Universidad de Concepción
Dirección de Postgrado
Facultad de Agronomía
Programa de Doctorado en Ciencias de la Agronomía

"Evaluación agronómica, fisiológica, nutricional y funcional en genotipos de frejol (*Phaseolus vulgaris* L.) cultivados bajo estrés hídrico terminal en la Región Centro-sur de Chile"

Tesis para optar al grado de Doctor en Ciencias de la Agronomía

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CHILLÁN-CHILE
2025

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DEDICATORIA

A Dios por darme la energía y la claridad para perseverar.

A mi esposa María Elena, por su amor incondicional, paciencia infinita y por caminar a mi lado en cada etapa de este proceso.

A mis hijas Eloisa y Maite, fuente constante de inspiración, alegría y esperanza, con esfuerzo, todo es posible.

AGRADECIMIENTOS

.

Destacar y agradecer al Dr. Nelson Zapata SM, por su valiosa guía, paciencia y compromiso durante todo el desarrollo de esta tesis. Gracias por confiar en mí, por sus oportunas observaciones y por motivarme a completar este trabajo. Haber contado con su apoyo ha sido un privilegio y una experiencia de gran aprendizaje, tanto profesional como personal.

Agradezco sinceramente al Dr. Carlos Urrea por haber facilitado el material genético de frejol y los instrumentos utilizados en esta investigación, por su apoyo en la revisión del manuscrito, y especialmente por su guía en el mejoramiento genético del frejol. Su generosidad intelectual y amistad han dejado una profunda huella en mi formación profesional.

Mi sincera gratitud al Dr. Miguel Garriga y al Dr. Abdelhalim Khaled Elazab por su tiempo y dedicación en el desarrollo del análisis estadístico, así como sus valiosas correcciones al manuscrito. Sus recomendaciones oportunas y certeras contribuyeron significativamente a mejorar la calidad de este trabajo.

Mi agradecimiento a la Dra. María Dolores López Belchí por haber facilitado el uso de su laboratorio durante el desarrollo de esta investigación y su apoyo en la corrección del manuscrito. Su generosidad y disposición contribuyeron significativamente a la realización de esta investigación.

Agradecimientos a la Dra. Susana Fischer, directora del programa de Doctorado, por su constante preocupación, apoyo y motivación. Sus palabras de aliento fueron fundamentales para culminar esta etapa académica.

CONTENIDOS

Página

ÍNDICE DE TABLAS

ÍNDICE DE FIGURAS

RESUMEN

El frejol (*Phaseolus vulgaris* L.) es un cultivo estratégico para la seguridad alimentaria y nutricional, tanto a nivel mundial como nacional, debido a su alto valor nutricional, y relevancia socioeconómica en la agricultura familiar campesina. En Chile, su producción está concentrada en el valle central y representa cerca del 50% del consumo nacional, Sin embargo, el cambio climático y la creciente escasez de agua amenazan la sostenibilidad y productividad de este cultivo, particularmente en etapas críticas como la floración y el llenado de vainas. Estas condiciones también pueden afectar negativamente la calidad nutricional y funcional del grano,

En este contexto, el presente estudio tuvo como objetivo evaluar rasgos agronómicos, fisiológicos, nutricionales, funcionales y de calidad culinaria en genotipos de frejol bajo condiciones contrastantes de disponibilidad hídrica en Chile. Esta evaluación busca contribuir a la identificación de genotipos superiores que combinen resiliencia al estrés hídrico con atributos nutricionales y calidad, con miras a su incorporación en programas de mejoramiento genético adaptados a escenarios de cambio climático bajo condiciones contrastantes de disponibilidad hídrica en Chile.

Se evaluó el desempeño de veinte genotipos de frejol que comprendían líneas avanzadas y cultivares comerciales durante dos temporadas (2021–2022 y 2022–2023) bajo condiciones de riego normal (ND) y sequía terminal (DS). La sequía tuvo un impacto severo en varios componentes del rendimiento, incluyendo el rendimiento de grano (–22,7%), biomasa aérea (–37%), índice de cosecha (–19,5%), número de granos por vaina (–61,3%) y peso de cien granos (–10,1%). Sin embargo, se observó una significativa variabilidad genotípica, destacando los genotipos 452, 473 y 483 por mantener altos rendimientos y un desempeño fisiológico superior bajo condiciones de estrés. Características fisiológicas como el contenido de clorofila y el rendimiento cuántico del fotosistema II (ΦPSII) mostraron fuertes asociaciones con la tolerancia a la sequía y la estabilidad del rendimiento. Estos resultados destacan la importancia de seleccionar rasgos fisiológicos de resiliencia para mejorar el rendimiento bajo sequía terminal, reforzando el potencial de las estrategias de fenotipado integradas en programas de mejoramiento. Los atributos nutricionales, funcional y de calidad culinaria, como cocción, contenido de proteína cruda, capacidad de hidratación, contenido de fenoles totales y actividad antioxidante, mostraron una variación genotípica significativa e interacciones genotipo × ambiente. El tiempo de cocción tendió a incrementarse bajo DS en distintos genotipos, aunque algunos mostraron perfiles estables o incluso mejorados, lo que resalta el potencial de selección en función de sus atributos. El contenido de fenoles y la actividad antioxidante se vieron significativamente afectados por la sequía, aunque ciertos genotipos como Curi y 458 mantuvieron altos valores en ambas condiciones hídricas. Además, se observó una correlación positiva y estadísticamente significativa entre el contenido de fenoles totales y la actividad antioxidante, lo que confirma la contribución funcional de los fenoles en la defensa antioxidante del frejol.

Este estudio aporta valiosos conocimientos sobre las respuestas agronómicas, fisiológicas, nutricional, funcionales y calidad culinaria de los genotipos del frejol, permitiendo integrar datos para la identificación de líneas élite con buen rendimiento, tanto en condiciones de riego como bajo estrés hídrico. Estos resultados proporcionan información fundamental para apoyar la selección de genotipos con mayor tolerancia a la sequía y valor nutricional, lo cual contribuirá al desarrollo de cultivares resilientes y funcionales, adaptados a los escenarios agroclimáticos cambiantes en Chile. Asimismo, los genotipos destacados por su desempeño agronómico, fisiológico, nutricional y funcional constituyen una base valiosa de material genético que podrá ser incorporada en el programa de mejoramiento genético nacional, fortaleciendo de esta manera la seguridad alimentaria y la sostenibilidad agrícola frente al cambio climático.

SUMMARY

Common bean (*Phaseolus vulgaris* L.) is a strategic crop for food and nutritional security at both global and national levels, due to its high nutritional value and its socioeconomic relevance for smallholder farming systems. In Chile, its production is concentrated in the central valley and accounts for approximately 50% of national consumption. However, climate change and increasing water scarcity threaten the sustainability and productivity of this crop, particularly during critical stages such as flowering and pod filling. These conditions may also negatively affect the nutritional and functional quality of the grain. In this context, the present study aimed to evaluate the agronomic, physiological, nutritional, functional, and culinary quality traits in common bean genotypes under contrasting water availability conditions in Chile. This evaluation seeks to support the identification of superior genotypes that combine drought resilience with favorable nutritional and quality attributes, with the goal of incorporating them into breeding programs adapted to climate change scenarios.

Twenty common bean genotypes, including advanced breeding lines and commercial cultivars, were evaluated over two growing seasons (2021–2022 and 2022–2023) under normal irrigation (ND) and terminal drought stress (DS) conditions. Terminal drought had a severe impact on several yield components, including grain yield (–22.7%), aboveground biomass (–37%), harvest index (–19.5%), number of grains per pod (–61.3%), and hundred-grain weight (–10.1%). However, significant genotypic variability was observed, with genotypes 452, 473, and 483 showing superior performance under stress, maintaining high yields and stable physiological behavior. Physiological traits such as chlorophyll content and the quantum yield of photosystem II (ΦPSII) were strongly associated with drought tolerance and yield stability. These findings highlight the importance of selecting physiological resilience traits to enhance productivity under terminal drought, reinforcing the value of integrating phenotyping tools into breeding strategies. Nutritional, functional, and culinary quality traits—including cooking time, crude protein content, hydration capacity, total phenolic content, and antioxidant activity (DPPH)—showed significant genotypic variation, and genotype-by-environment interactions were detected. Cooking time generally increased under DS in several

genotypes; however, some genotypes showed stable or even improved profiles, highlighting the potential for selection based on these attributes. Both phenolic content and antioxidant capacity were significantly affected by drought stress, although genotypes such as Curi and 458 maintained high values under both water regimes. Moreover, a statistically significant positive correlation was found between total phenolic content and DPPH antioxidant activity, confirming the functional role of phenolics in contributing to antioxidant activity in beans.

Overall, this research provides valuable insights into the agronomic, physiological, nutritional, and functional responses of common bean genotypes, allowing the identification of elite lines with good performance under both irrigated and drought-stressed conditions. The results offer critical information to support the selection of genotypes with enhanced drought tolerance and nutritional value, contributing to the development of resilient and functional cultivars adapted to changing agroclimatic scenarios in Chile. Furthermore, the genotypes identified for their superior agronomic, physiological, nutritional, and functional performance represent a valuable source of genetic material for incorporation into the national breeding program, thereby strengthening food security and agricultural sustainability in the context of climate change.

I. CAPÍTULO 1: INTRODUCCIÓN GENERAL

1.1. Características del frejol en Chile y el mundo

El frejol (*Phaseolus vulgaris* L.) desempeña un papel fundamental en la seguridad alimentaria y nutricional a nivel global, especialmente en regiones de América Latina y África, donde constituye un cultivo de alto valor estratégico. Es la leguminosa más consumida en el mundo, con una significativa contribución a la ingesta diaria de proteínas y representa una fuente vegetal accesible de nutrientes esenciales, incluyendo fibra, minerales y compuestos bioactivos (Lisciani et al., 2024; Didinger et al., 2022; Uebersax et al., 2022). Además de su valor nutricional, el frejol contribuye a la sostenibilidad de los sistemas agrícolas por su capacidad de fijar biológicamente nitrógeno atmosférico en asociación con bacterias del género Rhizobium, lo que reduce la necesidad de fertilizantes sintéticos y mejora la fertilidad del suelo. Estos atributos lo convierten en un componente clave en sistemas de rotación de cultivos, favoreciendo la diversificación y productividad de los sistemas agroalimentarios (Habibi et al., 2025).

A nivel mundial, se estima que el cultivo de frejol abarca más de 30 millones de hectáreas, principalmente bajo condiciones de secano, con una producción que supera los 30 millones de toneladas y un rendimiento promedio cercano a 1 t ha^{-1} (FAOSTAT, 2023). Los principales países productores son India, Brasil, México, Myanmar y Tanzania. En este contexto, Chile presenta un rendimiento promedio de aproximadamente 1,75 t ha^{-1} y una producción anual superior a las 10.000 toneladas, lo que representa cerca del 50% del consumo nacional (González y Tay, 2024; Odepa, 2025). Esta cifra pone de relieve la importancia de la producción local no solo en términos de soberanía alimentaria, sino también por su impacto en la economía de la agricultura familiar campesina. El cultivo del frejol se concentra tradicionalmente en el valle central del país, en las regiones del Maule, Ñuble y Biobío, donde es manejado mayoritariamente por pequeños agricultores bajo condición de riego (González y Tay, 2017).

En Chile, los principales tipos de frejol cultivados corresponden a las clases comerciales Tórtola y Cimarrón, variedades exclusivas del país que se distinguen por su alta aceptación culinaria y por alcanzar los precios más altos en el mercado nacional. Estas variedades, pertenecientes a la raza Chile, forman parte del acervo genético andino de (*P. vulgaris* L.) y su conservación y mejoramiento dependen exclusivamente del programa de selección y fitomejoramiento que se desarrolla a nivel nacional.

1.2. Cambio climático y sequía terminal

El cambio climático representa una amenaza creciente para la producción de frejol. El aumento de las temperaturas, la disminución de las precipitaciones y la reducción de la acumulación de nieve en la cordillera de Los Andes han intensificado la escasez hídrica en la zona central del país. Se proyecta que Chile esté entre las 30 naciones con mayor déficit hídrico para el año 2040 (Luo et al., 2015) y se estima que la precipitación invernal podría disminuir en más del 40% hacia finales del siglo XXI (Araya-Osses et al., 2020). Este escenario ha dado lugar a una "mega-sequía" prolongada, caracterizada por una reducción del 20–40% en las lluvias, disminución del deshielo andino y menor disponibilidad de agua en ríos y embalses, sobre todo en los meses de verano (Martínez-Barradas et al., 2023; Garreaud et al., 2019). Estas condiciones han generado una presión adicional sobre el cultivo del frejol en toda el área productiva del país, especialmente durante el periodo reproductivo, afectando negativamente la floración, formación de vainas y llenado de granos y, en consecuencia, el rendimiento (Rai et al., 2020; Labastida et al., 2023; Campos et al., 2021 y Polania et al, 2016).

1.3. Tolerancia a sequía y rasgos fisiológicos

Frente a este contexto, los programas de fitomejoramiento han priorizado el desarrollo de genotipos tolerantes a la sequía, enfocando tradicionalmente el proceso de selección en el rendimiento bajo condiciones de estrés hídrico. Sin embargo, se ha demostrado que la sequía terminal tiene efectos negativos sobre los principales componentes del rendimiento; número de vainas por planta, número de granos por vaina, peso de 100 granos y un menor índice de cosecha (Beebe et al., 2013). Este tipo de estrés puede provocar además una aceleración del desarrollo fenológico, generando madurez anticipada como mecanismo de escape, además de una disminución de la fotosíntesis que limita la partición de fotoasimilados hacia los órganos reproductivos, lo que acorta el período de llenado de grano y reduce significativamente la producción de granos (Assefa et al., 2017).

En este sentido, enfoques más integrales en el mejoramiento genético han incorporado índices complementarios como el Índice de Susceptibilidad a la Sequía (DSI) y la Productividad Media Geométrica (GMP), los cuales permiten una evaluación más equilibrada del comportamiento genotípico en condiciones contrastantes (Parker et al., 2023; Memari et al., 2022; Mutari et al., 2022). Mientras el DSI cuantifica la sensibilidad relativa del genotipo al estrés hídrico, el GMP favorece la selección de genotipos que combinan productividad y estabilidad en distintos ambientes. Además, la incorporación de rasgos fisiológicos, como el contenido de clorofila, la conductancia estomática, el contenido relativo de agua y la eficiencia cuántica del fotosistema II (ΦPSII), ha mejorado la precisión en la identificación de genotipos más eficientes en el uso del agua, al ofrecer una visión más detallada y temprana de las respuestas adaptativas al déficit hídrico (Khadka et al., 2020; Gracia-Romero et al., 2025; Tefera et al., 2022; Papathanasiou et al., 2022; Traub et al., 2018; Gonçalves et al., 2019). La integración de estas herramientas fisiológicas y agronómicas en los programas de mejoramiento contribuye a acelerar el desarrollo de variedades más resilientes a los efectos del cambio climático.

1.4. Calidad nutricional, funcional y culinaria del grano

Además de los aspectos agronómicos y fisiológicos, es de gran relevancia la evaluación de la calidad nutricional, funcional y culinaria de las semillas. El frejol no solo es una fuente vital de proteínas, sino también de compuestos bioactivos como los fenoles, conocidos por su capacidad antioxidante y sus beneficios para la salud (Messina, 2014). Estos compuestos son sensibles a las condiciones ambientales, particularmente a la disponibilidad hídrica, que puede modificar el metabolismo de la planta y, con ello, su composición química (Sica et al., 2021). Investigaciones previas han demostrado que el estrés ambiental puede inducir la síntesis de compuestos fenólicos, aunque la magnitud de esta respuesta depende del genotipo (Smith et al., 2022).

Esta legumbre es muy versátil ya que su consumo puede ir de preparaciones muy básicas a muy sofisticadas, por lo que los rasgos tecnológicos, como la capacidad y velocidad de hidratación y el tiempo de cocción, son claves para la aceptabilidad del producto final. Estas características están influenciadas por la estructura y composición del grano y afectan tanto el procesamiento como las preferencias del consumidor (Wang et al., 2016). La capacidad de hidratación refleja la dinámica de absorción de agua durante el remojo y se asocia con la permeabilidad de la testa y la integridad interna del grano (Katuuramu et al., 2020). Los genotipos que absorben agua rápido y eficientemente requieren menos tiempo de cocción, lo cual favorece la conservación de nutrientes termosensibles y resulta menos costosa su preparación (Brito et al., 2013). Por ello, comprender la interacción entre genotipo, régimen hídrico y calidad de semilla es esencial para el desarrollo de cultivares con buen desempeño agronómico y alto valor funcional.

1.5. Hipótesis

La disponibilidad hídrica restringida en etapa reproductiva (sequía terminal) afecta significativamente los parámetros agronómicos, fisiológicos, de calidad nutricional, funcional y culinaria del grano en el frejol, siendo los genotipos susceptibles a sequía los que presentan mayores reducciones en rendimiento y calidad funcional del grano.

1.6. Objetivos

1.6.1. Objetivo general

Evaluar el efecto de la sequía terminal sobre los parámetros agronómicos, fisiológicos y de calidad nutricional y funcional del grano en genotipos de frejol, con el propósito de identificar materiales con tolerancia a sequía terminal y alto valor funcional, que puedan ser incorporados en programas de mejoramiento genético.

1.6.2. Objetivos específicos

1. Determinar la influencia de la sequía terminal sobre factores agronómicos, fisiológicos y productividad en genotipos de frejol cultivados en condiciones de campo en la Región Centro-sur de Chile.

