d	ns	20.4 ^a	29.6 ^{bcde}	ns	46.8 ^{cdefg}	54.0 ^e	ns
456	22.4 ^{bcdef}	20.9 ^{abc}	ns	213.9 ^a	176.4 ^a	*	16.0 ^a	14.1 ^a	ns	37.3 ^{bcd}	30.8 ^{cdef}	ns	40.2 ^{abcde}	36.6 ^{abc}	ns
457	21.1 ^{abc}	20.6 ^{abc}	ns	3233.0 ^c	3269.7 ^c	ns	71.5 ^c	34.5 ^b	**	32.5 ^{abcd}	42.6 ^{fg}	ns	45.0 ^{bcdefg}	39.5 ^{abcd}	ns
458	24.3 ^{efg}	22.2 ^{cde}	ns	3536.2 ^c	3125.3 ^b	ns	57.9 ^b	46.9 ^c	ns	67.5 ^f	73.0 ^h	ns	51.2 ^g	46.5 ^{cdefg}	ns
463	23.6 ^{cdefg}	22.5 ^{cde}	ns	215.3 ^a	179.4 ^a	ns	16.5 ^a	21.6 ^a	ns	24.9 ^{abc}	36.4 ^{ef}	**	39.0 ^{abcd}	39.4 ^{abcd}	ns
464	21.2 ^{abc}	20.7 ^{abc}	ns	250.6 ^a	181.8 ^a	ns	17.5 ^a	13.3 ^a	***	21.4 ^{ab}	28.4 ^{bcde}	ns	48.0 ^{efg}	40.8 ^{abcde}	ns
467	22.3 ^{bcdef}	21.0 ^{abcd}	ns	238.5 ^a	175.4 ^a	**	17.6 ^a	15.7 ^a	*	35.2 ^{abcd}	20.1 ^{abc}	ns	46.2 ^{bcdefg}	42.8 ^{bcdef}	ns
473	21.8 ^{abcde}	20.9 ^{abc}	ns	227.0 ^a	139.2 ^a	***	16.7 ^a	21.1 ^a	ns	23.0 ^{ab}	20.9 ^{abc}	ns	47.7 ^{efg}	50.4 ^{efg}	ns
475	26.0 ^g	24.1 ^e	ns	237.4 ^a	162.1 ^a	***	19.8 ^a	19.5 ^a	ns	40.0 ^{cd}	36.0 ^{ef}	ns	44.5 ^{bcdefg}	46.3 ^{cdefg}	ns
478	20.9 ^{ab}	21.5 ^{bcd}	ns	211.0 ^a	143.2 ^a	**	18.8 ^a	18.5 ^a	ns	25.6 ^{abc}	15.7 ^a	ns	45.2 ^{bcdefg}	45.2 ^{bcdefg}	ns
479	23.2 ^{bcdef}	22.7 ^{cde}	ns	208.0 ^a	156.8 ^a	*	18.3 ^a	20.4 ^a	ns	59.6 ^{ef}	52.0 ^g	ns	38.4 ^{ab}	39.3 ^{abcd}	ns
483	21.6 ^{abcd}	19.8 ^{ab}	ns	220.8 ^a	175.1 ^a	**	17.7 ^a	16.1 ^a	ns	31.0 ^{abc}	30.4 ^{cde}	ns	36.3 ^a	35.0 ^{ab}	ns
485	24.1 ^{defg}	22.7 ^{cde}	ns	224.8 ^a	165.8 ^a	**	22.4 ^a	19.7 ^a	ns	29.4 ^{abc}	18.2 ^{ab}	ns	42.2 ^{bcdefg}	41.2 ^{abcde}	ns
487	24.3 ^{efg}	22.2 ^{cde}	ns	219.5 ^a	154.7 ^a	**	14.6 ^a	23.3 ^a	ns	29.1 ^{abc}	23.7 ^{abcd}	ns	45.3 ^{bcdefg}	42.2 ^{bcdef}	ns
Blanco Español	26.0 ^g	23.1 ^{de}	*	195.8 ^a	146.6 ^a	*	18.9 ^a	14.2 ^a	**	64.4 ^f	51.0 ^g	*	45.0 ^{bcdefg}	44.5 ^{bcdefg}	ns
Curi	21.5 ^{abc}	20.8 ^{abc}	ns	4820.3 ^e	3630.2 ^d	**	64.4 ^{bc}	83.9 ^e	*	60.6 ^{ef}	70.2 ^h	ns	47.2 ^{defg}	49.5 ^{defg}	ns
Lpci	24.4 ^{fg}	23.8 ^e	ns	396.4 ^a	135.9 ^a	**	18.7 ^a	15.0 ^a	ns	29.1 ^{abc}	23.1 ^{abcd}	ns	42.0 ^{bcdefg}	41.8 ^{bcdef}	ns
Sel.6	22.6 ^{bcdef}	21.5 ^{bcd}	ns	378.6 ^a	172.1 ^a	**	14.4 ^a	17.4 ^a	ns	22.7 ^{ab}	35.9 ^{ef}	*	48.0 ^{efg}	52.0 ^{fg}	ns
Zorzal	22.4 ^{bcdef}	22.5 ^{cde}	ns	210.6 ^a	164.8 ^a	ns	19.8 ^a	21.9 ^a	ns	34.8 ^{abcd}	33.6 ^{def}	ns	49.2 ^{fg}	52.2 ^{fg}	ns

