

Evaluation of Productive Performances of Common Bean (*Phaseolus Vulgaris* L.) Genotypes under Drought Stress Conditions at ARDS Turda

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Abstract. Common bean (*Phaseolus vulgaris* L.) is a key legume crop, serving as an essential source of plant-based protein worldwide. In the context of climate change and the increasing frequency of drought events, developing and selecting drought-tolerant cultivars is a major priority in agricultural research. This study aims to identify valuable genotypes of common bean (*Phaseolus vulgaris* L.) with high productive potential and drought resistance, for their integration into breeding programs. The research was conducted at Agricultural Research and Development Station Turda during the 2024 agricultural year, which was characterized by high temperatures and significant water deficit. The field experiment evaluated 50 common bean genotypes, revealing significant variability in yield and yield parameters. Grain yields ranged widely from 690 kg/ha to 2682 kg/ha, demonstrating considerable genetic diversity in productivity potential under the given environmental conditions. Notably, 14 genotypes exceeded 2000 kg/ha, identifying them as promising candidates for breeding programs focused on improving yield. The integration of yield data with drought tolerance scores suggests that certain genotypes combine both high productivity and tolerance to drought conditions, making them valuable genetic resources. These findings support the selection of high-performing genotypes for future breeding efforts.

Keywords: adaptability, genotypes, common bean, yield, drought

INTRODUCTION

The common bean (*Phaseolus vulgaris* L.) is one of the most significant legume crops globally, cultivated due to its rich content of protein, dietary fiber, and complex carbohydrates. Species within the *Phaseolus* genus are remarkably diverse, being grown using various cultivation practices, across a wide range of environments and altitudes—from sea level up to 3,000 meters. The extensive variability in plant architecture and growth patterns places common beans among the most versatile and widely adapted crops in global agricultural systems (Broughton, 2003), surpassing other food legumes such as peas and chickpeas in both cultivation area and consumption (Shi, 2025). Its nutritional composition is remarkable, being rich in proteins, dietary fiber, vitamins, minerals, and antioxidants essential for human health (Sinkovič, 2024). When combined with cereals, beans provide a complete source of protein and essential micro- and macronutrients, making them a key component in combating malnutrition, especially in developing countries (Jain, 2016).

On the other hand, introduced into crop rotation, due to its biological nitrogen fixation and effects on the soil, as well as in weed control, it plays a key role in the diversification and sustainable intensification of agriculture, especially due to climate change (Bitocchi, 2017).

It is also cultivated all over the world since it adapts to different cultivation technologies, but also environmental conditions (Sinkovič, 2024). Beans arrived in Europe from the American continent in the 16th century, later spreading across the old continent due to their adaptation to different climatic and geographical conditions (Losa, 2025).

Local varieties, adapted to diverse climates, hold vital genetic traits (genetic diversity) for future food security, but are disappearing due to modern high-yield crops; thus, we must identify and conserve these endangered resources to maintain adaptability against climate change and ensure resilient agriculture (Losa, 2025; Šajgalík, 2019). And the domestication of the common bean led to the development of two distinct genetic bases, namely Mesoamerican and Andean (Sinkovič, 2024).

Genetic diversity between different populations belonging to the same genus resulted from the evolution of crops over time, due to different climatic conditions and agricultural practices (Sinkovič, 2019). In the more than five centuries since its introduction to Europe, specific variants of the common bean have been created. This development has been due to its adaptation to different soil types, climatic conditions, new pathogens and pests, subsequent divergent and extensive breeding processes, and new cultivation practices (Šajgalík, 2019).

Environmental conditions at the time of sowing are essential for successful crop development and productivity. Beans can grow in a wide range of climates, but vegetative development and yield are influenced by environmental factors such as temperature, rainfall, and soil type. Low temperatures after sowing affect

germination and emergence of plants, while lack of or excess rainfall can negatively affect yield (Gosgot, 2025). Also, the growth type of varieties, determinate or indeterminate, plays a key role in the adaptation of the crop to various environmental conditions and cultivation technologies (De Ron, 2019).