2. Evaluar el desempeño de la calidad nutricional, funcional (fenoles, capacidad antioxidante y proteína) y culinaria (capacidad de hidratación y tiempo de cocción) desde diversos genotipos de frejol sometidos a sequía terminal y su relación con el comportamiento agronómico.

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II. CAPÍTULO 2:

Screening Terminal Drought Tolerance in Dry Bean Genotypes and Commercial Bean Cultivars in Chile

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Published in Journal Agronomy on 20th June 2025 (ISSN 2073-4395)

2.1. Abstract

Drought significantly constrains common bean (Phaseolus vulgaris L.) production worldwide, and as climate change intensifies, projections indicate a subsequent reduction in yield. This study aimed to identify drought-resilient genotypes among twenty common bean lines in Chile under two water regimes: regular irrigation and terminal drought stress. The research was conducted over two seasons in south-central Chile. Drought significantly reduced grain yield (22.7%), aboveground biomass (37%), harvest index (19.5%), the number of grains per pod (61.3%), and hundred-grain weight (10.1%). Genotypes 452, 473, and 483 exhibited minimal yield reductions (<11%) and maintained stable physiological performance, including higher quantum yield of photosystem II and efficient photoprotective mechanisms (increased ΦNPQ) under stress. In contrast, sensitive genotypes like Blanco Español, showed a marked yield loss (54%) and lower photosynthetic efficiency. Chlorophyll retention emerged as a key trait for identifying high-yielding, drought-tolerant genotypes. Drought also accelerated crop maturation in susceptible genotypes, compromising yield potential. These findings highlight the importance of integrating agronomic, phenological, and physiological traits in breeding programs to develop drought-adapted varieties. The tolerant genotypes offer valuable genetic traits to improve drought resilience and contribute to food security in the face of climate change.

Keywords: agronomic traits; common beans; drought tolerance; physiological traits; yield stability.

2.2. Introduction

The common bean is a globally important crop in nutrition and food security, particularly in Latin America and Africa. As the most consumed legume worldwide, it contributes up to 15% of daily caloric intake and 36% of protein intake, making it a staple food source for people worldwide (Uebersax et al., 2022; Didinger et al., 2022; Lisciani et al., 2024). Beans also provide an affordable source of essential nutrients, including fiber, vitamins, and minerals, as a low-cost alternative to animal protein (Cominelli et al., 2022; Papanikolaou et al., 2024; Singh et al., 2022; Parker et al., 2023). 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 dietary staple (Farrow and Muthoni Andriatsitohaina, 2020; Jha et al., 2023). By 2040, Chile is projected to be among the 30 nations facing the most severe water scarcity if current trends continue (Luo et al., 2015). Furthermore, by the end of the 21st century, winter precipitation in Chile is expected to decrease by more than 40% (Araya-Osses et al., 2020).

Water scarcity affecting beans leads to reduced leaf area, lower photosynthetic activity, decreased biomass, and a significant reduction in seed yield (Rai et al., 2020). The extent of yield reduction varies depending on the bean genotype and the severity and timing of the drought (Labastida et al., 2023). In Chile, bean cultivation is predominantly affected by terminal drought, which severely impacts the reproductive stage, leading to a critical decrease in grain production; the production is primarily associated with smallholders who manage relatively small plots, with most of the crop being produced under irrigation (González and Tay, 2017). Most bean production is concentrated in the central valley, particularly in the south-central regions of Maule, Ñuble, and Biobío. However, these key production areas have been severely affected by an unprecedented mega-drought, characterized by a 20–40% reduction in rainfall and diminished snowpack in the Andes (Martínez-Barradas et al., 2023). As a result, river flow and water reservoir levels have significantly decreased, particularly during the summer months, exacerbating water shortages, which have placed additional pressure on bean production, making it increasingly challenging for Chilean farmers to achieve high yields under limited water availability (Garreaud et al., 2019; Jódar et al., 2023). Despite significant global progress in identifying drought-tolerant common bean genotypes, there is a lack of information on genotypes evaluated under Chilean conditions.

Traditionally, breeding programs have focused on selecting drought-resistant bean genotypes primarily based on grain yield under drought stress, as this trait has been considered the most important. However, a more comprehensive approach incorporating additional factors could enhance the identification of parent lines with complementary traits (Mutari et al., 2023; Mladenov et al., 2023). In this context, two widely used indices for evaluating genotypes under drought are the Drought Susceptibility Index (DSI) and Geometric Mean Productivity (GMP). The DSI measures the relative yield reduction of a genotype under drought compared to optimal conditions (Memari et al., 2022). However, it may penalize high-yielding genotypes when the drought is not severe. In contrast, GMP highlights stability and productivity (Mutari et al., 2022). Using both indices provides a balanced approach to genotype selection across different environments and selection criteria (Parker et al., 2023). Traditionally, plant drought tolerance has been evaluated using physiological parameters such as leaf water potential, stomatal conductance, and relative water content. However, incorporating advanced physiological traits, such as chlorophyll content, quantum yield of photosystem II, non-photochemical quenching, and proportion of light energy dissipated via non-regulated processes, provides a more complete physiological evaluation. Integrating these parameters into the selection process enhances efficiency and precision, allowing breeders to gain a more comprehensive understanding of the genotype's response to water scarcity, leading to more successful drought-tolerant selection (Khadka et al., 2020; Gracia-Romero et al., 2025; Tefera et al., 2022; Papathanasiou et al., 2022; Traub et al., 2018). Additionally, evaluating drought-tolerant bean lines using these methods enhances the accuracy of the selection criteria, making the genotype selection more effective and the breeding process more rapid, thereby reducing breeding costs (Gonçalves et al., 2019). Integrating these selected genotypes into breeding programs will facilitate the development of common bean varieties with improved adaptation to drought conditions (Parker et al., 2023; Mickelbart et al., 2015).

The goal is to identify parental lines with superior agronomic, phenological, and physiological traits suited to water-limited environments, ensuring high yield performance for their incorporation into breeding programs.

2.3. Materials and Methods

2.3.1. *Experimental site conditions and genetic materials*

The experiment was conducted for two consecutive seasons (from November to March) in 2021/2022 and 2022/2023 at the Santa Rosa Experimental Field of the Institute of Agricultural Research (INIA) Quilamapu, Chillán, Chile (36°31′ S; 71°54′ W, 196 m.a.s.l). The soil at the experimental site is volcanic (Melanoxerand) (USDA, 2014), with a loamy texture (Supplementary Table S1), and the climate is temperate Mediterranean, characterized by a hot, dry summer and 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, respectively. Meteorological data, including precipitation, evapotranspiration, and temperature, were obtained from an automated weather station at the research site and reported by the INIA Agrometeorological Network (Table 1). The trial received only 11 and 8 mm precipitation between flowering and harvest during the 2021/2022 and 2022/2023 seasons. After flowering, only the trial without drought receives irrigation. Detailed climatic and irrigation quantities during the two crop cycles are presented in Table 1.

The germplasm consisted of twenty common bean genotypes (Table 2). Fifteen genotypes were selected from the US dry bean breeding drought nursery at the University of Nebraska, USA. Additionally, five cultivars belonging to the Chilean race and Andean genetic pool were selected from the Bean breeding program of INIA.

Table 1. Monthly maximum (T Max), minimum (T Min), average (T Ave), evapotranspiration (ET0), rainfall (Rf), and applied irrigation (Irr) at the Santa Rosa Experimental Field, INIA-Quilamapu, Chillán, Chile, during the 2021/2022 and 2022/2023 seasons.

Season	**Month**	**T° Max (°C)**	**T° Min (°C)**	**T° Ave (°C)**	**ET0 (mm)**	**Rf (mm)**	**Irr (mm)**	**ND (mm)**	**DS (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	100
	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	00

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.

2.3.2. *Crop management and experimental design*

The genotypes were assigned to experimental units using a randomized complete block design with four replications. Each plot consisted of four 5.0-m rows spaced 0.6 m apart, targeting a plant density of 250000 plants per hectare. Furrow irrigation systems were used throughout the trial. Before sowing, the soil was fertilized with 60 kg ha^{-1} of N, 50 kg ha^{-1} of P2O5, 40 kg ha^{-1} of K2O, 18 kg ha^{-1} of S, and 12 kg ha^{-1} of MgO. (Supplementary Table S2). Seeds were treated with Fludioxonile and Thiamethoxam. Chemical control of weeds was applied with the Sodium salt of Fomesafen, and management of weeds also included manual labor.

Table 2. Genotypes from the University of Nebraska, USA, and the Institute of Agricultural Research (INIA), Chile, were evaluated at the Santa Rosa Experimental Field from 2021 to 2023.

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

Growth habit classifications standards of common bean: 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).

The genotypes were evaluated under two water regimes: regular irrigation (ND) and terminal drought stress (DS). Trials were irrigated from sowing until flowering to ensure proper plant establishment and early growth. In DS stressed plots, irrigation was discontinued on day 56 after sowing, coinciding with the period when all genetic materials 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.

2.3.3. *Agronomic evaluations*

To assess the plant's response to water stress, aerial biomass, grain yield, number of grains per pod, and hundred-grains weight were evaluated. At the mid-pod stage, a 21 cm row from each plot containing three plants were destructively sampled to measure above-ground biomass (AGB), which was then extrapolated to kg^{-1} per hectare. The collected plant samples were oven-dried at 70°C until they reached a constant weight, and the total dry weight was recorded. The grain yield (GY) was determined by harvesting seeds at the same moisture (14%) from two central rows of each plot, excluding 50 cm end plants, for both the irrigated and drought-stressed plots; the GY was then extrapolated to a per-hectare basis. For assessing the hundred-grains weight (HGW) at harvest, a random sample was taken to determine the weight of 100 seeds; the values were expressed as in grams. The number of grains per pod (NGP) was extrapolated to the number of grains per area (m^2). The harvest index (HI %) directly estimates how much of the plant's biomass was allocated to grain formation (Rodriguez et al., 2020). The HI for each genotype was calculated as the dry weight of seeds at harvest divided by the dry weight of aboveground biomass (leaves + stems + pods) at mid-pod filling and was expressed as a percentage.

2.3.4.*The drought intensity and susceptibility index calculations*

Multiple indices were evaluated, given the challenge of selecting germplasm with drought tolerance and high yield potential. For drought severity quantification, the Drought Intensity Index (DII) was calculated using Equation (1) as follows:

$$DII = 1 - \frac{Xd}{Xp} \tag{1}$$

where Xd represents the mean yield under drought conditions and Xp the mean yield under non-stress conditions. The Drought Susceptibility Index (DSI) and the Geometric

Mean (GM) were used to identify drought-tolerant germplasm. The DSI was calculated according to the following Equation (2):

$$DSI = \frac{1 - (\frac{Yd}{Yp})}{DII} \qquad (2)$$

where Yd is the mean yield under drought stress and Yp is the mean yield under non-stress conditions (Mutari et al., 2022; Beebe et al., 2013; Papathanasiou et al., 2022).

A low DSI value indicates less yield reduction under drought conditions. However, selection based solely on this index does not allow to distinguish between genotypes with a low DSI due to genuine drought tolerance (maintaining good yield even under water-limited conditions) and those with a low DSI due to poor yield performance in both drought and non-stress conditions, which may be associated with factors such as poor adaptation or inherently low yield potential. Therefore, relying exclusively on the DSI could lead to the selection of plants that are not truly drought-tolerant but do not have a low overall yield.

To address this limitation, this study proposes using additional indices, such as Geometric Mean Productivity (GMP), alongside the DSI to obtain a more comprehensive evaluation of genotype performance. The Geometric Mean was calculated using the following Equation (3):

$$GMP = \sqrt{Yp \ x \ Yd} \qquad (3)$$

where Yp is the mean yield under DS and Yd is the mean yield of the same genotype under ND. This index provides a more robust measure of a particular genotype’s yield stability across different water conditions (Parker et al., 2023; Beebe et al., 2013).

2.3.5. *Phenological evaluations*

Days to flowering (DF) are the days after sowing until 50% of the plants have at least one open flower. Days to physiological maturity (DPM) is the days after sowing until 50% of plants have at least one pod losing its green pigmentation.

2.3.6. *Physiological evaluations*

Physiological traits were measured using the MultispeQ v1.0 (PhotosynQ Inc., East Lansing, MI, USA), which simultaneously quantified chlorophyll fluorescence parameters such as ΦII (quantum yield of photosystem II), ΦNO (the proportion of light energy dissipated via non-regulated processes), ΦNPQ (proportion of light energy dissipated as heat through non-photochemical quenching), and chlorophyll content in leaves (SPAD units) [23,32,33]. The measurements were performed on three plants per plot that were randomly selected and evaluated per treatment at the flowering and pod-filling stage between 11:00 and 15:00

2.4. *Statistical analysis*

The study was performed as four separate trials (environments): ND1 (no drought 2021/2022), DS1 (terminal drought 2021/2022), ND2 (no drought 2022/2023), and DS2 (terminal drought 2022/2023). Each water regime (ND and DS) comprised a sample size of N = 160, resulting from 2 growing seasons × 20 genotypes × 4 replicates. Levene's test verified the equality of variances in the samples (homogeneity of variance). Thus, the combined analysis of variance (two-way ANOVA) for the two years was performed using the general linear model (GLM) procedure to calculate the effects of water regimes (WR) and genotypes (G), and the G × WR interactions. The means separation of water regimes (ND vs. DS) and genotypes for the different parameters was performed by the independent sample t-test *($p \leq 0.05$)* and Duncan's test, respectively. Data were analyzed using Stat-graphics Centurion, Version 18.1.12 (Statgraphics Technologies, Inc., The Plains, VA, USA, 2018). Figures were created using Sigma Plot 11.0 for

Windows (Sysat Software Inc., Point Richmond, CA, USA). Principal component analysis (PCA) and Genotype + Genotype × Environment interaction analysis (GGE) were conducted in RStudio, version 4.2.1 (R Core Team, Vienna, Austria, 2021).

2.5 Results and Discussion

2.5.1. *Agronomic and productive traits*

The field experiments, conducted under (DS) and (ND), provided a robust and comprehensive framework to evaluate how drought influences a diverse range of agronomic, phenological, and physiological traits in common bean genotypes. The results presented in the following sections reflect the importance of genotypic variability in response to water limitation.

Seed yield is the most important and reliable agronomic trait of interest in abiotic stress studies (Oliveira Neto et al., 2022). Under ND conditions, the mean yield for all tested genotypes was about 3891 kg ha^{-1}; under DS, the mean yield decreased to about 3023 kg ha^{-1}, a reduction of 22.7%. The main effects of genotype, water regime, and their interaction (G × WR) were highly significant (***, $p \leq 0.001$) (Table 3). The former indicates that water stress considerably impacted yield, and the variation among genotypes and their interaction with water availability suggests differences in genotype performance under water stress. Table 4 presents the analysis of variance for key phenological and physiological traits, further supporting the observed genotype-specific responses to drought. Blanco Español was the most affected by drought stress, with a 54% reduction in yield (Figure 1b), and also showed a high DSI value, and Sel 6 had a low yield under both conditions and the lowest GMP value (Table 5). These findings are consistent with previously reported studies on common beans, which have shown significant yield reductions ranging from 20% to 76% under drought conditions compared to well-watered conditions (Polanía et al., 2016; Androcioli et al., 2020). As demonstrated in previous studies in common bean (Beebe et al., 2013; Oliveira Neto et al., 2022). Drought occurring during early grain filling can severely reduce sink capacity and restrict the partitioning of assimilates to developing seeds. The (DS) in this study was imposed at flowering, a reproductive stage known to be highly sensitive to water deficit. The observed reductions in the number of grains per pod (NGP) by 61.3% and hundred-grain weight (HGW) by 10.1% (Table 3) reflect this stage vulnerability. These results indicate that pod formation and seed filling were negatively affected by water stress, corroborating previous findings that highlight the impact of terminal drought on yield components in common beans.

In contrast, the genotypes least affected by drought stress were 452, 473, and 483 (Figure 1; Table 3), with less than 11% reduction in yield; similar results were reported in common beans by Rezene et al. (2012) and Darkwa et al. (2016), who observed that specific genotypes were able to maintain rel-atively high yields under drought stress conditions, demonstrating high drought tolerance.

The water regime had a highly significant effect (*** $p \leq 0.001$) on aboveground biomass production (Table 3) since terminal drought reduced AGB by approximately 37%. The genotype effect was insignificant for AGB, suggesting that differences in biomass among the 20 genotypes are relatively minor compared to the strong influence of the water regime (Figure 1a). This finding aligns with previous reports describing how limited water availability reduces vegetative biomass by constraining photosynthesis, cell growth, and leaf expansion (Beebe et al., 2013; Oliveira Neto et al., 2022). The reduction observed underscores the impact on the plant’s capacity to capture and convert resources into dry matter, highlighting the critical role of water management in optimizing biomass production.

A high variability was observed among genotypes in their biomass response to water stress. Some genotypes, such as 473 and 463, showed smaller reductions in biomass (33%), indicating greater resilience to water deficit (Figure 1a). This variability in biomass response to water stress may be associated with differences among the genotypes regarding their water use efficiency, depth of root system, or capacity for osmotic adjustment (Dramadri et al., 2021; Androcioli et al., 2020; Darkwa et al., 2016). In contrast, genotypes such as Curi and Blanco Español exhibited more pronounced reductions (41.8% and 40.9%, respectively), suggesting lower drought tolerance.