The total phenolic content (TPC) revealed differences among genotypes ($p < 0.001$) (Table 3), as well as for the $G \times WR$ interaction, indicating that genotypes and water availability influence phenolic accumulation in common bean seeds. Genotype 'Curi' recorded the highest phenolic content under ND (85.84 mg 100 g⁻¹), which significantly declined under DS (65.72 mg 100 g⁻¹), though still among the highest TPC producers. This suggests that while some genotypes possess inherently high phenolic levels, they may not further enhance them under drought (Albergaria et al., 2020). Conversely, genotypes 452, 457, and 458 notably increased phenolic accumulation under drought conditions, demonstrating a plastic response (Figure 1b). Most genotypes showed an increased TPC under DS, suggesting an inducible antioxidant defense response to water deficit. This observation aligns with previous findings that drought conditions provoke an inducible antioxidant defense response to water deficit (Kuşvuran and Daşgan, 2017). Also, there were strong and significant correlations observed in this study between TPC and DPPH antioxidant activity ($r = 0.902$ under ND and $r = 0.867$ under DS; $p < 0.001$); these results support the functional contribution of phenolics to antioxidant activity as a primary antioxidant in common beans (Ganesan and Xu, 2017; Chávez-Mendoza et al., 2018; Sica et al., 2021) (Figures 3 and 4).

Significant variation in DPPH activity was observed among genotypes ($p < 0.001$), with a highly significant $G \times WR$ interaction (Table 3). The average DPPH values ranged from 135.9 to 4820.3 mg 100 g⁻¹, highlighting

substantial genotypic differences in antioxidant capacity under the different water regimes. Under ND conditions, genotypes 452, 457, 458, and 'Curi' exhibited notably high antioxidant activity ($> 3100 \text{ mg } 100 \text{ g}^{-1}$), with 'Curi' reaching the highest value. These genotypes maintained or even increased their antioxidant capacity under DS, with 'Curi' reaching $4820.3 \text{ mg } 100 \text{ g}^{-1}$, followed by 458 ($3536.2 \text{ mg } 100 \text{ g}^{-1}$) and 457 ($3232.9 \text{ mg } 100 \text{ g}^{-1}$). The DS has been reported to increase the accumulation of phenolics as part of the plant's adaptive response to oxidative stress since drought, enhanced by DPPH activity. Drought-induced oxidative stress stimulates phenylpropanoid pathway activity, thereby increasing the biosynthesis of phenolic compounds as a protective response (Kuşvuran and Daşgan, 2017; Desoky et al., 2021; Sica et al., 2021), which results in enhanced DPPH activity. This aligns with the findings of Chávez-Mendoza et al. (2018), who noted that phenolic-rich bean genotypes often retain strong antioxidant activity even under abiotic stress. The stability of DPPH values in several genotypes across both water regimes supports the hypothesis that antioxidant capacity is genotype-dependent and may be linked to drought tolerance mechanisms. Genotypes such as 473 and 'Lpci' exhibited consistently lower antioxidant activity, suggesting a potential susceptibility to oxidative stress or a reduced allocation of metabolic resources toward antioxidant defense mechanisms. Furthermore, differences in phenolic content and antioxidant activity among genotypes have been reported, even within the same seed coat color; this suggests that antioxidant capacity is largely influenced by genotype-specific phenolic composition, leading to substantial variation in antioxidant activity among genotypes despite similar external characteristics (Kuşvuran and Daşgan, 2017; Madrera et al., 2021).

