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APPLYING MARVIN SEED ANALYZER FOR PHENOTYPIC CHARACTERIZATION OF COMMON BEAN COLLECTION

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Abstract

The National Crop Genebank of Bulgaria was established in 1984 at the Institute of Plant Genetic Resources in Sadovo (Central South Region). It maintains extensive germplasm collections of local and foreign origin. Landraces constitute a strategic genetic reservoir, requiring systematic characterization and conservation. The study was conducted in the experimental field of the institute including 84 accessions of common bean (Phaseolus vulgaris L.). They were analysed through phenology observations and biometric measurements, using the international descriptors and analysed with MARViN VisionLine seed screening. Biological, morphological, and quality traits with averaged data across two replications were assessed. Statistical analyses were performed with Microsoft Excel and SPSS, applying diverse approaches to reveal trait variability. Seed colour and the used morphometric parameters from the analyzer may prove to be highly informative traits that can be used both for morphological classification and for genetic and breeding purposes. Local populations are the golden gene pool and they should not only be studied but also preserved and open access should be guaranteed. The research was carried out under the project IS-PGR-SADOVO (Contract KP-06-H86/9/09.12.2024 of Bulgarian National Science Fund).

Key words*: genebank, Phaseolus vulgaris, seed traits, data base, statistical analysis.*

INTRODUCTION

The common bean (*Phaseolus vulgaris* L.) is an important protein crop which is cultivated all over the world. In Bulgaria it is one of the valuable and traditional growing pulses. (Stoilova et al., 2014). It occupies a central and almost obligatory place in the local holiday tables. Due to its good taste and healthy qualities, it is mainly used for the preparation of various dishes as a main or additional food product or including it in the diverse diets.

The common bean is an excellent precursor for almost all field crops because it enriches the soil with nitrogen (Ivanova et al., 2019). Legume species are capable of meeting their nitrogen needs through both soil absorption and symbiotic nitrogen fixation, which provides an additional nitrogen source for the plant (Unkovich et al., 2008). In common bean, roughly 60% of nitrogen is obtained from the soil, whereas about 40% is contributed by the symbiotic fixation pathway (Unkovich and Pate, 2000; Peoples et al., 2009).

Different common bean subspecies, such as those with small seeds, tend to germinate and multiply their seed weight more rapidly than those with large seeds, depending on external factors (Laing et al., 1984). However, at lower temperatures (12°C), large-seeded varieties tend to germinate more rapidly than those with small seeds (Austin and Maclean, 1972). This is consistent with the observation that varieties adapted to cooler climates tend to have larger seeds. The seeds themselves can be from 0.5–2 cm long and exhibit remarkable colour variation across varieties, ranging from red, white, purple, grey, brown, black, a mix of colours, etc. (Smith and Rao, 2021). With the development of technology, it is now possible to more precisely assess genetic diversity. The devices designed for colour spectrophotometric and morphometry are equipped with high-resolution cameras that capture different shades of colour space and offer morphometric measurements of plant materials with high precision.

All *Phaseolus* plant genetic resources, ranging from landraces and ancient varieties to heterogeneous populations are essential for advancing breeding programs, supporting scientific research, and ensuring their preservation in genebanks for future use (Stoilova et al., 2024).

Capturing the full diversity of grain legumes and maintaining high-quality, accessible collections of well-characterized genetic resources are essential requisites for the advancement and improvement of the crop. The comprehensive characterization of gene bank accessions is crucial for unlocking their full potential (Brezeanu et al., 2025).

Situated in Sadovo and part of the Agricultural Academy, the Institute of Plant Genetic Resources "Konstantin Malkov" is committed to the collection, documentation, investigation, conservation, and sustainable use of Bulgaria's plant genetic resources. The National Seed Genebank, housed within the Institute, ensures long-term preservation of both local and introduced accessions in line with FAO Standards (2014). The Institute expands its ex-situ collections through targeted expeditions, international germplasm exchange, and the storage of breeding materials (Velcheva et al. 2024). Collecting activities aimed at acquiring local varieties and populations are conducted according to FAO Guidelines (2019). The full range of *Phaseolus* germplasm, encompassing landraces, old varieties, and heterogeneous populations are of significant importance for breeding and research activities and for safeguarding genetic resources through ex-situ genebank conservation (Stoilova et al., 2024).