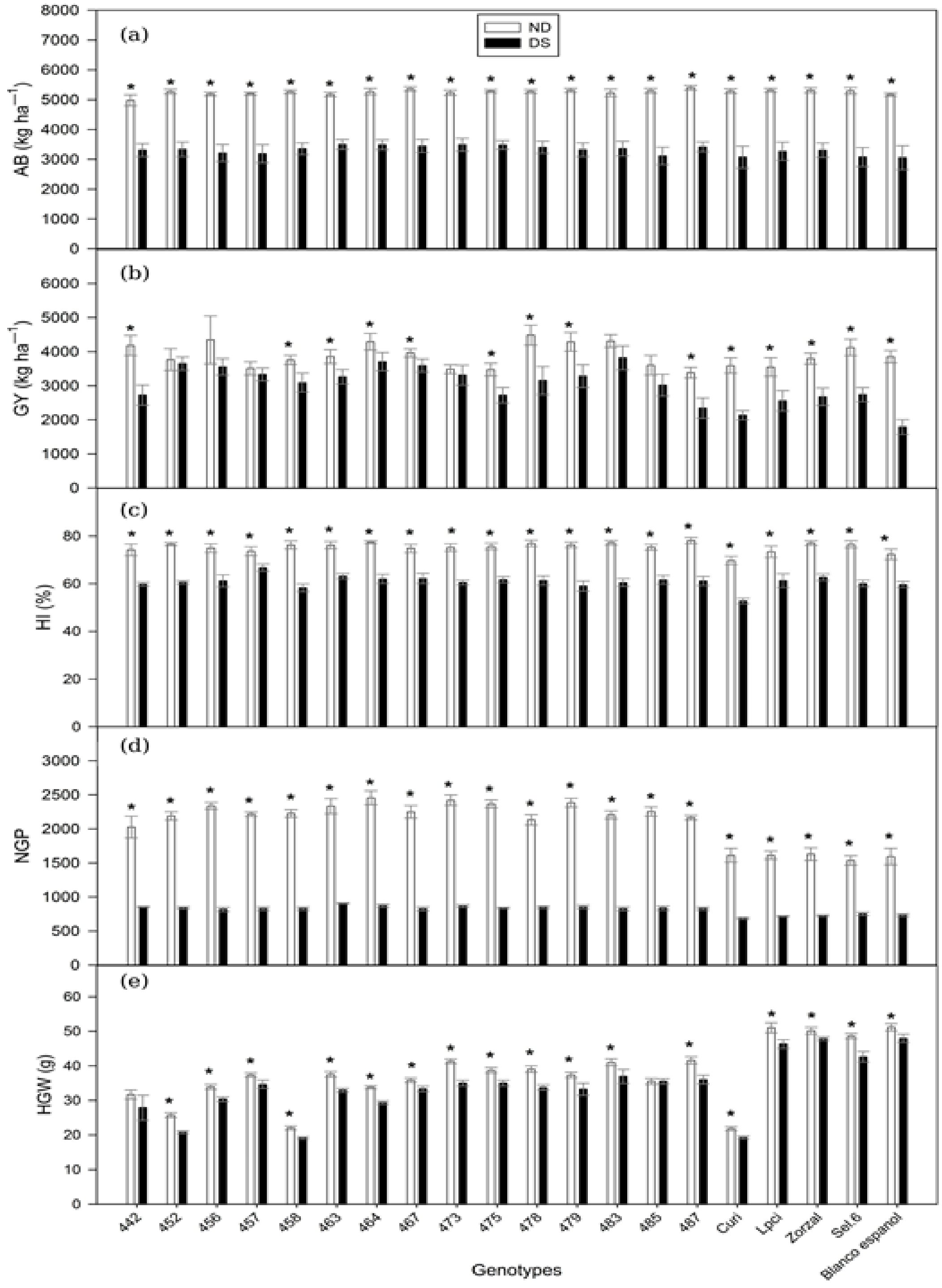

Figure 1. Agronomic and productive traits evaluated in twenty bean genotypes during two seasons under no stress (ND) and terminal drought stress (DS). (a) Aboveground biomass (AGB), (b) grain yield (GY) kg ha−1, (c) harvest index (HI), (d) number of grains m−2 (NGP), (e) hundred-grain weight (HGW). Error bars represent the standard error of the mean. Means followed by asterisks indicate the significant difference between ND and DS for the same genotype using the independent samples t-test *(p* ≤ 0.05).

Although biomass is important in grain yield formation, redistributing photoassimilates to reproductive organs (pods and grains) under water stress can modulate this relationship (Lynch, 2013). Genotype 464 maintained relatively high AGB (3489.9 kg ha^{-1}) and grain yield (3703.4 kg ha^{-1}) under ND, suggesting efficient resource allocation to grain production. This behavior could be associated with a high harvest index, indicating a prioritization of reproductive development over vegetative growth under adverse conditions (Sita et al., 2017; Gebeyehu, 2006).

The number of grains per pod was highly influenced by water regime (WR) and genotype (G) (** $p \leq 0.001$), with a significant genotype × water regime interaction (*** $p \leq 0.001$) (Table 3). Under terminal drought, NGP decreased sharply from 2105.1 ± 29.1 (ND) to 815.0 ± 6.3 (DS) (Figure 1d).

Under ND conditions, genotypes 464 and 473 achieve the highest numbers of grains per pod (exceeding 2400 seeds m^{-2}), while others like 463, 456, and 479 also stand out in the 2200–2300 range (Figure 1d), indicating excellent floral set when water is not a limiting factor. However, in the DS condition, most genotypes undergo a 55–65% reduction in NGP, underscoring the strong dependence on water during the reproductive phase.

Genotypes such as Curi, Blanco Español, Lpci, and Zorzal were particularly sensitive, with a 50–57% decrease and reaching only 686–754 grains per m^{-2}. In contrast, although reduced, 464, 473, and 463 still maintain relatively high counts (864–907) (Figure 1d), demonstrating a degree of drought tolerance. Similar results were reported Rodriguez et al. (2022) and Gebeyehu (2006), indicating that the seed number in drought-resistant genotypes is associated with more efficient water use, higher canopy biomass, and stronger dry matter partitioning to the pods. The variability in grain number per pod across genotypes emphasizes the agronomic importance of maintaining an adequate number of grains under water-limited conditions, which can promote more stable and competitive crop yields.

Hundred-grain weight is one of the main qualities and yield components in beans, influencing both the commercial value and the productive potential of the genotype. There was a significant effect of the water regime (*** $p \leq 0.001$) on HGW and a negative impact of drought on individual grain weight (Table 3). Differential responses among genotypes were observed, with several genotypes exhibiting high stability in HGW, with minimal changes under drought stress conditions (Figure 1e). Notably, genotype 485 maintained the same grain weight in both water regimes. Other genotypes, such as Zorzal (−4.51%), 467 (−6.91%), Blanco Español (−6.23%), and 457 (−7.17%), were slightly impacted by the terminal drought. The HGW stability in drought-tolerant genotypes enhances seed vigor through sustained sink strength, promoting carbohydrate and protein accumulation for improved germination (Hageman and Van Volkenburgh, 2021; Sánchez-Reinoso et al., 2020), this result also aligns with previous studies highlighting the importance of genetic variability in drought tolerance in common beans, where specific genotypes can maintain physiological processes and seed development under drought stress (Beebe et al., 2013; Androcioli et al., 2020). In contrast, genotypes 452, 458, 442, 456, and 463 experienced higher losses in HGW under drought stress, with reductions ranging from 10.43% to 19.38% (Figure 1e). The differential response of HGW across genotypes under drought stress can be attributed to various adaptive mechanisms, such as efficient water use, osmotic adjustment, and the prioritization of resources toward reproductive development (Assefa et al., 2017).

The harvest index reflects the efficiency of biomass partitioning into the grain. It was significantly affected by water regime and genotype (*** $p \leq 0.001$) (Table 3). Under DS, HI decreased from 75.4% (ND) to 60.81% (DS) (Figure 1c), indicating that drought not only reduces biomass but also impairs the plant's ability to allocate resources to grain production (Polania et al., 2016).

Table 3. Effect of water regime, genotypes, and their interaction on agronomic and productive traits evaluated in twenty bean genotypes during two seasons under no stress (ND) and terminal drought stress (DS).

	AGB	**GY**	**HI**	**NGP**	**HGW**
G	NS	***	***	***	***
WR	***	***	***	***	***
G × WR	NS	**	NS	***	NS
ND	5264.2 ± 17.2 b	3890.8 ± 62.6 b	75.49 ± 0.4 b	2105.1 ± 29.1 b	37.7 ± 0.7 b
DS	3310.7 ± 54.9 a	3022.8 ± 70.8 a	60.81 ± 0.4 a	815.0 ± 6.3 a	33.9 ± 0.7 a

The data show the mean of the twenty genotypes studied for each water condition. AGB, aboveground biomass (kg ha^{-1}); GY, grain yield (kg ha^{-1}); HI, harvest index; NGP, number of grains per pod (seeds m^{-2}); HGW, hundred-grain weight (g). 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 ($p \leq 0.05$). The probabilities (** $p \leq 0.01$; *** $p \leq 0.001$) are shown, and NS is insignificant.

2.5.2. Phenological traits

The study revealed significant variability in the phenological traits among the twenty common bean genotypes under terminal drought stress and regular irrigation conditions. These traits are critical for understanding the phenological responses and how genotypes adjust their development to cope with water limitations.

The ND and DS treatments did not affect the timing of flowering (Table 4), as both experimental conditions experienced the same moisture regime until flowering. The average number of days to the flowering stage was 48 across the genotypes (Figure 2a). Additionally, flowering within each genotype occurred within a relatively narrow timeframe of 3 days.

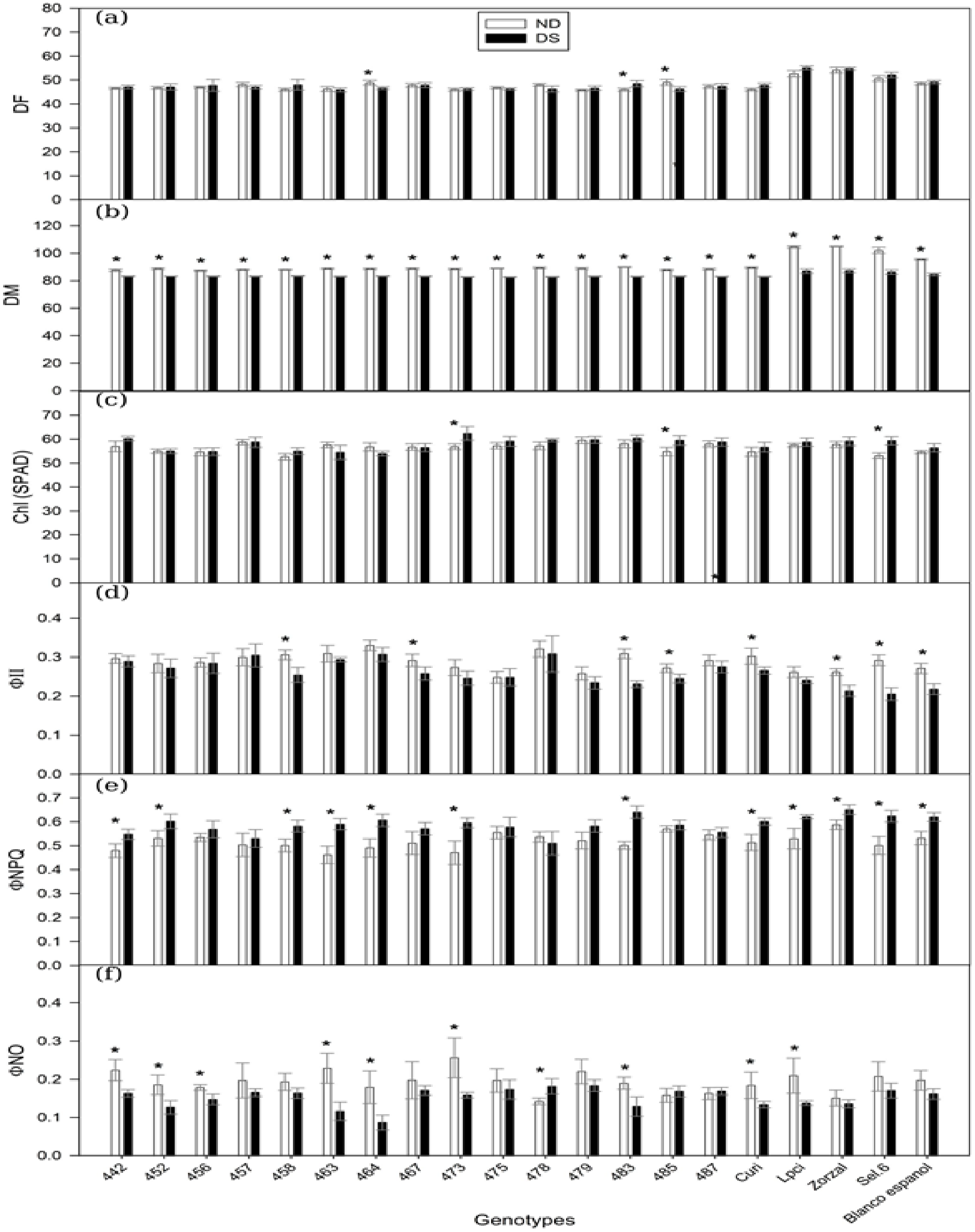

Figure 2. Phenological and physiological traits evaluated in twenty bean genotypes under no stress (ND) and terminal drought stress (DS) during two seasons. (a) Days to flowering (DF), (b) days to maturity (DM), (c) chlorophyll content (Chl; SPAD units), (d) quantum yield of photosystem II (ΦII), (e) proportion of light energy dissipated as heat through non-photochemical quenching means for the studied genotypes (ΦNPQ), (f) proportion of light energy dissipated via non-regulated processes (ΦNO). Error bars represent the standard error of the mean. Means followed by asterisks indicate the significant difference between ND and DS for the same genotype using the independent samples t-test *(p* ≤ 0.05)

Table 4. Effect of water regime, genotypes, and their interaction on phenological and physiological traits evaluated in twenty bean genotypes during two seasons under no stress (ND) and terminal drought stress (DS).

	DF	DM	Chl	ΦII	ΦNPQ	ΦNO
G	***	***	***	***	NS	NS
WR	NS	***	**	***	***	***
G × WR	NS	***	NS	NS	NS	NS
ND	47.9 ± 0.3 a	91.2 ± 0.5 b	56.4 ± 0.3 a	0.29 ± 0.00 b	0.52 ± 0.01 a	0.19 ± 0.01 b
DS	48.2 ± 0.3 a	83.6 ± 0.2 a	58.0 ± 0.4 b	0.26 ± 0.00 a	0.59 ± 0.01 b	0.15 ± 0.00 a

The data shown are the mean of the twenty genotypes studied for each water combination. DF, days to flowering; DM, days to physiological maturity; Chl, chlorophyll content (SPAD units); ΦII, the quantum yield of photosystem II; ΦNO, the proportion of light energy dissipated via non-regulated processes; ΦNPQ, the proportion of light energy dissipated as heat through non-photochemical quenching. G, genotypes; WR, water regime; G × WR, genotype by water regime interaction. Means followed by different letters were significantly different ($p \leq 0.05$) by the independent samples *t*-test ($p \leq 0.05$). The probabilities (** $p \leq 0.01$; *** $p \leq 0.001$) are shown, and NS is insignificant.

Under terminal drought conditions, significant variability was observed among genotypes in the number of days to maturity (DM). On average, the genotypes under water deficit reached maturity 8 days earlier compared to well-watered conditions (Figure 2b).

This acceleration in the developmental cycle is a typical adaptive response to terminal water deficit, as plants often complete their life cycle earlier to avoid prolonged stress (Beebe et al., 2013); however, the magnitude of this acceleration varies among cultivars. The genotypes Lpci and Zorzal reached maturity at 105 days under ND, but in DS, the development cycle was reduced, reaching maturity at 87 days. This reduction represents an 18% increase in crop precocity in these genotypes, which appear more sensitive to water scarcity. The former potentially led to a minor number of grains and, consequently, lower yield potential.

In contrast, genotypes 456 and 458 display only a 5% difference in DM between the two water regimes, suggesting more stable phenological behavior and an inherent drought tolerance. These findings highlighted that such variability could be linked to root architecture and water-use efficiency, which were not measured in this study but warrant further investigation (Assefa et al., 2017; Polania et al., 2022). The accelerated maturity in sensitive genotypes may compromise yield potential due to reduced grain filling periods, whereas tolerant genotypes balance stress avoidance and yield stability.

2.5.3. *Physiological Traits*

In addition to the observed phenological variation, substantial differences were also found in physiological traits among the evaluated genotypes. These traits are closely linked to adaptive mechanisms of drought tolerance in common bean.

The analysis of leaf chlorophyll content revealed variable responses across the bean genotypes under ND and DS conditions. A significant difference (*** $p \leq 0.01$) was observed between the genotypes and water regimes (Table 4; Figure 2a). In addition, the drought-resistant genotype 473 showed the highest chlorophyll content (Figure 2a). This increase in chlorophyll content under DS may be attributed to adaptive mechanisms avoiding oxidative damage and photoinhibition (Tapia et al., 2022; Chaves et al., 2008). Also, the higher chlorophyll content under DS could result from reduced leaf expansion (smaller leaf area with concentrated chlorophyll) or upregulation of chlorophyll biosynthesis as part of the stress response (Flexas et al., 2006).