Cluster analysis of phenotypic and quality traits

The hierarchical cluster heat map provided a comprehensive visual representation of the relationships among genotypes and traits under DS and ND conditions. This multivariate approach enabled the identification of genotype groups sharing similar physiological, agronomic, and seed quality profiles.

Two distinct clusters emerged, separating genotypes based on water regime, underscoring the significant influence of drought on trait expression. Within each condition, genotypes exhibiting higher antioxidant capacity DPPH and TPC, such as 458 and 'Curi', were clustered together regardless of water regime, and 452 and 457 were also clustered together, but within the main ND and DS clusters, suggesting a strong genotype effect and a notable increase in phenolic accumulation under drought conditions, demonstrating a significant response of these genotypes under water deficit. These genotypes also tended to show increased CT and lower hydration rates. In contrast, genotypes such as 442, 456, 479, and 483 grouped with lower DPPH and TPC alongside relatively favorable HC and CT, potentially reflecting different physiological adaptation strategies that are less reliant on oxidative stress defense. Genotypes like 'Sel 6', 'Zorzal', 'Lpci', and 'Blanco Español' formed a separate cluster characterized by high PC and HGW values, with a major antioxidant performance, suggesting a distinct allocation of resources toward seed biomass and nutritional traits rather than the production of antioxidants.

Furthermore, clustering revealed that agronomic traits like GY and NGP are inversely associated with phenolic-related traits, underlying a physiological trade-off or genotype-specific prioritization of yield vs. antioxidants accumulation-related processes under stress. For instance, clear associations between traits were observed between TPC and DPPH. Also, GY and NGP formed a coherent trait module that was inversely associated with phenolic-related traits in some clusters. This spatial opposition in the heat map may indicate underlying physiological trade-offs or genotype-specific prioritization of yield vs. quality biochemicals and antioxidants-related processes under stress.

The Figure 5 shows that clear trait clusters emerged, and TPC and DPPH clustered closely, reflecting their strong positive correlation. Genotypes such as 'Curi', 452, and 457 were grouped due to elevated antioxidant content, while others like 456 and 483 clustered with higher GY and HGW. This supports the differentiation of drought response, with genotypes prioritizing nutritional or stress-related traits while others maintain yield and biochemical and antioxidant performance.

Terminal drought significantly affected the productivity and quality of the evaluated genotypes under DS; GY, NGP decreased, and fewer DM. However, some genotypes are distinguished by maintain stable HGW, consistent protein content, and increased phenolic compounds content and antioxidant capacity as adaptive responses. These results reveal significant genotypic variability in response to water deficit during the reproductive stage, facilitating the identification of genotypes with superior agronomic performance and nutritional quality under drought. This knowledge is of great value for future breeding strategies to select genotypes that combine drought tolerance with improved grain quality.