Biotic and abiotic stresses are among the main factors that cause yield decline in beans. Extreme heat, drought, soil acidity, salinity, and heavy metal toxicity are significant abiotic stresses (Oner, 2025; Tüfekçi, 2025). In addition, environmental factors such as day length and temperature significantly affect flowering period and production (Łabuda, 2012).

At the heart of common bean breeding programs, one of the main objectives is the development of varieties with high yields and superior quality indices (Nadeem, 2021). Exploiting the diversity of plant genetic resources is a very effective strategy for increasing the nutritional quality of varieties, and for this, it is necessary to characterize plant resources. For that it is important to know the evolutionary history of crops that have shaped the current levels and structure of genetic diversity of germplasm (Murube, 2021).

Local varieties of common beans are not only treasures that need to be protected for the future, but also important genetic resources that can be used in bean breeding programs (Celmeli, 2018). Therefore, the success of a breeding program is based on the genetic variability/diversity existing in populations, and the extent to which the desired traits are heritable, and the effectiveness of selection depends on the extent and nature of the phenotypic and genotypic variability present in the different agronomic traits (Assefa, 2025; Kouam, 2023).

Current germplasm collections of common bean display substantial phenotypic diversity; however, this genetic variability is increasingly threatened by genetic erosion, as traditional local varieties are progressively being replaced by modern elite cultivars in many countries (De Ron, 2016).

Due to the significance of the common bean in Romania, A.R.D.S. Turda conducted studies on the behavior of 50 common bean genotypes from the Vegetable Research and Development Station Suceava germplasm collection under drought conditions. The objective of this study is to identify genotypes with high productive capacity under drought conditions, as a foundation for initiating a breeding program targeting drought resistance in common bean adapted to the central region of Romania.

MATERIAL AND METHODS

A total of 50 common bean genotypes were analyzed, coded from BGR1 to BGR42, BGM1-BGM4, BGU1-BGU2, and BGB1 (Table 1).

The experimental study was established on a vertic clay-illuvial phaeozem soil type (RSST, 2012), with a pH ranging between 6.80 and 7.00. In the 0–30 cm soil layer, the humus content varied from 2.14% to 3.12%, while the clay content ranged from 51.8% to 55.5%, classifying the soil as having a clayey texture (Bârdaş, 2024).

The experimental setup followed a single-factor design, arranged linearly without replications, with each variant occupying 1.5 m in length and 50 cm row spacing. Due to limited seed availability, the harvestable area per variant was restricted to 0.75 m², with a plant density of 25 plants/m². The overall experimental area also included a 7 m access path and 1 m protection buffer zone. Main yield components were analyzed using precision equipment (seed counters and analytical balances): plant height (cm), basal pod insertion (cm), pod length (cm), number of pods/plant, number of seeds/pod, seed weight/plant (g), hectoliter mass (kg/hl), thousand seed weight (g), grain yield (kg/ha). The number of plants that determinations were performed were 10 plants for each genotype.

To evaluate the drought response of the tested genotypes, a three-point scoring scale was used, where 1 indicates high drought tolerance, 2 indicates moderate tolerance, and 3 indicates low tolerance. This visual assessment was based on field observations during key growth stages under water-limited conditions (Table 2).

Statistical calculations were performed to support the selection of superior genotypes for future field trials.

As shown in Figure 1, the average monthly temperatures during the April–September period were consistently higher than the multiannual average (65-year mean). April registered an average temperature of 13.3°C, exceeding the long-term average by 3.3°C. The warmest months were July (24°C) and August (23.4°C), with deviations of +4.2°C and +3.9°C, respectively.

All six months of the vegetation period (April–September) recorded positive deviations from the long-term average, ranging between +0.8°C and +4.2°C. These values highlight a warmer than normal growing season, which likely increased evapotranspiration rates and placed greater stress on plants, particularly during the flowering and pod development stages.

Figure 2 shows the total monthly precipitation amounts with the most critical deficit occurring in June, with only 36.2 mm of precipitation compared to the multiannual average of 84.6 mm, a negative deviation of 48.4 mm. Similar deficits were recorded in July (-29 mm) and August (-19.1 mm), further exacerbating drought stress during key developmental phases. Only in September was precipitation relatively abundant (64 mm), exceeding the long-term average by 21.6 mm, which may have affected the final stages of pod maturation and harvesting operations.