By applying statistical analyses, the study aims to explore the diversity within a collection of local and introduced common bean (*Phaseolus vulgaris* L.) accessions and to highlight groups that could be valuable for breeding efforts and practical applications.

MATERIALS AND METHODS

The experiment was conducted in the field of IPGR "K. Malkov" (42.1197° N, 24.8997° E) in the town of Sadovo over two consecutive years, 2024 and 2025. In this study 84 accessions with diverse origin are included. Most of them are of Bulgarian (local) origin and four of them are breading varieties (Eliksir, Trackiya, Skitiya and Ustrem) created in Dobroudzha Agricultural Institute in General Toshevo, Dobrich Region (Figure 1).

All the variants were sown in rows 2 m long with an inter-row spacing of 0.7 m. A non-standard method for establishing a field experiment with randomized allocation of the variants was used.

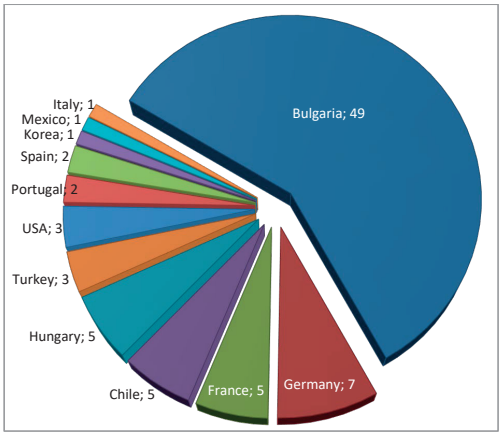

Figure 1. Origin of the accessions included in the study

Key developmental stages of the crop were evaluated and the length of the vegetation period was recorded, based on which the accessions were classified as early, medium-early, and late. The number of days from emergence to mass flowering, the duration of flowering, and the number of days from emergence to bean formation were calculated. A visual characterization is performed for the seed colour. For biometric measurements, a digital scale with an accuracy of 0.01 g was used to determine the mass of 100 seeds and seed mass per plant.

A digital clipper with data transfer cable was used for measure the seed dimensions (length, width, and thickness) measured in millimetres (mm). For the characterization and evaluation of the *Phaseolus vulgaris* L. accessions, the IBPGR (1982) and UPOV (2013) descriptors were used.

In 2025 an additional study was conducted and a morphometric analysis of the seeds was performed using a Marvin Seed Analyzer (MARViTECH GmbH, Germany), designed for precise, non-destructive seed measurements. The device uses a high-resolution camera and specialized software for automatic extraction of geometric and colour parameters. Before analysis, the seeds were arranged in a single layer on the standard measuring plate, ensuring uniform illumination and contrast. All measurements were carried out under constant lighting conditions. The morphometric analysis included the following parameters: seed area converted to square millimetres (mm^2); seed perimeter in millimetres (mm); mean values of the Red, Green, and Blue channels (RGB); I-

Max mean; mean values in the HSL colour space – H (hue), S (saturation), and L (lightness). Variation analysis was applied where variation is considered low if the coefficient does not exceed 10%, medium when it is between 10-20%, and high (significant) when it exceeds 20% (Dimova and Marinkov, 1999).

Experimental data from the Marvin Seed Analyzer and phenotyping were processed through descriptive, correlation, variation, and cluster analyses which revealed both positive and negative relationships among the studied traits.

Correlation between all traits was determined, using the correlation coefficient "r". In the correlation tables, the strength of relationships is indicated as follows: weak dependence – *($0.3 \leq |r| < 0.5$); medium dependence – **($0.5 \leq |r| < 0.7$); strong dependence – ***($|r| \geq 0.7$).