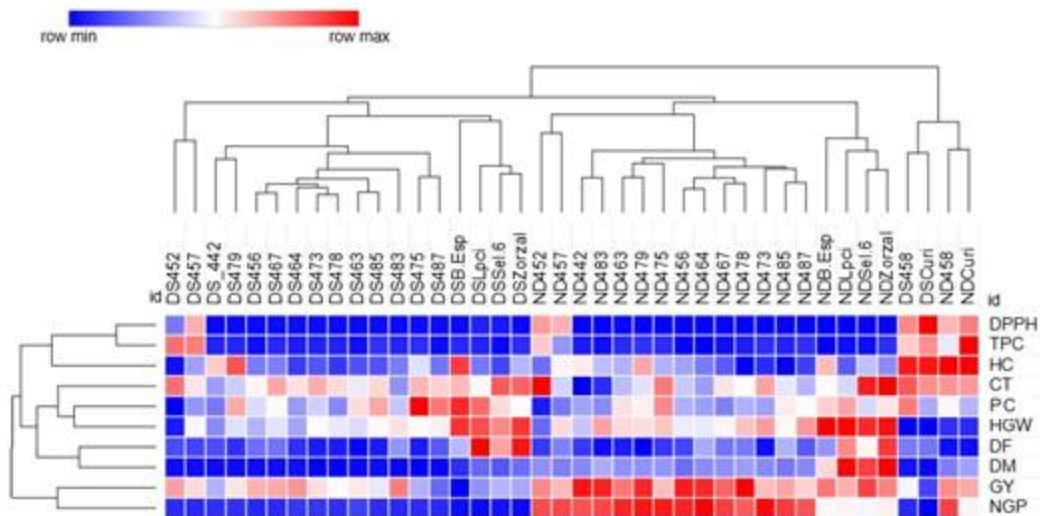


Figure 5. Heat map and hierarchical clustering of phenological, productive and quality traits among studied under no drought (ND) and drought stress (DS) evaluated in 20 common bean genotypes across two seasons. DPPH: Antioxidant capacity (2,2-diphenyl-1-picrylhydrazyl); TPC: total phenolic content; HC: hydration capacity; CT: cooking time; PC: crude protein content; HGW: hundred-grain weight; DF: days to flowering; DM: days to physiological maturity; GY: grain yield; NGP: number of grains per pod.

CONCLUSIONS

This study evaluated the agronomic performance and nutritional quality of 20 common bean genotypes under terminal drought conditions in south-central Chile over two growing seasons. The results indicate that terminal drought stress significantly reduces grain yield (GY) and number of grains per pod (NGP), with a moderate decrease of hundred-grain weight (HGW). However, genotypes 452, 464, 473, and 483 maintained GY and demonstrated resilience in HGW, highlighting their potential as promising breeding candidates for improve drought tolerance.

Regarding grain quality, terminal drought had variable effects across genotypes. Several genotypes showed increased total phenolic contents and enhanced antioxidant capacity (DPPH), suggesting an active biochemical response to stress. Protein content remained relatively stable across treatments, with some genotypes exhibiting significant increases under drought conditions. These findings underscore the importance of selecting genotypes combining agronomic stability with high nutritional quality. These dual-purpose genotypes are crucial for developing new cultivars adapted to the increasing water scarcity expected to increase in this region.

Author contribution

Conceptualization: N.Z., K.T. Methodology: N.Z., M.L., K.T., C.U. Software: A.K., M.G. Validation: N.Z., K.T., M.G., A.K. Formal analysis: A.K., M.G. Investigation: K.T., N.Z. Resources: K.T., N.Z. Data curation: A.K., M.G., K.T. Writing, original draft: K.T., N.Z. Writing, review and editing: M.G., A.K., C.U., M.L. Supervision: K.T., N.Z. Project administration: K.T., N.Z. Funding acquisition: K.T., N.Z. All co-authors reviewed the final version and approved the manuscript before submission.