The climatic data recorded during the 2024 growing season at Turda reveal a year marked by above-average temperatures and significant precipitation deficits, conditions which are generally unfavorable for common bean cultivation.

Table 1. The biological materials used in the experiment and their origin

No.	Genotype Code	Origin	No.	Genotype Code	Origin
1	BGR1	RO	26	BGR26	RO
2	BGR2	RO	27	BGR27	RO
3	BGR3	RO	28	BGR28	RO
4	BGR4	RO	29	BGR29	RO
5	BGR5	RO	30	BGR30	RO
6	BGR6	RO	31	BGR31	RO
7	BGR7	RO	32	BGR32	RO
8	BGR8	RO	33	BGR33	RO
9	BGR9	RO	34	BGR34	RO
10	BGR10	RO	35	BGR35	RO
11	BGR11	RO	36	BGR36	RO
12	BGR12	RO	37	BGR37	RO
13	BGR13	RO	38	BGR38	RO
14	BGR14	RO	39	BGR39	RO
15	BGR15	RO	40	BGR40	RO
16	BGR16	RO	41	BGR41	RO
17	BGR17	RO	42	BGR42	RO
18	BGR18	RO	43	BGM1	MDA
19	BGR19	RO	44	BGM2	MDA
20	BGR20	RO	45	BGM3	MDA
21	BGR21	RO	46	BGM4	MDA
22	BGR22	RO	47	BGM5	MDA
23	BGR23	RO	48	BGU1	HUN
24	BGR24	RO	49	BGU2	HUN
25	BGR25	RO	50	BGB1	BGR

RO – Romania

MDA – Republic of Moldova

HUN – Hungary

BGR – Bulgaria

Table 2. Drought Tolerance Scoring Scale

Score	Drought Tolerance Level	Description
1	Highly tolerant	Plants maintain good growth and productivity under drought conditions; yield is relatively unaffected
2	Tolerant	Plants with partial pod filling, yield was affected, maintaining a reasonable level of productivity
3	Low tolerance	Plants show strong sensitivity to drought stress, reduced growth, poor pod formation, and yield loss observed

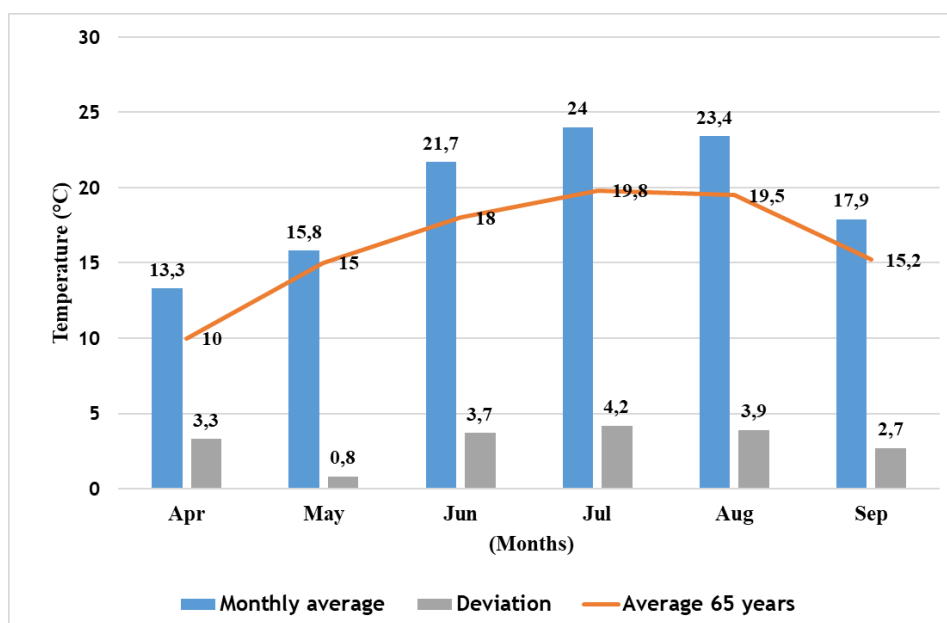


Figure 1. Average temperature (°C) during the common bean vegetation period, A.R.D.S. Turda, 2024