The quantum yield of PSII (ΦII) is a dimensionless parameter that quantifies the efficiency with which absorbed light is converted into excited electrons that drive the electron transport chain and, ultimately, the synthesis of chemical energy (Genty et al., 1989). The results of the present study revealed significant variations in ΦII among genotypes and under both well-watered and drought-stress conditions (*** $p \leq 0.001$) (Table 4). There was a decline in ΦII under drought (Figure 2d), indicating reduced photosynthetic performance, likely due to stomatal closure and the consequent reduction in CO2 availability (Flexas et al., 2006), which is consistent with previous studies showing how drought stress negatively impacts PSII efficiency (Polania et al., 2016).

Notably, some genotypes, such as 464 and 478 (Figure 2d), maintain relatively high ΦII values under both ND and DS, suggesting they possess mechanisms that sustain photosynthetic activity and protect the photosynthetic apparatus under water deficit (Bashir et al., 2021). On the other hand, genotypes like Zorzal and Sel 6 showed the lowest ΦII values under drought, which may render them more susceptible to photooxidative damage and PSII in activation under stress. In addition, the lowest grain yield genotype, Blanco Español, showed reduced ΦII values under drought.

Furthermore, the absence of a significant genotype × water regime interaction (NS) suggests that the inherent genetic differences in ΦII remain consistent regardless of the water conditions (Table 4).

The non-photochemical quenching (ΦNPQ) values across multiple genotypes under irrigation and drought conditions reveal significant variability in photoprotective capacity. In general, ΦNPQ values increase under drought stress, and there were significant differences between water regimes (*** $p \leq 0.001$) (Table 4). The enhanced NPQ under DS suggests that plants actively dissipate excess light energy as heat to protect the photosynthetic apparatus from photodamage (Chaves et al., 2008; Ruban et al., 2016). This response is consistent with the known role of NPQ as a critical photoprotective mechanism under conditions of water limitation, where stomatal closure reduces CO2 availability and increases the risk of excess light energy accumulation.

Among the genotypes, 483 and Zorzal (Figure 2e) stand out for their robust photoprotective responses, with ΦNPQ values increasing significantly under drought. These genotypes likely possess efficient mechanisms for dissipating excess energy, which helps maintain photosynthetic efficiency and minimize damage under stress (Živcák et al., 2014). In contrast, genotype 457 showed a little increase in ΦNPQ under drought, suggesting less effective photoprotection and potentially greater susceptibility to photooxidative stress (Muller et al., 2001).

The non-regulated energy dissipation parameter (ΦNO) also showed significant differences (*** $p \leq 0.001$) between water treatments. This parameter decreased in plants under DS, indicating a shift towards regulated energy dissipation (Table 4). Lower ΦNO under DS can indicate a reduction in energy dissipation, which may indicate improved regulation of energy use under stress and could be beneficial, as it minimizes energy loss through unregulated processes that can lead to photoinhibition and highlight the plant's ability to adjust energy dissipation pathways to cope with drought stress (Porcar-Castell et al., 2014). These results underscore that maintaining low ΦNO values under water deficit indicates adaptive physiological mechanisms such as sustained CO2 assimilation and effective osmotic adjustment, collectively contributing to enhanced drought tolerance.

Therefore, a notable association was observed between physiological traits and yield performance, particularly under DS. Genotypes that exhibited elevated values of quantum yield of photosystem II (ΦII) and non-photochemical quenching (ΦNPQ) consistently maintained higher grain yields. This trend suggests that the ability to sustain efficient photochemical activity and activate photoprotective mechanisms under water-limited conditions contributes significantly to drought tolerance in common beans.

The combined analysis of agronomic, phenological, and physiological traits with drought tolerance indices (DSI and GMP) (Table 5) revealed distinct genotypic responses to terminal drought stress. Genotypes 452, 473, and 483 exhibited superior drought tolerance, characterized by minimal yield reductions (<11%), but also recorded the lowest DSI (≤0.5) and highest GMP (>3400 kg ha^{-1}), confirming their superior drought tolerance and yield stability. This genotype also had a superior physiological performance (high ΦII and ΦNPQ). These responses suggest that these genotypes employ stress tolerance mechanisms, such as maintaining photochemical activity, efficient energy dissipation, and physiological stability, through delayed senescence and chlorophyll retention under water deficit (Muller et al. 2001; Porcar-Castell et al., 2014). In contrast, genotypes such as Blanco Español, Sel 6, and Curi showed high DSI values (>1.5) and low GMP, aligning with their poor yield performance under drought. In contrast, genotypes like Blanco Español showed high DSI values (>1.5) and low GMP (Table 5), reflecting greater susceptibility. These findings emphasize the value of combining yield-based indices with physiological parameters, such as chlorophyll retention and photosystem II efficiency, to identify genotypes with high drought adaptation. This approach highlights the differential impact of water scarcity on bean productivity. Also, it provides a framework for selecting parental lines for breeding programs to enhance drought resilience in water-scarce environments.

The findings of this study are consistent with previous research conducted in semi-arid regions of South America, where common bean genotypes with enhanced photosynthetic efficiency and greater capacity for non-photochemical energy dissipation have shown superior performance under terminal drought. For instance, Rosales et al., (2012) reported that drought-tolerant cultivars exhibited smaller reductions in photosystem II efficiency and higher ΦNPQ values, which contributed to improved adaptation to water stress in semi-arid environments; another study (Lana et al., 2018), also emphasized the significance of physiological traits such as chlorophyll content and efficiency of photosystem II in select-ing drought-resilient genotypes in Mexico and northeast Brazil. These studies reinforce the value of integrating physiological parameters as selection criteria in breeding programs aimed at enhancing drought tolerance in common bean.

The genotypes identified as drought-tolerant in this study, particularly 452, 473, and 483, demonstrated stable yield performance, efficient photosynthetic functioning, and favorable phenological adjustment under terminal drought. These traits make them strong candidates for use as parental lines in the national breeding program of INIA in the central valley of Chile.

Table 5. Mean yield (kg ha^{-1}), percent yield reduction (PR in %) under drought-stressed (DS) relative to the non-stressed (ND) conditions, geometric mean productivity (GMP), drought susceptibility index (DSI), 100-seed weight (g), and days to maturity (days) for 20 genotypes evaluated during two seasons at the Santa Rosa Experimental Field, INIA-Quilamapu, Chillán, Chile, during the seasons 2021/2022 and 2022/2023.

Code	**Yield (kg ha^{-1})**					**100-seed weight**		**Days to maturity**	
	NS	DS	PR (%)	GMP	DSI	ND	DS	ND	DS
442	4390	2727	38	3460	1.7	31.5	27.9	88	83
452	3768	3650	3	3708	0.1	25.7	20.7	89	83
456	4345	3555	18	3930	0.8	33.9	30.4	87	83
457	3509	3330	5	3419	0.2	37.3	34.7	88	83
458	3757	3091	18	3408	0.8	22	19.1	88	83
463	3857	3263	15	3512	0.6	37.5	32.9	89	83
464	4292	3703	14	3987	0.6	33.8	29.4	89	83
467	3963	3594	9	3774	0.4	35.8	33.4	89	83
473	3484	3311	5	3427	0.1	41.3	35	88	83
475	3473	2722	22	3074	1	38.7	35	89	83
478	4486	3154	30	3761	1.3	39	33.7	89	83
479	4287	3284	23	3752	1.1	37.3	33.2	89	83
483	4312	3819	11	4058	0.5	41	37	90	83
485	3604	3017	16	3297	0.7	35.5	35.5	88	83

487	3382	2343	31	2815	1.4	41.6	36	88	83
Curi	3591	2134	41	2624	2.4	21.8	19.2	90	83
Lpci	3548	2558	28	2768	1.8	51	46.3	104	87
Zorzal	3796	2678	29	3012	1.3	50.1	47.9	105	87
Sel 6	4125	2738	34	3361	1.5	48.6	42.6	102	86
Blanco Español	3850	1788	54	3189	1.3	51.5	47.9	95	85
Overall mean	3891	3023			0.98	37.7	33.8	91	84
LSD (0.05)	684.601	643.149				1.93	3.51	2.04	1.87
CV%	20.33	29.64				23.0	26.1	7.47	9.1

2.5.4. *Relationships between traits and yield stability*

Principal Component Analysis (PCA) was used to reduce the dimensionality of the dataset and to explore relationships between genotypes and the physiological and produc-tive traits of common beans under different water conditions. The analysis (Figure 3) explained 71.6% of the total data variability through the first two principal components (PC1 and PC2). The traits AGB, HI, NGP, ΦNPQ, and GY explained more than 50% of the data variability. These findings agree with previous studies indicating that drought-adapted common beans rely on efficient biomass partitioning (harvest index) and sustained photosynthetic efficiency under stress two well-established traits that contribute to yield stability in water-limited conditions (Beebe et al., 2013; Wentworth et al., 2006; Rao et al., 2017).

The PCA reveals a clear separation of genotypes based on environmental conditions, which were distributed at opposite ends of PC1. Within each environment, two distinct groups of genotypes were observed. Under ND conditions, the genotypes Zorzal, Lpci, Sel 6, and Blanco Español were separated from the others, indicating different performances. This separation was primarily driven by traits such as HGW and DM. These four genotypes exhibited higher grain weight but produced fewer grains overall, resulting in an average yield compared to the full set of genotypes under control conditions (Figure 1). Additionally, they showed a tendency for delayed maturity (Figure 2).

Under drought conditions, crop productivity is primarily limited by water availability. To maximize water-use efficiency, three key factors must be considered: (1) optimizing the uptake of available water, (2) enhancing its utilization to improve dry matter accumulation, and (3) efficiently partitioning the accumulated biomass into harvestable grain yield (Beebe et al., 2009). The observed delay in DM suggests an extended vegetative phase, which may reduce resource allocation to reproductive structures—a trade-off commonly associated with conservative drought-avoidance genotypes (Rao et al., 2017).

The remaining group of genotypes under irrigated conditions showed a strong positive association with HI, AGB, NGP, and GY, as well as the photosynthetic parameters ΦII and ΦNO. These associations suggest a strong link between photosynthetic efficiency, biomass accumulation, and yield under non-stressful conditions (Beebe et al., 2013; Lanna et al., 2018; Keller et al., 2024).

A similar pattern of genotype separation was observed under terminal drought conditions (Figure 3). In this environment, Zorzal, Lpci, Sel 6, and Blanco Español again formed a distinct group, characterized by low yield and marked by high values of ΦNPQ and low values of ΦII (Figures 1 and 2). This suggests that the low yields observed under water stress were primarily due to a marked decline in photosynthetic efficiency (decrease in ΦII), coupled with an increase in thermal energy dissipation processes (increase in ΦNPQ) to protect PSII from oxidative damage, a hallmark of drought-sensitive common bean genotypes (Bashir et al., 2021; Macedo et al., 2019).

The analysis also showed no association between GY and DF, which was expected given that water stress occurred after flowering. Additionally, a negative correlation was observed between GY and Chl, although the contribution of leaf chlorophyll content to the overall variability in the analysis was very low. This negative association may be explained by two key mechanisms: 1) photo-oxidative stress in high-chlorophyll genotypes: under drought stress, genotypes with elevated chlorophyll content may experience excessive reactive oxygen species (ROS) production, leading to photooxidative damage (Foyer et al., 2009). and 2) enhanced nutrient remobilization in low-chlorophyll genotypes: conversely, low-chlorophyll genotypes may exhibit accelerated senescence, promoting more efficient nutrient redistribution to developing grains (Gregersen et al., 2013).

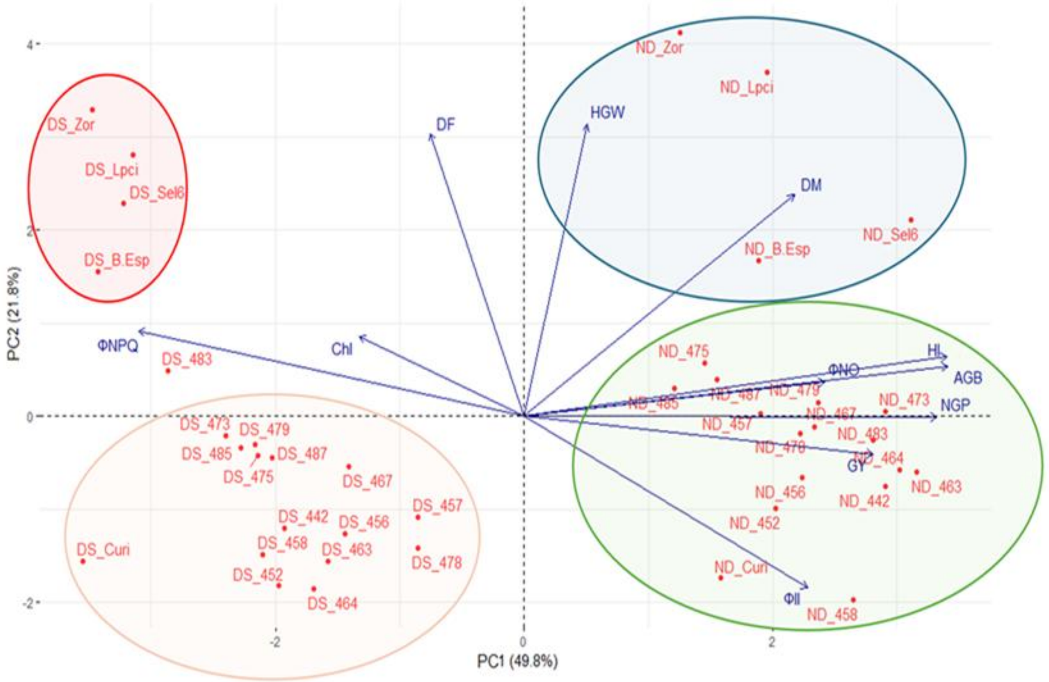

Figure 3. Principal components analysis (PCA) biplot of agronomic and physiological traits of twenty common bean genotypes assessed under no stress (ND) and terminal drought stress (DS) conditions over two years. AGB: Above ground biomass, GY: Grain yield, HI: Harvest index, NGP: Number grains per square meter, HGW: Hundred grains weight, DF: Days to flowering, DM: Days to maturity, Chl: Chlorophyll content, ΦII: Quantum yield of photosystem II, ΦNPQ proportion of light energy dissipated as heat through non-photochemical quenching means for the studied genotypes, ΦNO: proportion of light energy dissipated via non-regulated processes. Zor: Zorzal and B.Esp: Blanco Español.

The Genotype + Genotype-by-Environment interaction (GGE) analysis is widely used in plant breeding for evaluating data from multi-environment trials. It facilitates the identification of stable genotypes that perform consistently across diverse environments and those with superior performance in specific conditions (Esan et al., 2022; Omrani et al., 2022; Wang et al., 2023). The GGE analysis revealed that the first principal component accounted for 56% of the variance attributed to the genotype-by-environment interaction for grain yield, while the second component explained 26% (Figure 4), capturing together a substantial proportion of the yield variability (Gauch et al., 2008).

The high cumulative explained variance (82%) is consistent with findings from common bean trials of Acosta-Díaz et al. (2009), reinforcing that genotype × environment (G×E) interactions are the primary drivers of yield adaptation in this crop. These results underscore the critical importance of multi-environment testing to distinguish genotypes with broad adaptability from those suited to specific conditions.

Several genotypes, such as Blanco Español, Sel 6, Zorzal, Lpci, Curi, 442, 475, and 487, were classified as unstable. Although they exhibited relatively high yields under irrigated conditions, their performance declined sharply under terminal water stress (Figure 1), as reflected in above-average DSI values. Similarly, genotypes 478 and 479 were closely associated with irrigated conditions (Figure 4), characterized by high yields under ND environments. However, both experienced significant yield reductions under water stress, showing below-average DSI values (Figure 1, Table 5). This observed pattern aligns with the "water-spending" strategy documented in Andean bean genotypes by Polania et al. (2016), characterized by vigorous growth under well-watered conditions but poor drought avoidance mechanisms, such as shallow root systems and limited osmotic adjustment. The high drought susceptibility index (DSI) values further support this trend, mirroring results from drought-sensitive bean lines (Rao et al 2017). The observed dramatic yield reduction under drought conditions is consistent with findings from Rosales et al. (2012), who attributed such patterns to impaired photosynthate remobilization during stress periods. Despite this, their high performance in well-watered conditions makes them suitable candidates for breeding targeting non-limiting water environments.

In contrast, genotypes 452, 456, 457, 464, 473, and 483, along with 458, 463, 467, and 485, demonstrated stability across environments (Figures 1 and 4) and consistently low DSI values (Table 5). These genotypes exhibit greater versatility and could be used in environments with variable water availability. These genotypes exhibit characteristics similar to the high-yielding but drought-sensitive varieties reported by Beebe et al. (2013), where breeding for irrigated conditions favors harvest index improvement at the expense of stress resilience.