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References

- Albergaria, E.T. de, Oliveira, A.F.M. de, Albuquerque, U.P. 2020. The effect of water deficit stress on the composition of phenolic compounds in medicinal plants. *South African Journal of Botany* 131:12-20.
- Androcioli, L.G., Zeffa, D.M., Alves, D.S., Tomaz, J.P., Moda-Cirino, V. 2020. Effect of water deficit on morphoagronomic and physiological traits of common bean genotypes with contrasting drought tolerance. *Water* 12(1):217.
- AOAC. 1996. Official method of analysis of the Association of Official Analytical Chemists (AOAC). AOAC International, Arlington, Virginia, USA.
- Assefa, T., Rao, I.M., Cannon, S.B., Wu, J., Gutema, Z., Blair, M.W., et al. 2017. Improving adaptation to drought stress in white pea bean (*Phaseolus vulgaris* L.): Genotypic effects on grain yield, yield components and pod harvest index. *Plant Breeding* 136(4):548-561.
- Barros, M. de, Prudêncio, S.H. 2016. Physical and chemical characteristics of common bean varieties. *Semina: Ciências Agrárias* 37(2):751-762.
- Bondet, V., Brand-Williams, W., Berset, C. 1997. Kinetics and mechanisms of antioxidant activity using the DPPH free radical method. *LWT-Food Science and Technology* 30(6):609-615.
- Brito, L., Rodrigues, P., Martins, G., Silva, W. 2013. Water absorption in bean seeds (*Phaseolus vulgaris* L.) during processing. *Revista Brasileira de Engenharia Agrícola e Ambiental* 31(2):285-292.
- Brunet-Loredo, A., López, M.D., Cordero-Lara, K.I., Noriega, F., Cabeza, R.A., Fischer, S., et al. 2023. Assessing grain quality changes in white and black rice under water deficit. *Plants* 12(24):4091.
- Bulyaba, R., Winham, D.M., Lenssen, A.W., Moore, K.J., Kelly, J.D., Brick, M.A., et al. 2020. Genotype by location effects on yield and seed nutrient composition of common bean. *Agronomy* 10(3):347.
- Campos, K.M., Schwember, A.R., Machado, D.L.M., Ozores-Hampton, M., Gil, P.M. 2021. Physiological and yield responses of green-shelled beans (*Phaseolus vulgaris* L.) grown under restricted irrigation. *Agronomy* 11(3):562.
- Chávez-Mendoza, C., Hernández-Figueroa, K.I., Sánchez, E. 2018. Antioxidant capacity and phytonutrient content in the seed coat and cotyledon of common beans (*Phaseolus vulgaris* L.) from various regions in Mexico. *Antioxidants* 8(1):5.
- Corrêa, M.M., Carvalho, L.M.J. de, Nutti, M.R., Carvalho, J.L.V. de, Neto, A.R.H., and Ribeiro, E.M.G. 2010. Water absorption, hard shell and cooking time of common beans (*Phaseolus vulgaris* L.) *African Journal of Food Science* 1(1):13-19.
- Desoky, E.M., Mansour, E., El-Sobky, E.E.A., Abdul-Hamid, M.I.E., Taha, T.F., Elakkad, H.A., et al. 2021. Physio-biochemical and agronomic responses of faba beans to exogenously applied nano-silicon under drought stress conditions. *Frontiers in Plant Science* 12:637783. doi:10.3389/fpls.2021.637783.
- Didinger, C., Thompson, H.J. 2022. The role of pulses in improving human health: A review. *Legume Science* 4(4):e147.
- Elias, J.C.F., Gonçalves-Vidigal, M.C., Vaz Bisneta, M., Valentini, G., Vidigal Filho, P.S., Gilio, T.A.S., et al. 2021. Genetic mapping for agronomic traits in IAPAR 81/LP97-28 population of common bean (*Phaseolus vulgaris* L.) under drought conditions. *Plants* 10(8):1568.
- Farrow, A., Muthoni-Andriatsitohaina, R. 2020. Atlas of Common Bean Production in Africa. 2nd ed. Pan-Africa Bean Research Alliance (PABRA) International Center for Tropical Agriculture (CIAT), Nairobi, Kenya.
- Ganesan, K., Xu, B. 2017. Polyphenol-rich dry common beans (*Phaseolus vulgaris* L.) and their health benefits. *International Journal of Molecular Sciences* 18(11):2331.
- Gonçalves, J.G.R., Andrade, E.R. de, Silva, D.A. da, Esteves, J.A. de F., Chiorato, A.F., Carbonell, S.A.M. 2019. Drought tolerance evaluated in common bean genotypes. *Ciência e Agrotecnologia* 43:e001719.
- Hamabwe, S.M., Kuwabo, K., Urrea, C.A., Cichy, K.A., Kamfwa, K. 2024. Cooking time, seed darkening, and iron and zinc concentrations of selected Andean genotypes of common bean. *Legume Science* 6(4):e70012.