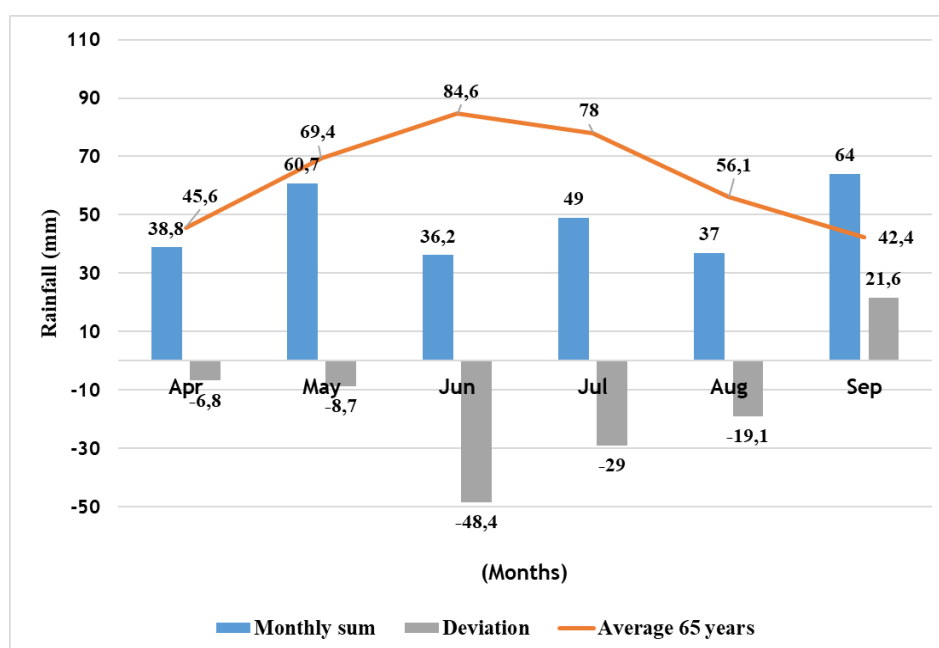


Figure 2. Precipitation (mm) during the common bean vegetation period, A.R.D.S. Turda, 2024

RESULTS AND DISCUSSIONS

The descriptive statistics in Table 3 highlight a wide range of variation among the 50 common bean genotypes evaluated under drought stress conditions at A.R.D.S. Turda in 2024. Plant height recorded the highest variability (CV = 65.8%), with values ranging from 16 cm to 130 cm (growth habits recorded was determinated but also indeterminated), suggesting strong genotypic differences in vegetative growth under drought conditions. Basal pod insertion showed moderate variability (CV = 41.69%), which may reflect adaptations to avoid pod exposure to soil moisture deficits. Yield traits revealed high variability, especially seed weight per plant (CV = 75.21%) and number of pods per plant (CV = 66.13%), underlining the strong impact of

drought stress on productivity. The results reveal substantial phenotypic diversity within the evaluated genotypes, both in terms of morphological traits and yield components. Such variability is crucial for selecting drought-tolerant and high yielding genotypes in the conditions of Central Transilvania.

Table 3. Descriptive statistics of morphological and yield parameters for the analyzed genotypes

	Plant height (cm)	Basal pod insertion (cm)	Pod length (cm)	No. pods/plant	No. seeds/pod	Seed weight/plant (g)
Count	50					
Minim	16	4	3.7	0	0	0
Maxim	130	40	15	10	4	6.7
Mean	43.5	16.7	9.71	3	2	1.7
Standard Deviation	28.63	6.96	2.34	2.29	1.03	1.6
CV %	65.8	41.69	24.14	66.13	43.19	75.21

Thousand Seed Weight (TSW) ranged from 100 to 389 g. The largest group (14 genotypes) fell within the 293–389 g interval, suggesting a significant number of genotypes with large seed size, an important trait for marketability and breeding. Another 13 genotypes had TSW values between 197–244 g, representing medium-sized seeds. The variability was again high (CV% = 34.83%), underlining the diversity of seed size among the tested germplasm (Figure 5).