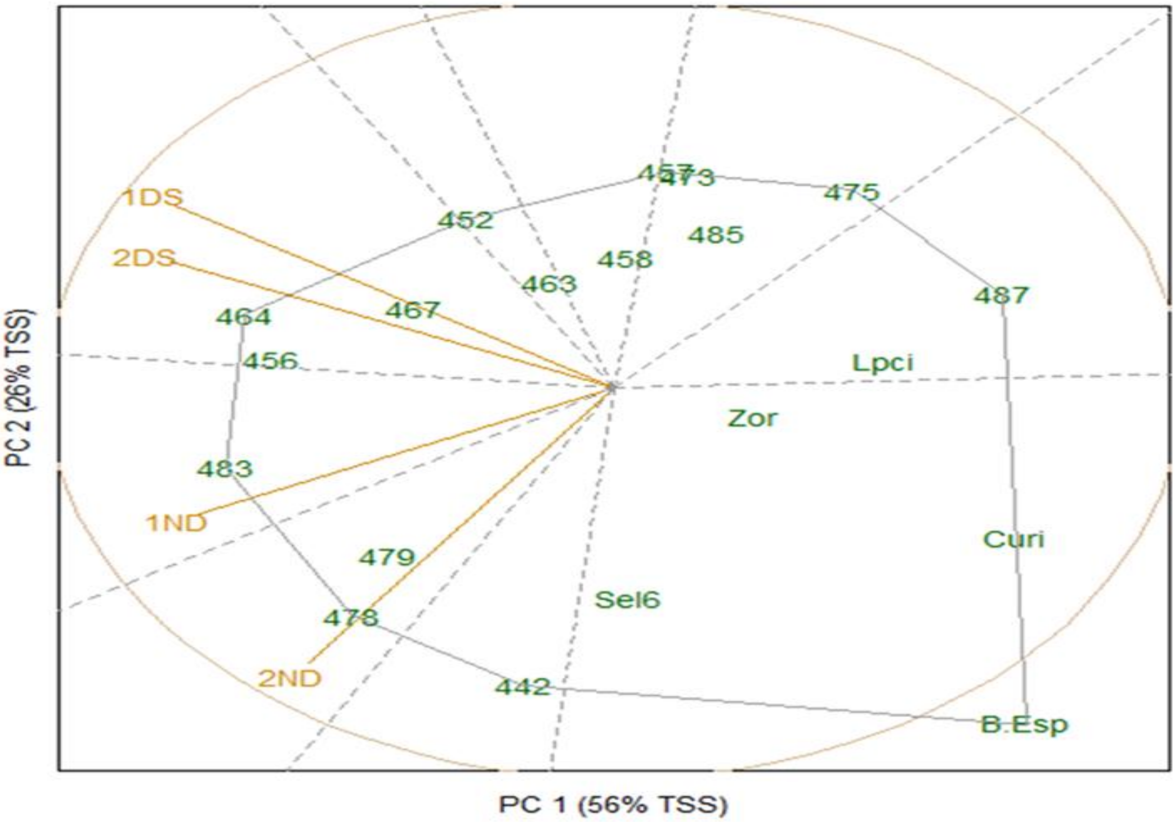

Figure 4. Genotype + Genotype × Environment interaction (GGE) biplot based on the grain yield of twenty common bean genotypes assessed under no stress (ND) and terminal drought stress (DS) conditions during two years. Zor: Zorzal and B.Esp: Blanco Español.

2.6. *Conclusions*

The study demonstrated that drought significantly reduced grain yield (22.3%), aboveground biomass (37%), harvest index (19.5%), grains per pod (61.3%), and hundred-grain weight (22.7%), highlighting water scarcity's severe impact on bean productivity. Drought also accelerated physiological maturity in susceptible genotypes, shortening the crop cycle—a stress-avoidance mechanism that may compromise yield potential. Notably, genotypes 452, 473, and 483 exhibited exceptional drought tolerance with minimal yield reductions and the lowest drought susceptibility index (DSI). These genotypes maintained high, stable photosystem II quantum yield (ΦII) under both non-drought (ND) and drought-stressed (DS) conditions, crucial for sustaining photosynthesis under stress. In contrast, sensitive genotypes like Blanco

Español suffered severe yield declines (54%) and reduced photosynthetic efficiency, underscoring cultivar-dependent drought adaptation. PCA analysis explained 71.6% of trait variability, with >50% driven by biomass, harvest index, grain number, non-photochemical quenching (ΦNPQ), and grain yield. Drought-sensitive genotypes (Zorzal, Lpci, Sel 6, Blanco Español) showed low yields, reduced ΦII, and ΦNPQ, while genotypes 452 and 456 excelled in yield and ΦII under ND, indicating efficient biomass partitioning. These results emphasize the value of combining physiological traits (ΦII, ΦNPQ) with agronomic metrics in breeding drought-resilient beans. Future research should assess selected genotypes under sustained moderate drought from sowing, alongside root architecture analysis (depth and density) to identify tolerance traits. Multi-location farmer-field trials are also critical to verify their stability and yield performance across diverse environments. This integrated approach will accelerate the development of climate-resilient bean varieties.

2.7. *Funding*

This research was funded by Subsecretaría de Agricultura, Gobierno de Chile, and Programa de Fitomejoramiento del Frejol (500155-70).

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Supplementary materials

Table S1. Physical soil analysis results at the Santa Rosa Experimental Field, INIA-Quilamapu, Chillán, Chile. The data represent three depth intervals and include texture classification, bulk and particle densities, water retention capacity, and porosity.

Depth (cm)	% Sand	% Silt	% Clay	Textural Class	Bulk Density (g/cm^{-3})	Particle Density (g/cm^{-3})	Moisture Retention 1/3 Atm (%HBSS)	Total Porosity (%)	Moisture Retention 15 Atm (%HBSS)
0–20	33.8	40.9	25.3	Loam	1.19	2.48	40.24	52.02	24.27
20–40	29.0	39.7	25.4	Loam	1.25	2.50	30.04	50.00	18.03
40–60	54.5	31.8	13.7	Sandy Loam	1.47	2.52	27.37	41.67	16.42

Note: %HBSS = Moisture percentage based on oven-dry soil weight.

Table S2. Soil chemical results analysis at the Santa Rosa Experimental Field, INIA-Quilamapu, Chillán, Chile. The table includes texture, pH, organic matter, conductivity, available nutrients, and exchangeable bases.

Parameters	Value
pH (soil: water 1:5)	6.04
Organic matter, %	11.57
EC, dS m^{-1}	0.11
Available N, mg kg^{-1}	14.7
Available P, mg kg^{-1}	11.81
Exchangeable K, cmol$_+$ kg^{-1}	0.38
Exchangeable Ca, cmol$_+$ kg^{-1}	6.71
Exchangeable Mg, cmol$_+$ kg^{-1}	0.94
Exchangeable Na, cmol$_+$ kg^{-1}	0.16
Exchangeable Al, cmol$_+$ kg^{-1}	0.02
Available S, mg kg^{-1}	26.31

Note: EC = electrical conductivity; N = nitrogen; P = phosphorus; K = potassium; Ca = calcium; Mg = magnesium; Na = sodium; Al = aluminum; S = sulfur.

Supplementary Table S3. Agronomic, Phenological, and Physiological Traits of 20 Common Bean (*Phaseolus vulgaris* L.) Genotypes under Non-Drought (ND) Conditions in Chillán, Chile. (2021–2023).

Code	AB (kg/ha)	GY (kg/ha)	HI (%)	NGP	HGW (g)	DF (days)	DM (days)	Chl (SPAD)	ΦII	ΦNPQ	ΦNO
442	5148,06 a	4390,00 ab	76,17 abc	2174,19 bc	31,49 g	46,75 de	88,38 de	56,77 abcd	0,290 abcd	0,486 bcd	0,224 ab
452	5266,31 a	3767,50 abcdef	76,64 ab	2190,04 bc	25,73 h	46,75 de	88,75 de	55,02 abcd	0,284 abcd	0,530 abcd	0,186 ab
456	5192,94 a	4344,69 abc	74,94 abc	2339,54 abc	33,90 f	47,00 de	87,25 e	54,65 bcd	0,287 abcd	0,535 abcd	0,179 ab
457	5203,59 a	3509,38 def	73,62 bc	2216,35 abc	37,33 de	48,13 cde	88,00 de	58,75 ab	0,300 abc	0,503 abcd	0,197 ab
458	5260,95 a	3756,88 abcdef	76,23 abc	2226,94 abc	22,04 i	46,00 e	88,00 de	52,64 d	0,306 abc	0,501 abcd	0,194 ab
463	5175,28 a	3856,56 abcdef	76,17 abc	2334,46 abc	37,53 de	46,25 de	88,75 de	57,59 abc	0,309 ab	0,462 d	0,229 ab
464	5272,78 a	4292,19 abcde	77,40 ab	2456,33 a	33,78 f	48,88 cd	88,63 de	56,79 abcd	0,330 a	0,491 bcd	0,179 ab
467	5358,21 a	3963,13 abcdef	74,81 abc	2249,19 abc	35,84 ef	47,88 de	88,75 de	56,73 abcd	0,292 abcd	0,511 abcd	0,198 ab
473	5236,15 a	3484,06 def	75,20 abc	2420,11 ab	41,31 c	46,00 e	88,50 de	56,86 abcd	0,273 bcd	0,470 cd	0,256 a
475	5281,94 a	3472,50 ef	75,68 abc	2367,04 abc	38,69 d	46,75 de	89,00 de	57,27 abcd	0,248 d	0,555 abc	0,197 ab
478	5271,87 a	4485,63 a	76,95 ab	2133,21 c	39,03 d	48,00 de	89,38 de	57,23 abcd	0,321 a	0,536 abcd	0,143 b
479	5310,79 a	4286,88 abcde	76,31 abc	2385,40 abc	37,34 de	45,75 e	88,88 de	59,54 a	0,258 cd	0,521 abcd	0,221 ab
483	5225,16 a	4311,56 abcd	77,25 ab	2206,58 abc	41,00 c	46,00 e	90,00 d	58,07 ab	0,309 ab	0,501 abcd	0,190 ab
485	5299,29 a	3603,75 bcdef	75,33 abc	2254,32 abc	35,53 ef	49,00 cd	87,75 de	54,83 abcd	0,272 bcd	0,570 ab	0,158 b
487	5401,11 a	3382,19 f	78,12 a	2164,22 c	41,61 c	47,38 de	88,38 de	58,03 ab	0,292 abcd	0,545 abcd	0,163 b
Curi	5286,51 a	3590,94 bcdef	69,70 d	1611,40 d	21,80 i	46,00 e	89,50 de	54,71 bcd	0,303 abc	0,513 abcd	0,185 ab
Lpci	5311,91 a	3547,81 cdef	73,38 bcd	1612,66 d	51,00 a	52,63 ab	104,50 a	57,55 abc	0,262 bcd	0,529 abcd	0,209 ab
Zorzal	5316,47 a	3795,94 abcdef	77,07 ab	1629,14 d	50,13 ab	54,13 a	104,75 a	57,81 ab	0,262 bcd	0,587 a	0,151 b
Sel,6	5296,27 a	4125,00 abcdef	76,50 abc	1537,85 d	48,60 b	50,63 bc	102,00 b	53,08 cd	0,292 abcd	0,501 abcd	0,208 ab

Blanco Español	5167,90 a	3850,31 abcdef	72,31 cd	1593,48 d	51,15 a	48,50 cde	95,38 c	54,63 bcd	0,271 bcd	0,531 abcd	0,198 ab

Data represent means from two growing seasons (2021/2022 and 2022/2023) under non-drought (ND) conditions in Chillán, Chile, Different lowercase letters within a column indicate significant differences among genotypes according to Duncan's test (*p* ≤ 0,05), **Abbreviations**: AB, aboveground biomass; GY, grain yield; HI, harvest index; NGP, number of grains per pod; HGW, hundred-grain weight; DF, days to flowering; DM, days to maturity; Chl, chlorophyll content; ΦII, quantum yield of photosystem II; ΦNPQ, non-photochemical quenching; ΦNO, non-regulated energy dissipation.

Supplementary Table S4. Agronomic, Phenological, and Physiological Traits of 20 Common Bean (*Phaseolus vulgaris* L.) Genotypes under Drought Stress (DS) Conditions in Chillán, Chile (2021–2023).

Code	**AB (kg/ha)**	**GY (kg/ha)**	**HI (%)**	**NGP**	**HGW (g)**	**DF (days)**	**DM (days)**	**Chl (SPAD)**	**ΦII**	**ΦNPQ**	**ΦNO**
442	3310,794 abc	2726,875 cdef	59,813 b	853,571 ab	27,856 f	47,125 c	83,125 c	60,255 ab	0,289 abcde	0,547 cde	0,163 abc
452	3333,849 abc	3650,000 ab	60,580 b	840,476 b	20,738 g	47,125 c	83,125 c	55,081 bc	0,272 abcdefg	0,602 abcd	0,127 bcd
456	3212,817 abc	3554,688 ab	61,178 b	819,048 b	30,363 def	47,750 c	83,125 c	54,851 bc	0,284 abcde	0,568 bcde	0,148 abc
457	3187,540 abc	3330,000 abc	66,725 a	829,762 b	34,650 c	47,000 c	83,125 c	58,763 abc	0,305 abc	0,530 de	0,165 abc
458	3353,373 abc	3090,625 abcd	58,264 b	830,952 b	19,100 g	48,000 c	83,375 c	55,014 bc	0,254 abcdefgh	0,582 abcde	0,164 abc
463	3499,127 a	3262,500 abcd	63,110 ab	907,143 a	32,938 cde	45,875 c	82,875 c	54,515 bc	0,294 abcd	0,590 abcd	0,116 cd
464	3489,881 a	3703,438 ab	62,006 b	871,429 ab	29,363 ef	46,625 c	83,250 c	54,000 c	0,307 ab	0,606 abcd	0,087 d
467	3448,413 a	3594,375 ab	62,182 b	827,381 b	33,363 cd	47,875 c	83,125 c	56,518 bc	0,258 abcdefgh	0,571 abcde	0,171 ab
473	3490,873 a	3310,938 abcd	60,489 b	864,286 ab	35,013 c	46,250 c	82,625 c	62,404 a	0,246 cdefgh	0,595 abcd	0,159 abc
475	3482,778 a	2721,875 cdef	61,716 b	839,286 b	35,013 c	46,250 c	82,500 c	59,114 abc	0,249 bcdefgh	0,578 abcde	0,174 ab
478	3406,944 ab	3153,750 abcd	61,344 b	850,000 ab	33,738 cd	46,250 c	82,625 c	59,609 abc	0,308 a	0,510 e	0,182 a
479	3321,825 abc	3283,750 abcd	59,012 b	854,762 ab	33,225 cd	46,625 c	83,000 c	59,730 abc	0,234 defgh	0,582 abcde	0,184 a
483	3358,413 abc	3818,750 a	60,481 b	828,571 b	36,950 c	48,500 c	82,875 c	60,404 ab	0,231 efgh	0,640 ab	0,129 bcd
485	3114,008 bc	3016,875 bcde	61,659 b	839,286 b	35,513 c	46,250 c	83,125 c	59,488 abc	0,245 cdefgh	0,586 abcde	0,169 ab
487	3417,778 ab	2342,500 efg	61,144 b	830,952 b	36,038 c	47,375 c	82,875 c	58,824 abc	0,275 abcdef	0,556 cde	0,169 ab

Curi	3073,968 c	2133,688 fg	52,746 c	685,714 d	19,225 g	47,875 c	82,875 c	56,666 abc	0,266 abcdefg	0,601 abcd	0,134 abc
Lpci	3272,460 abc	2557,500 def	61,247 b	716,667 cd	46,313 a	55,125 a	87,000 a	58,754 abc	0,241 defgh	0,621 abc	0,138 abc
Zorzal	3305,079 abc	2678,438 cdef	62,695 ab	723,810 cd	47,863 a	54,750 a	87,250 a	59,168 abc	0,214 gh	0,650 a	0,136 abc
Sel,6	3078,373 c	2737,813 cdef	60,082 b	753,571 c	42,625 b	52,125 ab	86,250 ab	59,364 abc	0,205 h	0,624 abc	0,171 ab
Blanco Español	3055,516 c	1788,375 g	59,632 b	733,333 cd	47,963 a	49,125 bc	84,500 bc	56,407 bc	0,218 fgh	0,620 abc	0,162 abc

Data represent means from two growing seasons (2021/2022 and 2022/2023) under drought stress (DS) conditions in Chillán, Chile. Different lowercase letters within a column indicate significant differences among genotypes according to Duncan's test *(p* ≤ 0.05). Abbreviations: AB, aboveground biomass; GY, grain yield; HI, harvest index; NGP, number of grains per pod; HGW, hundred-grain weight; DF, days to flowering; DM, days to maturity; Chl, chlorophyll content; ΦII, quantum yield of photosystem II; ΦNPQ, non-photochemical quenching; ΦNO, non-regulated energy dissipation.