- Katuuramu, D.N., Luyima, G.B., Nkalubo, S.T., Wiesinger, J.A., Kelly, J.D., Cichy, K.A. 2020. On-farm multi-location evaluation of genotype by environment interactions for seed yield and cooking time in common bean. *Scientific Reports* 10(1):3628.
- Kuşvuran, Ş., Daşgan, H.Y. 2017. Effects of drought stress on physiological and biochemical changes in *Phaseolus vulgaris* L. *Legume Research - An International Journal* 40(1):1-10.
- Lisciani, S., Marconi, S., Donne, C.L., Camilli, E., Aguzzi, A., Gabrielli, P., et al. 2024. Legumes and common beans in sustainable diets: Nutritional quality, environmental benefits, spread and use in food preparations. *Frontiers in Nutrition* 11:1385232.
- López, M.D., Toro, M., Riveros, G., Illanes, M., Noriega, F., Schoebitz, M., et al. 2022. Brassica sprouts exposed to microplastics: Effects on phytochemical constituents. *Science of the Total Environment* 823:153796.
- Luo, T., Young, R., Reig, P. 2015. Aqueduct projected water stress country rankings. World Resources Institute, Washington, D.C., USA.
- Madrera, R.R., Čampa, A., Valles, B.S., Fernández, J.J.F. 2021. Phenolic content and antioxidant activity in seeds of common bean (*Phaseolus vulgaris* L.) *Foods* 10(4):864.
- Messina, V. 2014. Nutritional and health benefits of dried beans. *American Journal of Clinical Nutrition* 100(Suppl 1):437S-442S.
- Mojica, L., Berhow, M.A., Mejía, E.G.de. 2017. Black bean anthocyanin-rich extracts as food colorants: Physicochemical stability and antidiabetes potential. *Food Chemistry* 229:628-639.
- Mutari, B., Sibiyi, J., Matova, P.M., Gasura, E., Simango, K. 2023. Drought stress impact on agronomic, shoot, physiological, canning and nutritional quality traits of navy beans (*Phaseolus vulgaris* L.) under field conditions in Zimbabwe. *Field Crops Research* 292:108826.
- Neto, S.S.O., Pereira, F.F.S., Zóz, T., Oliveira, C.E.S., Cirino, V.M. 2022. Effect of water deficit on morphoagronomic traits of black common bean genotypes (*Phaseolus vulgaris* L.) with contrasting drought tolerance. *Journal of Agronomy and Crop Science* 209(1):83-95.
- Polania, J., Poschenrieder, C., Beebe, S., Rao, I.M. 2016. Effective use of water and increased dry matter partitioned to grain contribute to yield of common bean improved for drought resistance. *Frontiers in Plant Science* 7:660.
- Polania, J., Rao, I.M., Cajiao, C., Grajales, M., Rivera, M., Velasquez, F., et al. 2017. Shoot and root traits contribute to drought resistance in recombinant inbred lines of MD 23-24 × SEA 5 of common bean. *Frontiers in Plant Science* 8:296.
- Sica, P., Galvao, A., Scariolo, F., Maucieri, C., Nicoletto, C., Pilon, C., et al. 2021. Effects of drought on yield and nutraceutical properties of beans (*Phaseolus* spp.) traditionally cultivated in Veneto, Italy. *Horticulturae* 7(2):17.
- Silva, M.B.O., Carvalho, A.J.de, David, A.M.S.S., Aspiazú, I., Alves, É.E., Carneiro, J.E.S., et al. 2019. Technological quality of grain of common bean genotypes of the black commercial class. *Revista Brasileira de Ciências Agrárias* 14(3):e5660.
- Smith, M.R., Dinglasan, E., Veneklaas, E.J., Polanía, J., Rao, I.M., Beebe, S., et al. 2022. Effect of drought and low P on yield and nutritional content in common bean. *Frontiers in Plant Science* 13:814325. doi:10.3389/fpls.2022.814325.
- Tapia, G., Méndez, J., Inostroza, L., Lozano, C. 2022. Water shortage affects vegetative and reproductive stages of common bean (*Phaseolus vulgaris*) Chilean landraces, differentially impacting grain yield components. *Plants* 11(6):749.
- USDA. 2014. Keys to soil taxonomy. 12th ed. United States Department of Agriculture, Washington, D.C., USA.
- Wang, N., Hou, A., Santos, J.L.S., Maximiuk, L. 2016. Effects of cultivar, growing location, and year on physicochemical and cooking characteristics of dry beans (*Phaseolus vulgaris*). *Cereal Chemistry* 94(1):128-134.
- Zhao, X., Chambers, E., Matta, Z., Loughin, T.M., Carey, E.E. 2007. Consumer sensory analysis of organically and conventionally grown vegetables. *Journal of Food Science* 72(2):S87-S91.