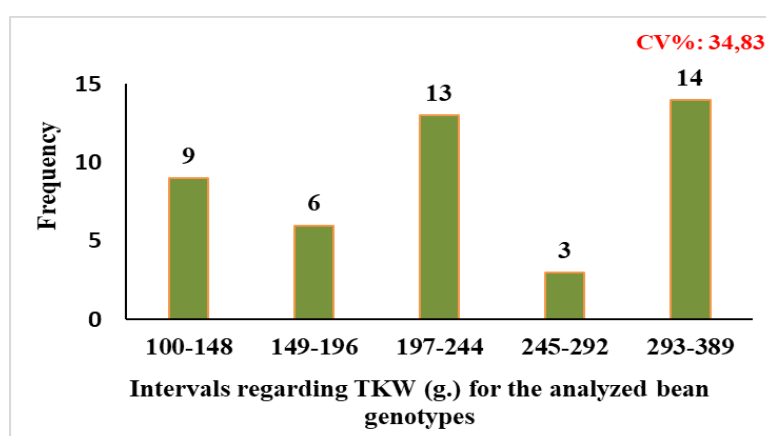


Figure 5. Distribution of Thousand Seed Weight (TSW) (g.) among the analyzed common bean genotypes, Turda 2024

Hectoliter mass (HM) values were distributed between 50 and 194 kg/hl, with 14 genotypes concentrated in the highest interval (147–194 kg/hl), and 13 genotypes in the 99–122 kg/hl class. Only three genotypes showed values between 123–146 kg/hl, suggesting a polarization towards either low or high density. The coefficient of variation for this trait was 34.77%, which, like the other traits, confirms the broad phenotypic variability among the germplasm (Figure 6).

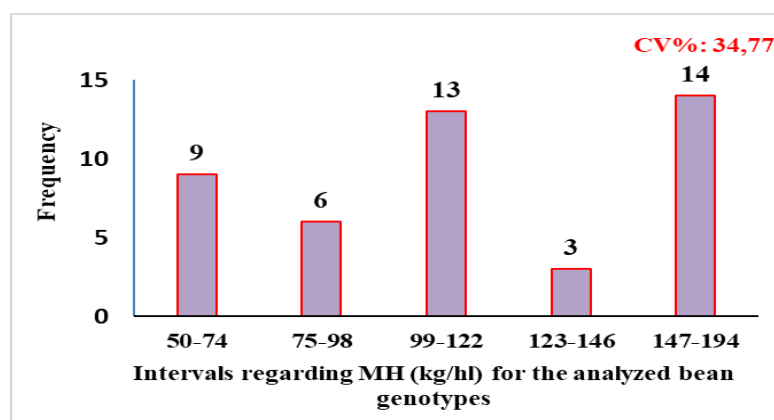


Figure 6. Distribution of Hectoliter Mass (HM) (kg/hl) among the analyzed common bean genotypes, Turda 2024

Grain yield (kg/ha) varied widely among the genotypes, ranging from 690 to 2682 kg/ha. The highest number of genotypes (13) fell within the 1355–1686 kg/ha yield interval, followed by 10 genotypes in the 2019–2350 kg/ha class. Four genotypes achieved yields above 2350 kg/ha, reflecting their high adaptability and performance under drought-prone conditions. The coefficient of variation (CV%) was 34.81%, indicating high variability in yield potential among the tested material.