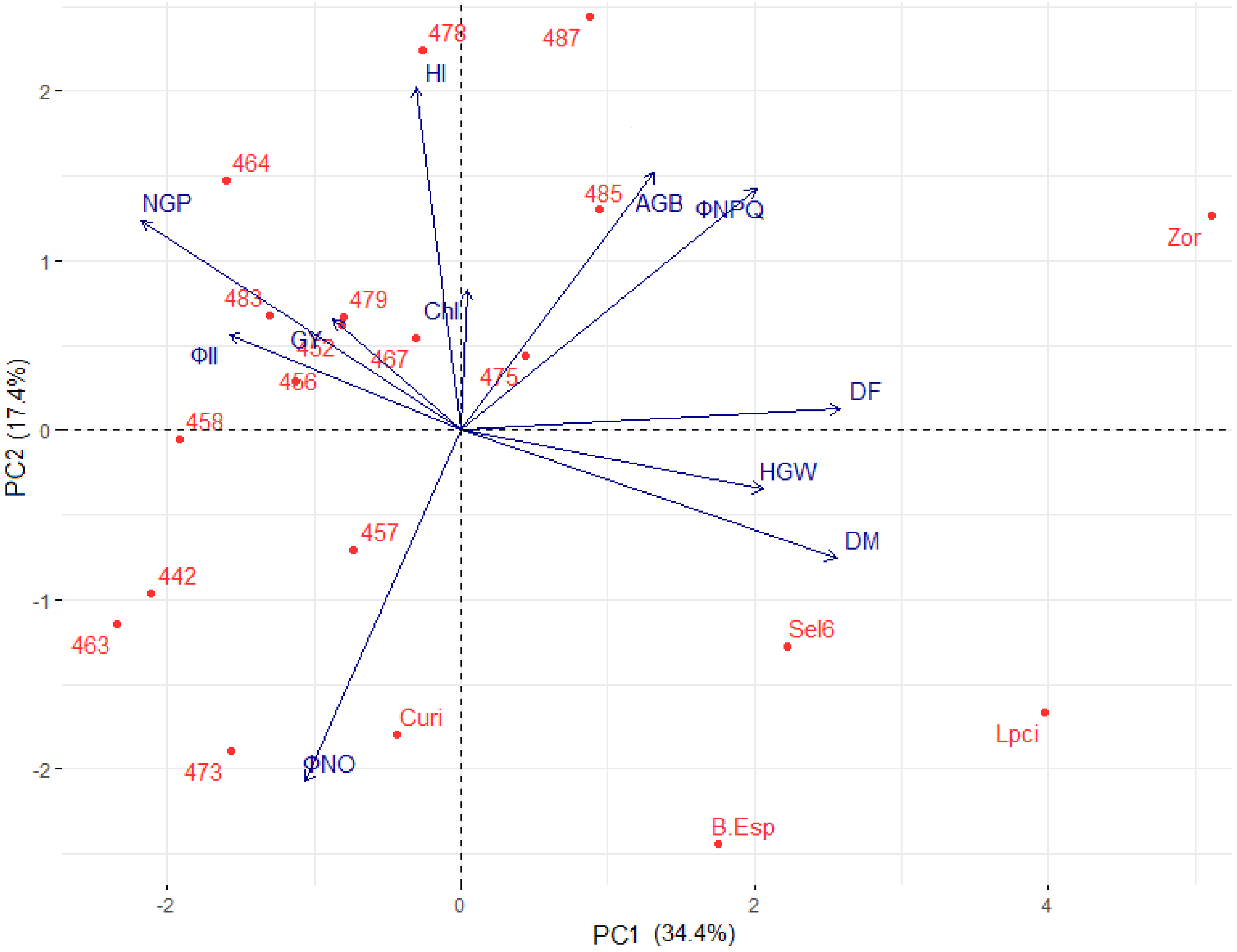

Figure S1. Principal components analysis (PCA) biplot of agronomic and physiological traits of twenty common bean genotypes assessed under no stress conditions over two years. AGB: Above ground biomass, GY: Grain yield, HI: Harvest index, NGP: Number grains per square meter, HGW: Hundred grains weight, DF: Days to flowering, DM: Days to maturity, Chl: Chlorophyll content, ΦII: Quantum yield of photosystem II, ΦNPQ proportion of light energy dissipated as heat through non-photochemical quenching means for the studied genotypes, ΦNO: proportion of light energy dissipated via non-regulated processes. Zor: Zorzal and B.Esp: Blanco Español.

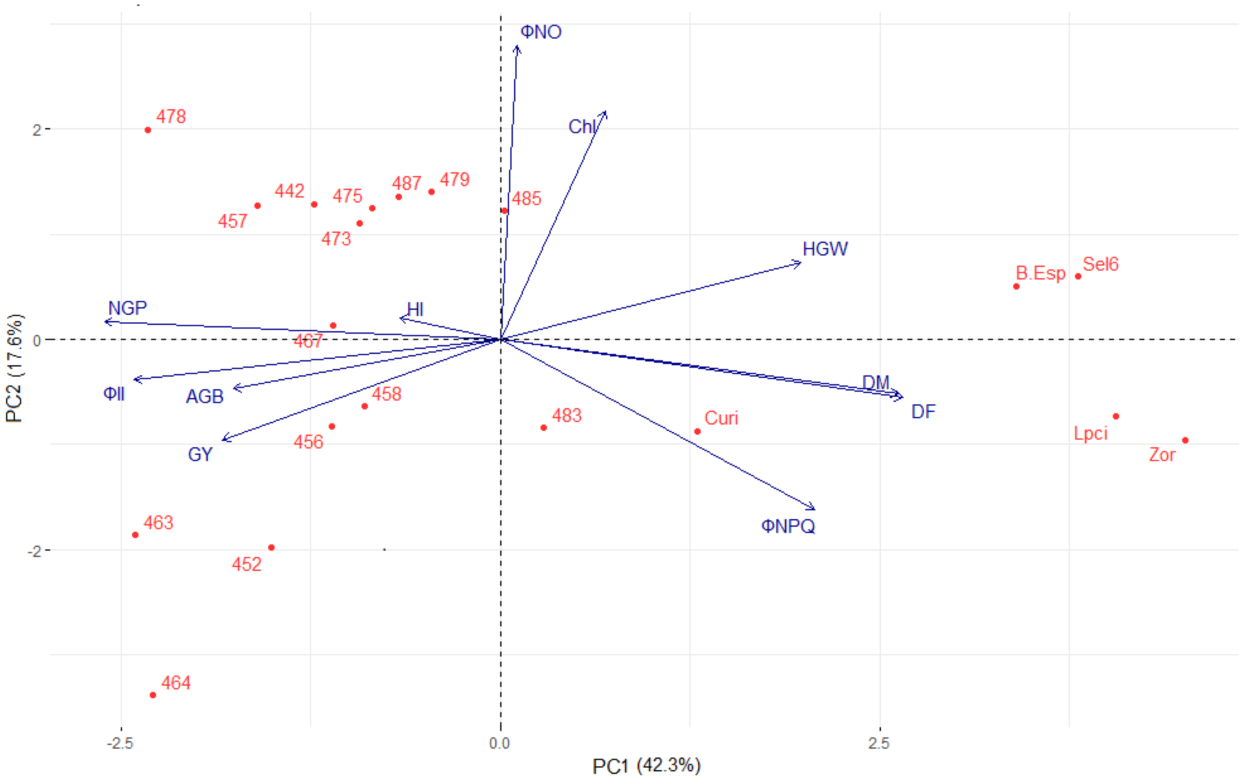

Figure S2. Principal components analysis (PCA) biplot of agronomic and physiological traits of twenty common bean genotypes assessed under terminal drought stress (DS) conditions over two years. AGB: Above ground biomass, GY: Grain yield, HI: Harvest index, NGP: Number grains per square meter, HGW: Hundred grains weight, DF: Days to flowering, DM: Days to maturity, Chl: Chlorophyll content, ΦII: Quantum yield of photosystem II, ΦNPQ proportion of light energy dissipated as heat through non-photochemical quenching means for the studied genotypes, ΦNO: proportion of light energy dissipated via non-regulated processes. Zor: Zorzal and B.Esp: Blanco Español.

III. CAPÍTULO 3:

Agronomic Performance, Nutritional Quality and Cooking Traits of Common Bean Genotypes Grown Under Terminal Drought Conditions in South-Central Chile

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Artículo enviado a: Chilean Journal of Agricultural Research. Número asignado: CJAR250169

3.1. Abstract

Drought stress significantly impacts the agronomic and nutritional properties of common bean (*Phaseolus vulgaris* L), affecting agronomic traits, the 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 twenty 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 (CT), crude protein content (PC), total phenolic content (TPC), and DPPH-based antioxidant activity. Results showed a significant reduction 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 (> 3,600 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 could contribute to improving the genotype selection process and development of common bean cultivars, indicating that selecting genotypes for both high yield and quality under water-limited conditions, thereby contributing to the sustainability of the crop and its adaptation to future climate scenarios.”

Keywords: common bean, drought stress, grain yield, hydration capacity, antioxidant, phenolic content.

3.2. Introduction

Common beans 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 et al., 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 in plants, leading to variations in the concentration of bioactive compounds 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 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 conserving nutritional content in the seed regardless of 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 refers to the rate and extent of water uptake during soaking, serving 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 result in the loss of heat-sensitive vitamins and minerals. (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 aims 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, including phenolic content, DPPH-based antioxidant activity, protein content, hydration capacity, and cooking time.

3.3. Materials and Methods

3.3.1. Experimental site conditions and plant materials

The experiment was conducted at the Santa Rosa Experimental Field of the Institute of Agricultural Research (INIA) Quilamapu, Chillán, Chile (36°31′ S; 71°54′ W, 196 m.a.s.l). The soil at the experimental site is classified as volcanic (Melanoxerand) according to the USDA classification system (USDA, 2014), with a loamy texture. The climate is temperate Mediterranean, characterized by 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 November 5th, 2021, and November 3rd, 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 of precipitation between flowering and harvest during the 2021-2022 and 2022-2023 seasons, respectively.

The germplasm consisted of twenty common bean genotypes (Table 2). Fifteen genotypes were selected from the US dry bean breeding drought nursery at the University of Nebraska, USA. Additionally, five cultivars belonging to the Chilean race and Andean genetic pool were selected from the Bean breeding program of INIA.

3.3.2. Crop management and experimental design

Genotypes were assigned to experimental units using a randomized complete block design with four replications. Each plot consisted of four 5.0-meter rows spaced 0.6 meters apart, targeting a plant density of 250,000 plants per hectare. Furrow irrigation systems were used throughout the trial. Before sowing, the soil was fertilized with 60 kg ha^{-1} of N, 50 kg ha^{-1} of P_2O_5, 40 kg ha^{-1} of K_2O, 18 kg ha^{-1} of S, and 12 kg ha^{-1} of MgO (Supplementary Table 1). Seeds were treated with Fludioxonil (0,35 g a.i. kg^{-1} seed) and Thiamethoxam (0,35 g a.i. kg^{-1} seed). Chemical control of weeds was applied using the Sodium salt of Fomesafen (375 g a.i. 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-meter buffer zone was maintained between adjacent trials to minimize water movement from the non-stressed to the drought-stressed plots.

Table 1. Monthly maximum (T Max), minimum (T Min), average (T Ave), evapotranspiration (ET0), rainfall (Rf), and applied irrigation (Irr) at the Santa Rosa Experimental Field, INIA-Quilamapu, Chillán, Chile, during the 2021-2022 and 2022-2023 seasons.

Season	**Month**	**T° Max (°C)**	**T° Min (°C)**	**T° Ave (°C)**	**ET0 (mm)**	**Rf (mm)**	**Irr (mm)**	**ND (mm)**	**DS (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	100
	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	00

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.

3.3.3. 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 irrigated and drought-stressed plots. Then, the data were extrapolated to a per-hectare basis. For the hundred-grain weight (HGW) at harvest, a random sample of 100 seeds was used, and the values were expressed in grams. The number of grains per pod (NGP) was extrapolated to the number of grains per square meter. Days to flowering (DF) refers to the 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.

Table 2. Genotypes from the University of Nebraska, USA, and the Institute of Agricultural Research (INIA), Chile, evaluated at the Santa Rosa Experimental Field from 2021 to 2023.

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

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).

3.3.4. *Grain quality traits*

The determination of anthocyanins, total phenolics, and antioxidant capacity of whole bean seeds was ground using an IKA A10 mill (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 of homogenized bean powder (particle size 430 nm) was extracted with 5 mL of a 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 for 24 h in sealed tubes. Afterward, the samples were subjected to ultrasound for 1 h, then centrifuged at 3,500 rpm for 15 minutes, and the supernatant was collected.

3.3.5. *Total phenolic content* (TPC)

The 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 of 0.5 N Folin–Ciocalteu reagent, 25 µL of the sample, blank, or standard, and 200 µL of distilled water were added to each well of a 96-well microplate. The plate was shaken for 30 seconds and incubated in the dark for 5 minutes at 25 °C. Subsequently, 25 µL of 10% Na_2CO_3 was added to each well, and the absorbance was measured at 765 nm using a Synergy H1 multimode microplate reader (Biotek, Winooski, VT, USA). Results were expressed as mg of gallic acid equivalents per 100 g sample (mg GAE·100 g^{-1} sample).

3.3.6. *Antioxidant activity* (DPPH)

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

3.3.7. *Crude protein content* (PC)

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

3.3.8. *Hydration capacity* (HC) *and cooking time* (CT)

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

$$(\%)\,\boldsymbol{Hydration\ capacity} = \left(\frac{\boldsymbol{seed\ weight\ after\ soaking - seed\ weight\ before\ soaking}}{\boldsymbol{seed\ weight\ before\ after\ soaking}}\right) \boldsymbol{x\ 100}$$

The cooking time was assessed using 25-seed samples that had been previously hydrated in 100 mL of distilled water for 12 hours (Katuuramu et al., 2020). After hydration, the 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.

3.4. *Statistical analysis*

The study was conducted as four independent trials (environments): ND1 (no drought, 2021-2022), DS1 (drought stress, 2021-2022), ND2 (no drought, 2022/2023), and DS2 (drought stress, 2022-2023). Each water treatment (ND and DS) consisted of a total sample size of 160, derived from two growing seasons, 20 genotypes, and four replicates. Levene’s test confirmed the homogeneity of variances among the samples. Consequently, a combined two-way analysis of variance (ANOVA) was performed across both years using the general linear model (GLM) procedure to assess the effects of water regimes (WR), genotypes (G), and their interaction (G × 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 conducted using the Morpheus tool (https://software.broadinstitute.org/morpheus/; Broad Institute. Morpheus Software. Cambridge, MA, USA).

3.5. Results

3.5.1. *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 (Supplementary Tables S1 and S2).

Under DS conditions, the average GY was 3,023 kg ha^{-1}, ranging from 2,148 to 4,071 kg ha^{-1}. The genotype 464 achieved the highest yield, while Blanco Español exhibited the lowest value. Within the DS regime, differences were found 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 3,890 kg ha^{-1}, a 19.3% gain compared to DS and ranged between 3,223 and 4,379 kg ha^{-1}. The genotype 483 displayed the highest yield, while 452 recorded the lowest; both were significantly different ($p < 0.05$). 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}. The 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 2,136 grains m^{-2}, ranging from 1,586 to 2,657 grains m^{-2}. The 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 (1,586, 1,624, and 1,611 grains m^{-2}, respectively).

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 no significant 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 ($p < 0.05$).

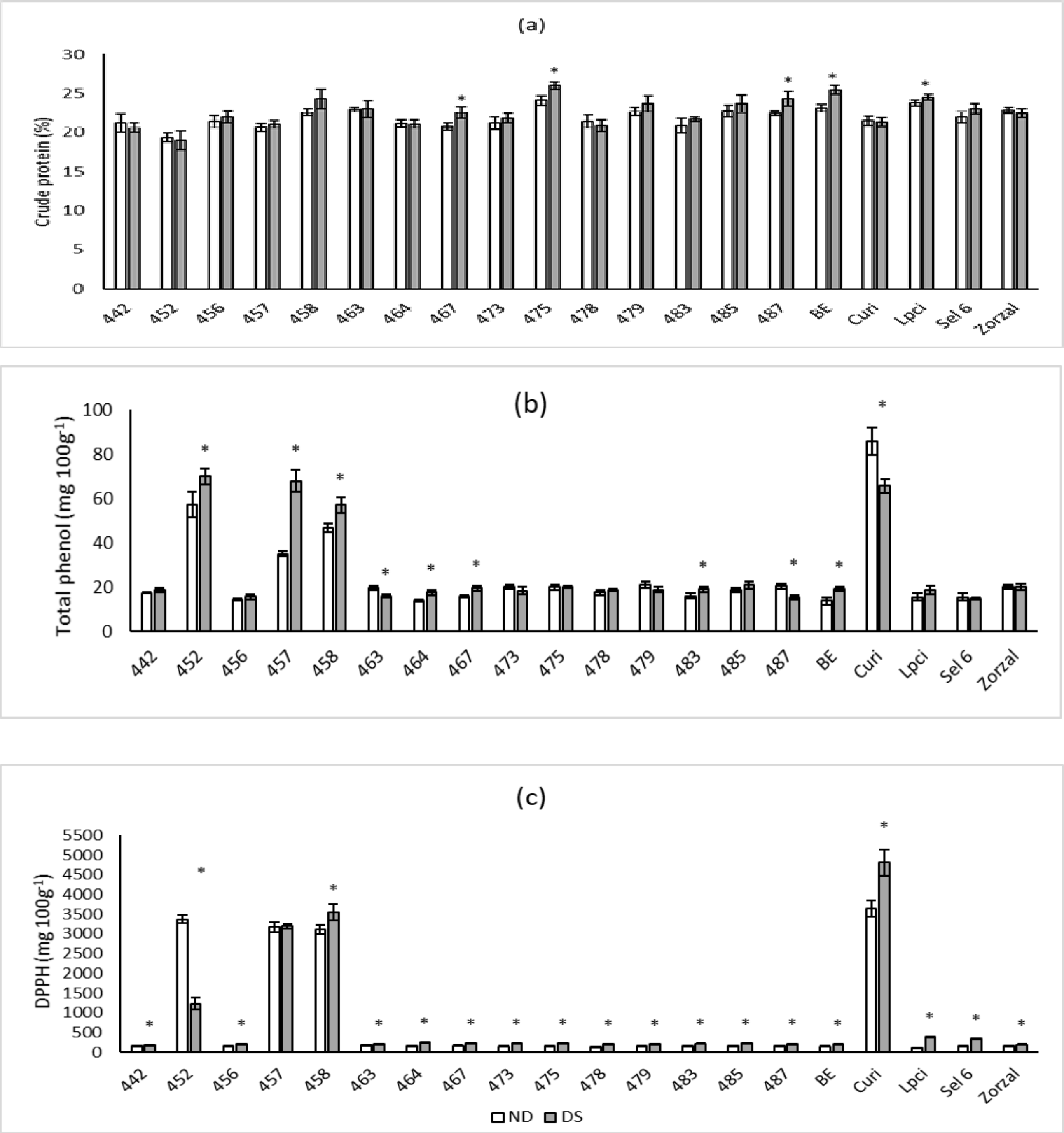
3.5.2. C*rude protein, total phenolics, and antioxidant capacity*

Stress moderately affected the protein content; only a few genotypes exhibited statistically significant differences between water regimes (Figure 1a). Genotypes 467, 475, 487, Blanco Español, 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 variety 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}. The genotype 458 exhibited a statistically 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 the accumulation of phenolic compounds 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 µmol TE g^{-1}), followed by genotypes 452 and 457 (3,340.71 and 3,269.73 µmol TE g^{-1}, respectively), which are statistically different from all other genotypes. No significant differences were observed among the remaining genotypes. In DS treatment, Curi again exhibited the highest antioxidant activity (4,825.46 µmol TE g^{-1}) ($p < 0.05$), followed by 458 (3,536.22 µmol TE g^{-1}), 457, and 452. Most genotypes remained in the same statistical group with values below 400 µmol 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 test indicates 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 such as Curi and 458 consistently exhibited superior antioxidant power under both conditions.