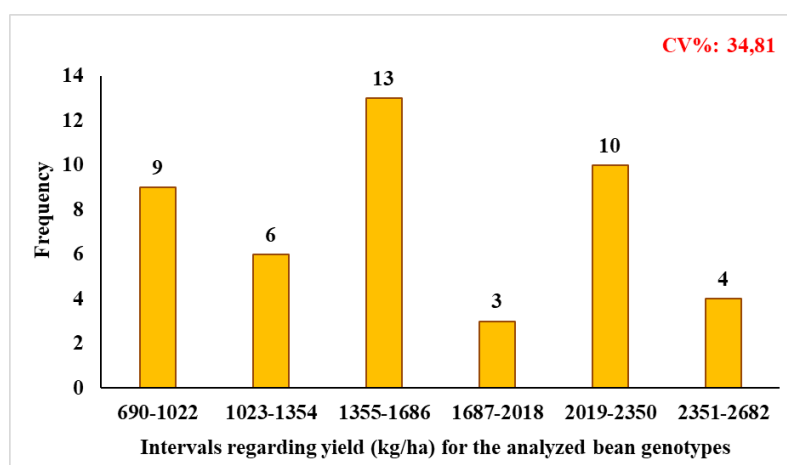


Figure 7. Distribution of yield (kg/ha) among the analyzed common bean genotypes, Turda 2024

Most genotypes demonstrated moderate tolerance to drought stress, with the majority scoring 2 on the tolerance scale. A smaller set of genotypes were classified as highly drought tolerant (score 1), showing strong potential for cultivation under drought conditions. 20% of genotypes received a score of 3, indicating lower drought tolerance and likely reduced performance under dry environments (Figure 8). While highly tolerant genotypes (score 1) showed generally good yields, the highest yields were actually recorded in genotypes classified as moderately tolerant (score 2). This may indicate that some genotypes combine drought tolerance with superior genetic potential for productivity, making them optimal candidates for breeding. On the other hand, low drought tolerance (score 3) is clearly associated with reduced yield potential, especially under the drought conditions recorded during the 2024 growing season. This variability provides valuable genetic resources for breeding programs aiming to improve drought resilience in common bean.

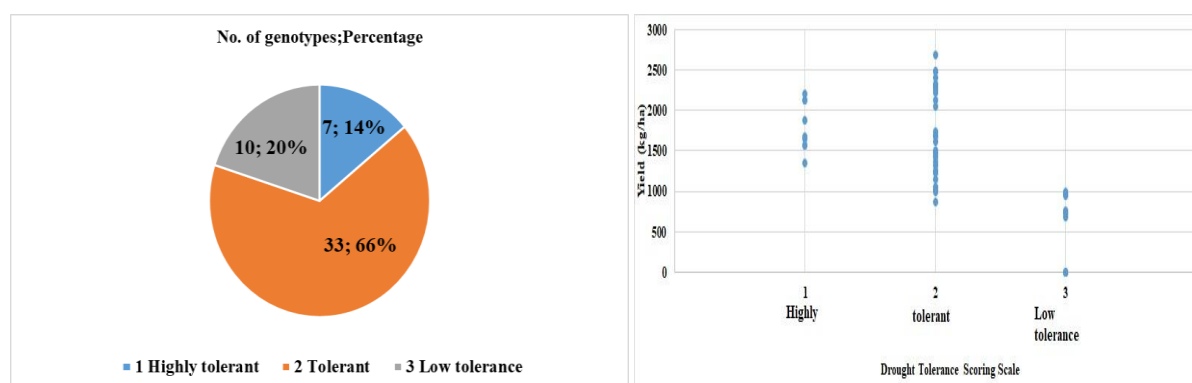


Figure 8. Analysis of drought tolerance scores and grain yield among the 50 common bean genotypes, Turda 2024

CONCLUSIONS

The climatic data for the 2024 growing season showed average temperatures generally above the 65-year mean, especially during June to August, indicating a warmer growing season. Precipitation levels were below the long-term average in most months, particularly in June and July, which created moderate drought stress

conditions for the crops. These climatic factors influenced the growth and productivity of the bean genotypes tested.

The field experiment evaluated 50 common bean genotypes, revealing significant variability in yield and yield parameters. Grain yields ranged widely from 690 kg/ha to 2682 kg/ha, demonstrating considerable genetic diversity in productivity potential under the given environmental conditions. Notably, 14 genotypes exceeded 2000 kg/ha, identifying them as promising candidates for breeding programs focused on improving yield.

The genotypes were classified for drought tolerance using a three-point scale: 1 (highly tolerant), 2 (tolerant), and 3 (low tolerance). The majority of genotypes were rated as tolerant (score 2), with a smaller number demonstrating high drought tolerance (score 1). Only a few genotypes were low tolerant (score 3). This variability highlights the potential for selecting drought-resilient lines within the tested germplasm.

This study highlights the genetic diversity in common beans germoplasm and due to limited seed availability future assessment will determine stronger conclusions.

The integration of yield data with drought tolerance scores suggests that certain genotypes combine both high productivity and resilience to drought conditions, making them valuable genetic resources. These genotypes can serve as parental lines in breeding programs aimed at developing cultivars adapted to the increasingly variable and dry climate conditions predicted in the future.

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REFERENCES

1. Assefa, A., Mekonnen, D., Bantayehu, M., Asres, F., ab. Genetic variability and association of traits in common bean (*Phaseolus vulgaris* L.) genotypes in Sekota, North Eastern Ethiopia. CABI Agriculture and Bioscience, 2025, 0003, doi:10.1079/ab.2025.0003.
2. Bârdaş M., Popa A., Ceclan A., Cheţan F., Cheţan C., Gaga I. Influence of herbicides in winter wheat crop at Agricultural Research and Development Station Turda. Life Science and Sustainable Development, 2024, Vol. 5, No. 2:145-152.
3. Bitocchi Elena, Rau, D., Bellucci Elisa, Rodriguez Monica, Murgia Maria L., Gioia Tania, Santo Debora, Nanni Laura, Attene Giovanna, Papa R. Beans (*Phaseolus* spp.) as a Model for Understanding Crop Evolution. Frontiers in Plant Science, 2017, volume 8, DOI:10.3389/fpls.2017.00722.
4. Broughton W. J., Hernandez G., Blair M. W., Beebe S. E., Gepts P., Vanderleyden J. - Beans (*Phaseolus* spp.): model food legumes. Plant Soil, 2003, 252:55-128.
5. Celmeli, T., Sari, H., Canci, H., Sari, D., Adak, A., Eker, T., Toker, C. The Nutritional Content of Common Bean (*Phaseolus vulgaris* L.) Landraces in Comparison to Modern Varieties. Agronomy, 2018, 8, 166, doi.org/10.3390/agronomy8090166.
6. De Ron, A. M., Kalavacharla, V. K., Casquero, P. A., Gutiérrez, S., Lorenzana, A., Villanueva, A. B., Rosa, L. De Genomic Designing of Climate-Smart Pulse Crops. Springer International Publishing: Berlin/Heidelberg, Germany, 2019, ISBN 9783319969329.
7. De Ron A. M., González A. M., Rodiño A. P., Santalla M., Godoy L., Papa R.. History of the common bean crop: its evolution beyond its areas of origin and domestication. Arbor, 2016, 192 (779): a317.
8. Gosgot Angeles, W., Banda Martinez, D., Barrera Gurbillón, M. Á., Espinoza Canaza, F. I., Santillan Gomez, H., Mori Servan, D. C., Yalta Chappa, M., Huanes Mariños, M. A., Gamarra-Torres, O. A., Oliva-Cruz, M. Productivity and Morphological Adaptation of *Phaseolus vulgaris* L. in Agrivoltaic Systems with Different Photovoltaic Technologies: A Case Study in Chachapoyas, Amazonas, Peru. Agronomy, 2025, 15, 529, doi.org/10.3390/agronomy15030529.
9. Jain, S., Chittem, K., Brueggeman, R., Osorno, J. M., Richards, J., Nelson, B. D. Jr. Comparative Transcriptome Analysis of Resistant and Susceptible Common Bean Genotypes in Response to Soybean Cyst Nematode Infection. PLoS ONE, 2016, 11(7): e0159338, doi.org/10.1371/journal.pone.0159338.
10. Kouam, E. B., Kamga-Fotso, A. Marc-Aurèle, Anoumaa, M. Exploring agro-morphological profiles of *Phaseolus vulgaris* germplasm shows manifest diversity and opportunities for genetic improvement. Journal of Agriculture and Food Research, 2023, Volume 14, ISSN 2666-1543, doi.org/10.1016/j.jafr.2023.100772.
11. Łabuda, H., Brodaczevska, A. The Influence of Environmental Factors on Flowering of French Bean (*Phaseolus vulgaris* L.). Acta Agrobot., 2012, 60, 153–159.