Figure 1. Nutritional and functional quality traits evaluated in twenty bean genotypes during two seasons under no stress (ND) and terminal drought stress (DS). (a) Crude Protein Content (PC), (b) Total Phenolic Content (PCT), and (c) Antioxidant Capacity (DPPH).



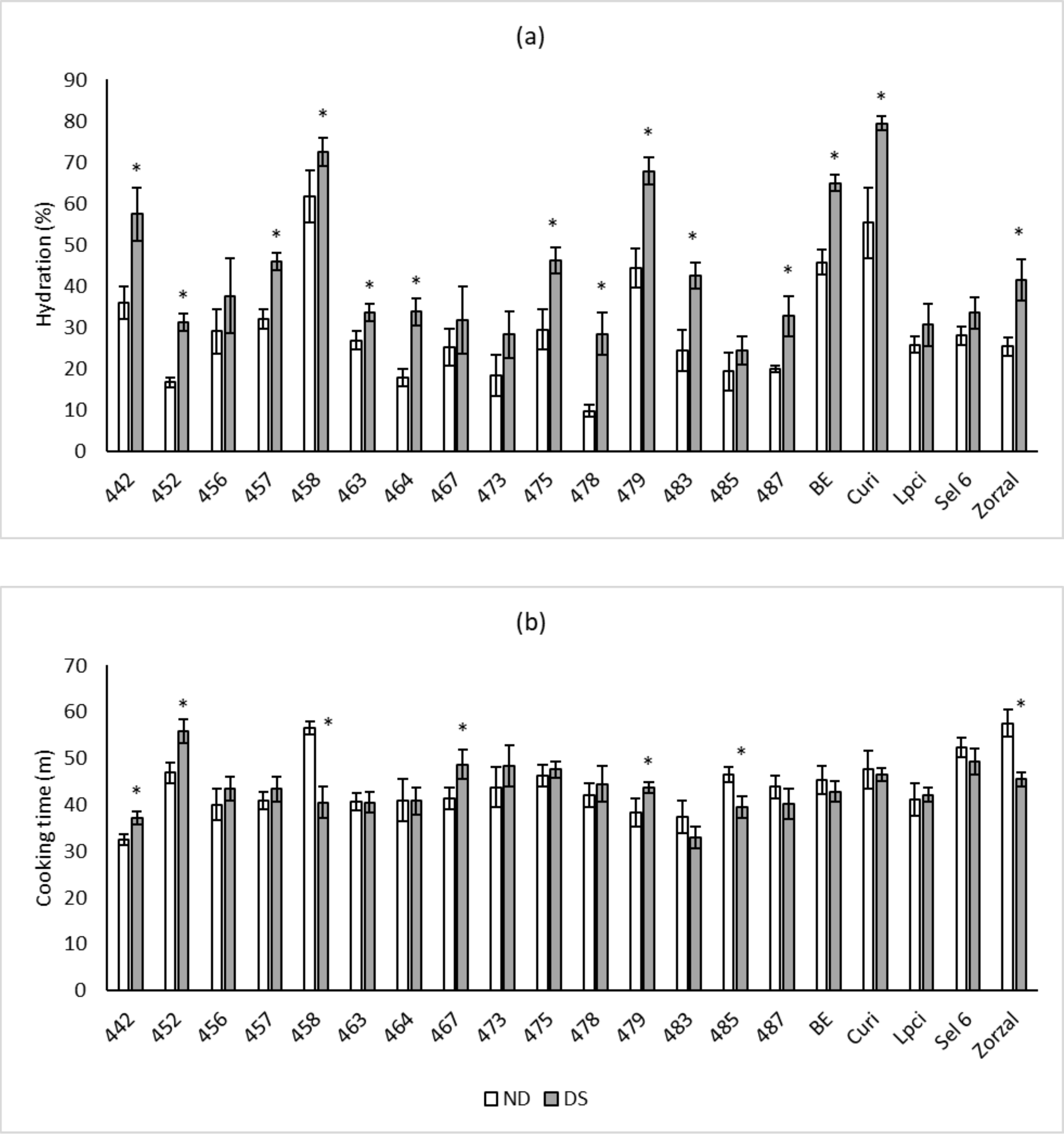
Error bars represent the standard error of the mean. Means followed by asterisks indicate significant differences between ND and DS for the same genotype, as determined by the independent samples t-test (*p* ≤ 0.05).

3.5.3. *Hydration capacity and cooking time*

Significant differences ($p < 0.05$) in hydration capacity 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 cooking time between irrigation regimes revealed genotype-dependent responses in several genotypes under DS and ND (Figure 2b). Significant increases in cooking time under DS were observed in genotypes 442, 452, 467, and 479 ($p < 0.05$); for instance, CT in genotype 452, its cooking time increased from 46.88 minutes under normal irrigation to 55.83 minutes 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 cooking time under DS. Similarly, the Zorzal genotype decreased its cooking time from 57.58 minutes in ND to 45.46 minutes under DS conditions.

Figure 2. Technological quality traits evaluated in twenty bean genotypes during two seasons under no stress (ND) and terminal drought stress (DS). (a) Hydration Capacity (HC) and (b) Cooking Time (CT)

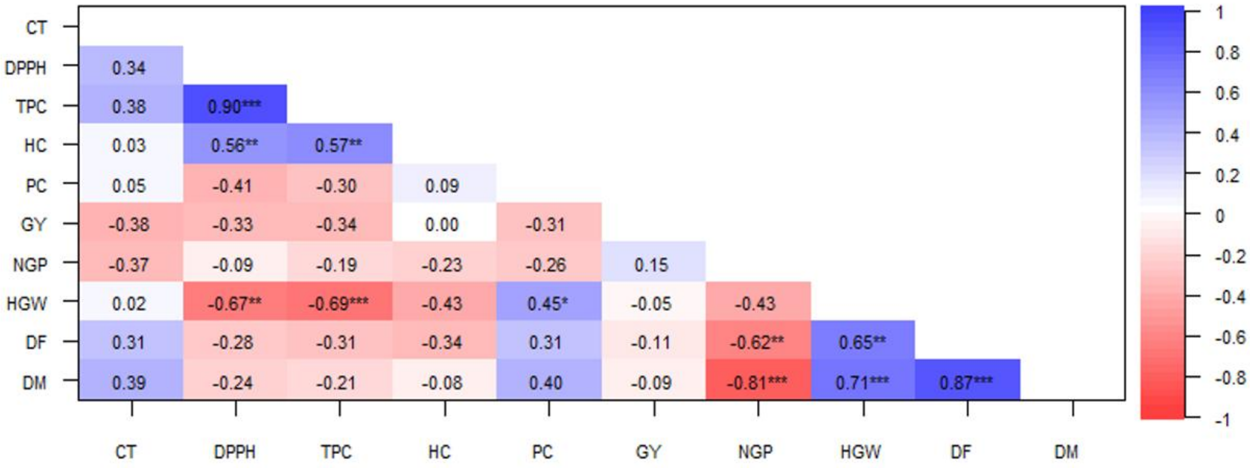


Error bars represent the standard error of the mean. Means followed by asterisks indicate significant differences between ND and DS for the same genotype, as determined by the independent samples t-test (*p* ≤ 0.05).

3.5.4. *Correlation analysis*

The correlations among the traits were consistent under both water conditions (Figures 3 and 4). The TPC and antioxidant capacity, measured by DPPH, showed strong and positive correlations, with coefficients of 0.90 and 0.87 for ND and DS, respectively. Similarly, HC was positively and significantly correlated with both DPPH and TPC, although the correlation with TPC was only significant under non-stress conditions. Additionally, a positive and significant association was observed between HGW and PC under both irrigation regimes. Conversely, HGW showed a significant negative correlation with both TPC and DPPH in both ND and DS conditions. Under water deficit, further negative and significant correlations were found between GY and HC, as well as between GY and PC.

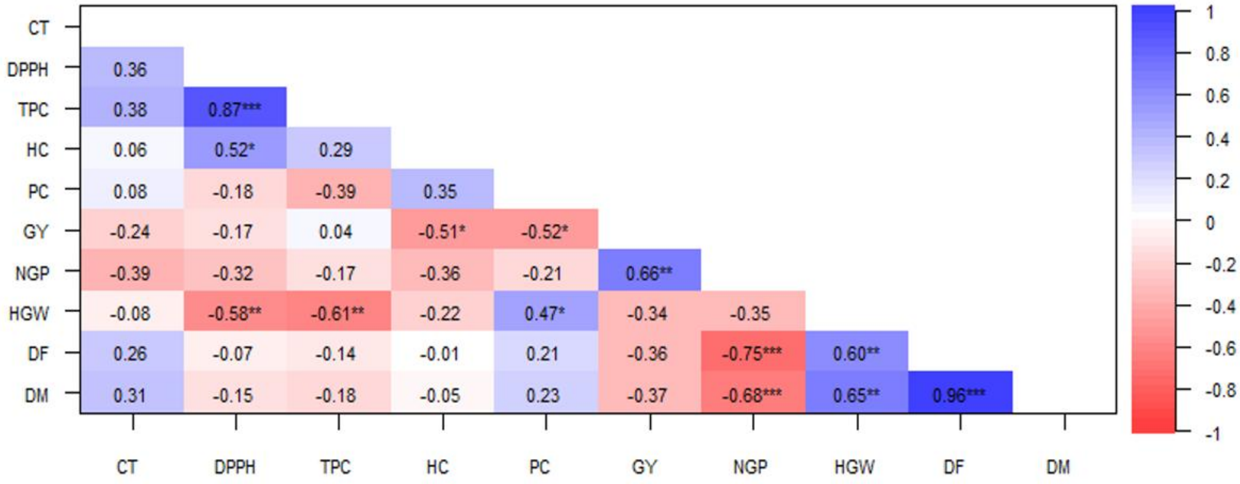
Figure 3. Pearson correlation analysis among traits evaluated in twenty bean genotypes under No Drought (ND) during two seasons.



	CT	DPPH	TPC	HC	PC	GY	NGP	HGW	DF	DM
CT										
DPPH	0.34									
TPC	0.38	0.90***								
HC	0.03	0.56**	0.57**							
PC	0.05	-0.41	-0.30	0.09						
GY	-0.38	-0.33	-0.34	0.00	-0.31					
NGP	-0.37	-0.09	-0.19	-0.23	-0.26	0.15				
HGW	0.02	-0.67**	-0.69***	-0.43	0.45*	-0.05	-0.43			
DF	0.31	-0.28	-0.31	-0.34	0.31	-0.11	-0.62**	0.65**		
DM	0.39	-0.24	-0.21	-0.08	0.40	-0.09	-0.81***	0.71***	0.87***	

Cooking time (min); DPPH, 2,2-diphenyl-1-picrylhydrazyl (mg $100g^{-1}$); total phenolic content (mg $100g^{-1}$); Hydration capacity (%); crude protein content (%); GY, grain yield (kg ha^{-1}); NGP, number of grains per pod (seeds m^{-2}); HGW, hundred-grain weight (g); DF, days to flowering; and 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 *** $p \leq 0.001$.

Figure 4. Pearson correlation analysis among traits evaluated in twenty bean genotypes under Drought Stress (DS) during two seasons.



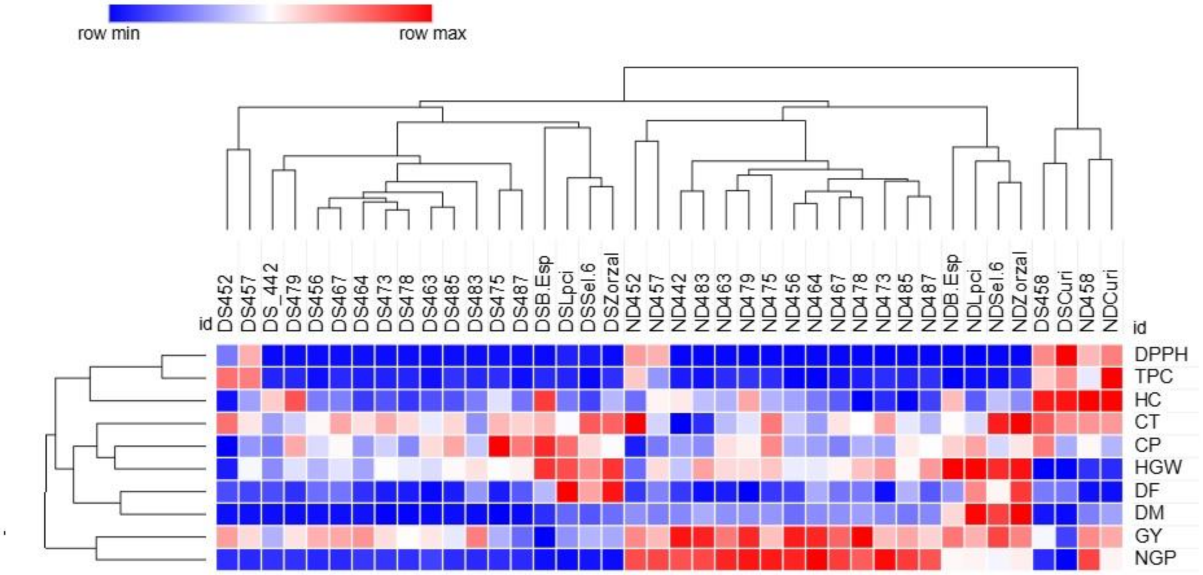
Cooking time (min); DPPH, 2,2-diphenyl-1-picrylhydrazyl (mg $100g^{-1}$); total phenolic content (mg $100g^{-1}$); Hydration capacity (%); crude protein content (%); GY, grain yield (kg ha^{-1}); NGP, number of grains per pod (seeds m^{-2}); HGW, hundred-grain weight (g); DF, days to flowering; and DM, 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 *** $p \leq 0.001$.

3.5.5. *Heatmap and cluster analysis*

All evaluated traits were subjected to heatmap and cluster analyses, which revealed distinct patterns of association among traits, genotypes, and environments (Figure 5). A clear segregation based on water regime emerged, resulting in two main clusters that grouped 18 genotypes according to water availability. The remaining two genotypes, DS458 and Curi, also clustered together based on water regime but formed separate groups from the other genotypes. This segregation of DS458 and Curi was primarily driven by high values of DPPH, TPC, HC, and CT, and low values of HGW, compared to the other genotypes. The separation between environments was primarily driven by reductions in DM, GY, and NPG under water stress conditions. As previously described, clear associations were observed among TPC, DPPH, and HC, as well as between PC and HGW.

Regarding the genotypes, beyond the association between DS458 and Curi, several other noteworthy relationships were identified. Independent of the environment, the genotypes Blanco Español, Lpci, Sel.6, and Zorzal consistently clustered together. High HGW and a longer time to flowering were characteristic of these genotypes. Additionally, the grouping of Blanco Español and Lpci was primarily driven by their high protein content, while Sel.6 and Zorzal were distinguished by their elevated CT. Another notable association was observed between genotypes 452 and 457, which also grouped independently of environmental conditions. These genotypes exhibited relatively high values of TPC and DPPH and achieved above-average yields (Figure 5).

Figure 5. Heat map and cluster analysis of phenological, productive, and quality traits evaluated in twenty bean genotypes under No Drought (ND) and Drought Stress (DS) during two seasons.



CT, cooking time (min); DPPH, 2,2-diphenyl-1-picrylhydrazyl (mg 100g^{-1}); TPC, total phenolic content (mg 100g^{-1}); HC, hydration capacity (%); CP, crude protein content (%); GY, grain yield (kg ha^{-1}); NGP, number of grains per pod (seeds m^{-2}); HGW, hundred-grain weight (g); DF, days to flowering; and DM, days to physiological maturity.

3.6. Discussion

GY is the most important and reliable agronomic trait in common bean; it was significantly affected by water regime, genotype, and their interaction (WR x G) ($p <$ 0.001) (Table 3). Across all genotypes, the mean grain yield under non-stress conditions was 3,891 kg ha^{-1}, which decreased to 3,023 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 DS and ND conditions, indicating drought tolerance (Gonçalves et al., 2019). GY was positively correlated with HGW 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 Polanía 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 NGP *(p* < 0.001) on genotypes; the mean NGP was 2,117 grains m^{-2}, whereas DS reduced this value to 809 grains m^{-2}, a 61% reduction. Furthermore, it was confirmed that interaction (WR x 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 HGW, a trait that reflects seed size, exhibited significant differences among genotypes under both ND and DS conditions and displayed significant genotypic variation under both water regimes *(p* < 0.001), primarily due to the effect of DS (Table 3). On average, HGW 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 HGW within DS. Genotypes such as Blanco Español (48.12 g), Zorzal (47.68 g), Lpci (46.53 g), and Sel.6 (41.53 g) consistently ranked in the top statistical group across both environments (Figure 5; Supplementary Tables 1 and 2), showing resilience in maintaining seed weight. This stability suggests these lines possess favorable physiological traits related to seed filling and assimilating remobilization under terminal drought (Polanía et al., 2016). In contrast, drought-sensitive genotypes, such as 458 (19.12 g) and Curi (19.20 g), were among the lowest performers in both DS and ND conditions. The differential response of HGW across genotypes under 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).