12. Losa, A., Sala, T., Toppino, L., Fricano, A., Rossi, G., Gippli, V., Landoni, M. Genetic Diversity and Distinctiveness of Common Beans (*Phaseolus vulgaris* L.) Between Landraces and Formal Cultivars Supporting Ex Situ Conservation Policy: The Borlotti Case Study in Northern Italy. *Agronomy*, 2025, 15, 786. doi.org/10.3390/agronomy15040786.
13. Murube, E., Beleggia, R., Pacetti, D., Nartea, A., Frascarelli, G., Lanzavecchia, G., Bellucci, E., Nanni, L., Gioia, T., Marciello, U., et al. Characterization of Nutritional Quality Traits of a Common Bean Germplasm Collection. *Foods*, 2021, 10, 1572, doi.org/10.3390/foods10071572.
14. Nadeem, M. A., Yeken, M. Z., Shahid, M. Q., Habyarimana, E., Yilmaz, H., Alsaleh, A., et al. Common bean as a potential crop for future food security: an overview of past, current and future contributions in genomics, transcriptomics, transgenics and proteomics. *Biotechnol. Equip.*, 2021, 35, 758–786, doi:10.1080/13102818.2021.1920462.
15. Oner, B. M., Aygören, A. S., Kasapoğlu, A. G., et al. Genome-Wide Analysis of *Phaseolus vulgaris* L. miR172 Gene Family Members Under Heavy Metal Stress, PREPRINT (Version 1) available at Research Square, 2025, <https://doi.org/10.21203/rs.3.rs-6189246/v1>.
16. Šajgalík, M., Ondreičková, K., Hauptvogel, P., Mihálik, D., Glasa, M., Kraic, J. Higher Effectiveness of New Common Bean (*Phaseolus vulgaris* L.) Germplasm Acquisition by Collecting Expeditions Associated with Molecular Analyses. *Sustainability*, 2019, 11, 5270, doi.org/10.3390/su11195270.
17. Shi, A., Xiong, H., Michaels, T. E., Chen, S. Genome and GWAS analyses for soybean cyst nematode resistance in USDA world-wide common bean (*Phaseolus vulgaris*) germplasm. *Front. Plant Sci., Sec. Plant Breeding*, 2025, Volume 16, doi.org/10.3389/fpls.2025.1520087.
18. Sinkovič, L., Pipan, B., Sinkovič, E., & Meglič, V. Morphological Seed Characterization of Common (*Phaseolus vulgaris* L.) and Runner (*Phaseolus coccineus* L.) Bean Germplasm: A Slovenian Gene Bank Example *BioMed Research International*, 2019, 1–13, doi:10.1155/2019/6376948.
19. Sinkovič, L., Tavakoli Hasanaklou, H., Neji, M., Plestenjak, E., Dolničar, P., Meglič, V., & Pipan, B. Combining multi-criteria decision analysis with agro-morphological-biochemical-molecular traits of interest for use in breeding in promising common bean breeding lines (*Phaseolus vulgaris* L.). *Cogent Food & Agriculture*, 2024, 11 (1), doi.org/10.1080/23311932.2024.2439551.
20. Tüfekçi, E. D., Tellioglu B., Aygören, A. S., Yaprak, E., İlhan, E. Genome-wide characterization of ascorbate peroxidase (APX) gene family in *Phaseolus vulgaris* L. of response to multiple abiotic stresses. *South African Journal of Botany*, 2025, Volume 177, Pages 429-444, ISSN 0254-6299, doi.org/10.1016/j.sajb.2024.12.030.
21. RSST. Romanian System of Soil Taxonomy; Estfalia: Bucharest, Romania, 2012.