Table 3. Effect of water regime, genotypes, and their interaction on agronomic traits and biochemical compounds evaluated in twenty bean genotypes during two seasons under no stress (ND) and terminal drought stress (DS). p values, *, P≤0.05; ***, P≤0.001. media separation using an independent t-test at P≤0.05

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

The data show the mean of the twenty genotypes studied for each water condition. GY, grain yield (kg ha^{-1}); NGP, number of grains per pod (seeds m^{-2}); HGW, hundred-grain weight (g); DF, days to flowering; DM, days to physiological maturity; CT, cooking time (min); DPPH, 2,2-diphenyl-1-picrylhydrazyl, (mg $100g^{-1}$); TPC, total phenolic content (mg $100g^{-1}$); 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* ≤ 0.05), n=20, ** *p* ≤ 0.01; *** *p* ≤ 0.001).

The HGW was highly influenced by genotype and water regime. The genotype × water regime interaction was not significant (*p* = 0.183), indicating that genotypes responded similarly to water stress, suggesting that seed weight is a more genetically stable trait than seed number, and is less influenced by environmental fluctuations (Mutari et al., 2023). Genotypes 483, 478, and 473 exhibited high HGW and above-average GY under drought conditions, indicating efficient assimilate partitioning to the reproductive sink. These findings align with previous studies that emphasize the role of HGW in yield maintenance under stress (Elias et al., 2021).

A positive correlation was observed between HGW and PC content under both water regimes, the correlation (ND; *r* = 0.454, DS*; r* = 0.465) suggest 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) (Figures 3 and 4).

The HC is critical in dry beans because rapid and extensive water uptake shortens cooking time (Katuuramu et al., 2020). Under DS, the HC increased in most genotypes compared with ND, with an average increase from 29.5% under ND to 43.7% DS. 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 are correspondence genotype-specific ($p < 0.001$), which indicates that seed hydration alone does not entirely predict thermal softening in faster cooking times, depends on structural characteristics specific to each genotype, (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 physicochemical properties of seed coats and cotyledons, 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 (Corrêaa et al., 2010). In contrast, 442 and 475 demonstrated increased HC and moderate CT (45 min) under DS.

The TPC revealed differences among genotypes ($p < 0.001$) (Table 3), as well as for the Genotype × Water regime 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 conditions (Albergaria et al., 2020). Conversely, genotypes 452, 457, and 458 notably increased phenolic accumulation under drought conditions, demonstrating a plastic response (Figure 2). 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 (Kusvuran and Dasgan, 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 (Chávez-Mendoza et al., 2018; Sica et al., 2021; Ganesan and Xu, 2017; Sica et al., 2021) (Figures 4 and 5).

Significant variation in DPPH activity was observed among genotypes ($p < 0.001$), with a highly significant interaction G x WR (Table 3). The average DPPH values ranged from 135.9 to 4,820.3 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 (>3,100 mg 100 g^{-1}), with Curi reaching the highest value. These genotypes maintained or even increased their antioxidant capacity under DS, with Curi reaching 4,820.3 mg 100 g^{-1}, followed by 458 (3,536.2 mg 100 g^{-1}) and 457 (3,232.9 mg 100 g^{-1}). Drought stress has been reported to increase the accumulation of phenolics as part of the plant's adaptive response to oxidative stress, as drought enhances the DPPH activity. Drought-induced oxidative stress stimulates the phenylpropanoid pathway, thereby increasing the biosynthesis of phenolic compounds as a protective response (Desoky et al., 2021; Kuşvuran and Daşgan, 2017; Sica et al., 2021), which results in enhanced DPPH activity. This finding aligns with the results of Chávez-Mendoza et al. (2018), who noted that phenolic-rich bean genotypes often retain strong antioxidant activity even under abiotic stress conditions. 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 (Kusvuran and Dasgan, 2017; Madrera et al., 2021).

The cluster analysis provided a comprehensive visual representation of the relationships among genotypes and traits under DS and ND conditions (Figure 5). 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 total phenolic content 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, and demonstrating a significant response of these genotypes under water deficit. These genotypes also tended to show increased cooking time and lower hydration rates. In contrast, genotypes such as 442, 456, 479, and 483 grouped with lower DPPH and total phenol contents alongside relatively favorable HC and CT, potentially reflecting different physiological adaptation strategies that are less reliant on oxidative stress defense. Genotypes such as Sel 6, Zorzal, Lpci, and Blanco Español formed a separate cluster characterized by high PC and HGW values, indicating 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, such as GY and NGP, are inversely associated with phenolic-related traits, underscoring a physiological trade-off or genotype-specific prioritization of yield versus antioxidant 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 group 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 antioxidant-related processes under stress.

Figure 5 shows that distinct trait clusters emerged, with TPC and DPPH clustering 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 GS, GY, NGP decreased, and a faster DM. However, some genotypes are distinguished by maintaining stable HGW, consistent protein content, and increased phenolic compounds 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 that aim to select genotypes combining drought tolerance with improved grain quality.

3.7. Conclusions

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

Regarding grain quality, terminal drought exhibited varied effects depending on the genotype. Several genotypes showed increased TPC concentrations and enhanced antioxidant capacity (DPPH), regarding grain quality, terminal drought exhibited varied effects depending on the genotype. Genotypes 457 and 458 stood out for their high total phenolic content (TPC) and antioxidant capacity (DPPH), even under water-limited conditions, suggesting an active biochemical response to stress. The PC 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 that are adapted to water scarcity conditions. Overall, drought stress tended to increase hydration capacity in most genotypes, suggesting a stress-induced softening effect. However, its effect on cooking time was genotype-dependent. For instanceinstance genotype 458 showed improved cooking performance under drought, while others like 473 and 475 had relatively stable CT across both conditions.

3.8. Authors contribution

An individual contributor may be assigned to multiple roles, and a given role may be assigned to multiple contributors.

Example: Conceptualization: NZ-KT. Methodology: NZ-ML-KT-CU. Software: AK-MG. Validation: NZ-KT-MG-AK. Formal analysis: AK-MG. Investigation: KT-NZ. Resources: KT-NZ. Data curation: AK-MG-KT. Writing-original draft: KT-NZ. Writing-review and editing: MG-AK-CU-ML. Supervision: KT-NZ Project administration: KT-NZ Funding acquisition: KT-NZ. All co-authors reviewed the final version and approved the manuscript before submission.

3.9. Funding

This research was funded by the Subsecretaría de Agricultura, Gobierno de Chile, Programa de Fitomejoramiento del Fréjol (500155-70) and the University of Concepción, Chile, VRID #2022000635INT.

4.0. Conflict of interest

Just include this item if consider pertinent.

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Supplementary Materials

Table S1. Agronomic, productive, and quality traits evaluated in 20 common bean genotypes under No Drought (ND) during two seasons at the Santa Rosa Experimental Field, INIA-Quilamapu, Chillán, Chile, during the seasons 2021/2022 and 2022/2023.

Genotype	GY ($kg\ ha^{-1}$)	NGP ($seeds\ m^{-2}$);	HGW (g)	DF	DM	Cooking time (min)	DPPH (mg/100g)	Total phenolic content (mg/100g)	Hydration (%)	Crude protein (%)
442	4188,817 abcd	2149,356 b	31,248 h	47,556 bcde	87,474 cd	31,094 f	158,651 d	17,764 e	47,179 bc	20,727 cdef
452	3223,817 e	2212,138 b	25,448 i	46,306 de	87,474 cd	53,844 a	3340,713 b	61,209 b	29,146 cde	19,180 f
456	3502,254 abcde	2358,988 ab	33,515 gh	46,994 cde	87,160 d	36,376 def	179,799 d	14,380 e	30,263 cde	20,747 cdef
457	3430,000 bcde	2205,764 b	36,850 def	48,500 bcd	88,000 cd	39,500 cdef	3269,735 b	34,547 d	42,579 bc	20,646 def
458	3708,192 abcde	2279,932 b	21,848 j	45,806 de	87,974 cd	46,344 abcd	3128,022 c	46,962 c	72,477 a	22,187 abcde
463	3620,754 abcde	2226,356 b	37,235 def	46,994 cde	88,560 cd	39,176 cdef	182,869 d	21,835 e	35,890 bcd	22,351 abcd
464	4328,874 ab	2657,382 a	34,008 fgh	47,126 cde	88,049 cd	40,997 bcdef	178,513 d	12,437 e	28,729 cde	20,868 bcdef
467	3922,751 abcde	2146,372 b	35,621 defg	48,687 bcd	87,725 cd	42,627 bcde	176,983 d	16,131 e	19,873 de	20,958 bcdef
473	3526,254 abcde	2333,123 ab	41,995 b	46,194 de	88,360 cd	50,176 abc	142,610 d	21,304 e	20,345 de	20,745 cdef
475	3345,417 cde	2395,238 ab	38,467 cde	46,667 de	88,667 cd	46,333 abcd	162,143 d	19,499 e	36,009 bcd	24,104 a
478	4372,446 a	2171,443 b	38,641 cd	46,955 cde	89,821 c	45,325 abcde	141,102 d	18,551 e	16,072 e	21,529 bcdef
479	4192,083 abcd	2343,191 ab	37,233 def	45,833 de	88,333 cd	39,333 cdef	156,812 d	20,386 e	52,036 b	22,671 abcd
483	4262,425 abc	2345,689 ab	41,120 bc	44,907 e	89,900 c	34,462 ef	183,039 d	17,097 e	29,276 cde	19,533 ef
485	3236,667 e	2236,842 b	35,350 efg	49,000 bcd	87,667 cd	41,167 bcdef	165,811 d	19,706 e	18,168 de	22,750 abc
487	3318,754 de	2221,143 b	41,875 b	47,794 bcde	87,360 cd	41,976 bcdef	158,113 d	23,519 e	23,176 de	22,096 abcde
BE	3674,583 abcde	1610,860 c	50,817 a	48,833 bcd	95,500 b	44,500 abcde	146,576 d	14,229 e	51,049 b	23,127 ab
Curi	3482,567 abcde	1585,571 c	22,323 j	46,056 de	89,474 cd	49,344 abc	3632,917 a	84,062 a	69,737 a	20,800 cdef
Lpci	3247,946 e	1623,974 c	49,961 a	50,755 ab	104,421 a	41,925 bcdef	133,794 d	15,115 e	23,480 de	23,884 a
Sel.6	3902,511 abcde	1620,151 c	48,363 a	50,236 abc	104,399 a	51,441 ab	180,679 d	18,060 e	34,525bcde	21,260 bcdef
Zorzal	3869,254 abcde	1650,517 c	49,435 a	52,994 a	104,760 a	51,976 ab	168,284 d	22,182 e	33,053 cde	22,404 abcd

Means followed by different letters were significantly different ($p \leq 0.05$) by the post hoc Duncan test ($p \leq 0.05$). GY, grain yield ($kg\ ha^{-1}$); NGP, number of grains per pod ($seeds\ m^{-2}$); HGW, hundred-grain weight (g); DF, days to flowering; and DM, days to physiological maturity; Cooking time (min); DPPH, 2,2-diphenyl-1-picrylhydrazyl ($mg\ 100\ g^{-1}$); total phenolic content ($mg\ 100\ g^{-1}$); Hydration capacity (%); crude protein content (%).

Table S2. Agronomic, productive, and quality traits evaluated in 20 common bean genotypes under Drought Stress (DS) during two seasons at the Santa Rosa Experimental Field, INIA-Quilamapu, Chillán, Chile, during the seasons 2021/2022 and 2022/2023.

Genotype	GY (kg ha^{-1})	NGP (seeds m^{-2})	HGW (g)	DF	DM	Cooking time (min)	DPPH (mg/100g)	Total phenolic content (mg/100g)	Hydration (%)	Crude protein (%)
442	2953.33 abcd	855.55 b	31.267 h	47.16 bcde	83.167 cd	38.83 f	185.86 d	19.26 e	47.44 bc	20.61 cdef
452	3650.16 e	820.66 b	20.491 i	46.55 de	82.994 cd	47.00 a	1189.21 b	64.69 b	20.36 cde	19.25 f
456	3653.33 abcde	787.17 ab	30.330 gh	45.96 cde	82.991 d	40.23 def	211.56 d	15.86 e	37.39 cde	22.37 cdef
457	3443.33 bcde	857.14 b	33.800 def	47.16 bcd	83.333 cd	45.00 cdef	3232.95 b	71.47 d	32.46 bc	21.05 def
458	3065.00 abcde	823.81 b	19.117 j	45.33 de	83.500 cd	51.16 abcd	3536.22 c	57.94 c	67.53 a	24.29 abcde
463	3166.85 abcde	894.67 b	33.198 def	44.43 cde	82.788 cd	38.41 cdef	228.21 d	17.28 e	24.83 bcd	23.79 abcd
464	4037.91 ab	847.97 a	29.286 fgh	46.05 cde	83.507 cd	47.74 bcdef	254.06 d	17.62 e	21.45 cde	21.24 bcdef
467	3491.66 abcde	809.23 b	32.791 defg	47.35 bcd	82.994 cd	46.40 bcde	235.72 d	17.48 e	35.12 de	22.22 bcdef
473	3574.16 abcde	857.14 ab	34.783 b	46.83 de	82.667 cd	47.66 abc	226.98 d	16.66 e	23.00 de	21.83 cdef
475	2775.83 cde	825.39 ab	34.683 cde	45.83 de	82.667 cd	44.50 abcd	237.42 d	19.80 e	40.04 bcd	25.97 a
478	3600.99 a	843.58 b	33.999 cd	46.67 cde	82.815 c	44.96 abcde	216.16 d	19.07 e	25.56 e	20.95 bcdef
479	3379.66 abcd	856.85 ab	31.951 def	46.35 de	82.794 cd	38.60 cdef	205.27 d	18.12 e	59.52 b	23.08 abcd
483	3804.42 abc	852.73 ab	34.082 bc	47.84 e	83.041 c	35.89 ef	233.38 d	18.46 e	30.83 cde	21.79 ef
485	3093.99 e	799.77 b	35.339 efg	45.67 bcd	83.015 cd	41.96 bcdef	229.93 d	22.73 e	29.37 de	24.21 abc
487	2558.75 de	850.79 b	36.433 b	48.00 bcde	83.000 cd	45.33 bcdef	219.50 d	14.63 e	29.09 de	24.31 abcde
BE	2056.39 abcde	731.20 c	48.119 a	49.47 bcd	83.815 b	44.76 abcde	200.94 d	19.20 e	64.35 b	26.08 ab
Curi	2181.39 abcde	674.06 c	19.199 j	47.47 de	83.015 cd	46.96 abc	4825.45 a	64.73 a	60.51 a	21.62 cdef
Lpci	2395.63 e	714.56 c	46.526 a	55.40 ab	87.231 a	42.29 bcdef	389.96 d	18.35 e	29.18 de	24.31 a
Sel.6	2994.66 abcde	733.04 c	41.531 a	51.55 abc	86.394 a	48.20 ab	375.86 d	14.25 e	22.65 bcde	22.55 bcdef
Zorzal	2483.33 abcde	720.63 c	47.683 a	54.50 a	87.500 a	49.16 ab	210.59 d	19.77 e	34.81 cde	22.44 abcd

Means followed by different letters were significantly different (*p* ≤ 0.05) by the post hoc Duncan test (*p* ≤ 0.05). GY, grain yield (kg ha−1); NGP, number of grains per pod (seeds m−2); HGW, hundred-grain weight (g); DF, days to flowering; and DM, days to physiological maturity; Cooking time (min); DPPH, 2,2-diphenyl-1-picrylhydrazyl (mg 100 g-1); total phenolic content (mg 100 g-1); Hydration capacity (%); crude protein content (%).

IV. CONCLUSIONES GENERALES

El estrés hídrico redujo significativamente el rendimiento, el número de granos y el índice de cosecha, evidenciando la sensibilidad del cultivo a la falta de agua durante la etapa reproductiva. No obstante, algunos genotipos mostraron estabilidad productiva y tolerancia al estrés, destacándose las líneas genéticas 452, 473 y 483 para su incorporación al programa nacional de mejoramiento genético de frejol.

Desde el punto de vista fisiológico, se identificaron genotipos que mantuvieron una alta eficiencia fotosintética y mecanismos fotoprotectores bajo estrés, lo que refleja adaptaciones clave frente a la sequía.

A nivel de calidad nutricional, la mayoría de los genotipos conservó su contenido proteico, mientras que varios aumentaron su concentración de compuestos fenólicos y capacidad antioxidante, lo que sugiere una respuesta bioquímica ventajosa frente al déficit hídrico.

En cuanto a los atributos de calidad nutricional y funcional, se observó un aumento en la capacidad de hidratación en DS y una respuesta variable en el tiempo de cocción, con algunos genotipos combinando buena calidad nutricional y tiempos de cocción reducidos.

Los resultados obtenidos resaltan la importancia de integrar múltiples dimensiones como productividad, fisiología, nutrición y cocción en los programas de mejoramiento del frejol, con el fin de seleccionar genotipos resilientes y de alto valor para enfrentar los desafíos del cambio climático y las demandas alimentarias actuales.