The hierarchical clustering was performed, using Ward's method, which minimizes within-cluster variation by merging the clusters that result in the smallest increase in the total sum of squared errors (Ward, 1963).

All data were processed, using the statistical programs Microsoft Excel - Analysis ToolPak and IBM SPSS Statistics.

RESULTS AND DISCUSSIONS

According to the length of the vegetation period, the samples are classified as early, medium-early, and late (Figure 2).

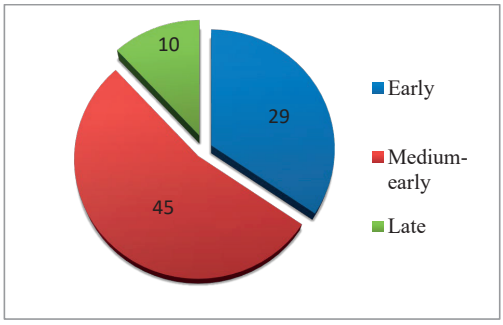

Figure 2. Classification of the accessions according to the number of days to maturity

Phenological data cover four key stages of plant development: length of the vegetation period, mass flowering, bean formation, and flowering duration. Descriptive statistics allow to assess the variability between samples and to determine the average values and ranges characteristic of the studied forms.

According to the vegetation, the mean duration is 77.54 days with a relatively low standard deviation of 5.37 days. The minimum value is 68 days (69886 - Germany; 771423 - Hungary) and the maximum 90 days (69847 - France; 69859 - Hungary; 84201015 - Germany), outlining a range of 22 days. The median (77 days) and the mode (77 days) coincide, which indicates a symmetrical distribution and the absence of extreme deviations. The variation is low, suggesting that the vegetation period is a stable trait with only minor differences among the genotypes.

Table 1. Descriptive statistic for the duration of the vegetation period and the number of days to flowering for 84 common bean accessions

Vegetation period		Mass flowering	
Mean	77.54	Mean	35.14
SE	0.59	SE	0.37
Med	77.00	Med	34.00
Mo	77.00	Mo	33.00
SD	5.37	SD	3.42
S^2	28.83	S^2	11.69
R	22.00	R	15.00
Min.	68.00	Min.	31.00
Max.	90.00	Max.	46.00
CV%	6.93	CV%	9.73
Count	84.00	Count	84.00

The days to mass flowering show that earliest forms enter mass flowering in the 31st (A7E0137 - Devin; C1E0051 - v. Rogozinovo; C4E0004v. Karavelovo; 91201091 - Hungary; 91201120 - Hungary) and latest at the 46 days (91201088 - Spain) after emergence, which corresponds well with the mean value of 35.14 days. The standard deviation is 3.42 days and the CV% = 9.73 falls within the category of low variability. This indicates that the timing of mass flowering is a relatively stable trait. The differences between genotypes are limited and do not lead to substantial divergence in the flowering phase, even though the range within the studied collection reaches 15 days. In most cases, however, due to sharply rising maximum temperatures at the beginning of summer, this two-week interval may be critical for this stage of crop development.

On table 2 the period of bean formation and the duration of flowering are presented. The mean

value for the period from emergence to bean development is 52.63 days, with a standard deviation of 2.79 days, which represents the lowest variability among all phenological traits. The range is 13 days. The median (52.5 days) and the mode (55 days) are close to the mean, suggesting a normal distribution. The earliest accession in this period is C4E0004 - from Karavelovo and the latest 69847 - France. This is the most stable indicator among all phenological traits. The low variability shows that bean formation is highly uniform across genotypes. However, the trait shows low variation and stability.

The phase of seed growth and flowering are most influenced by the agro-climatic conditions of the environment, as plants in these phases of development consume 60% of the water needed for the entire growing season (Ivanova et al., 2019). The year, growing conditions, and genotype are related and directly affect the realization of good yields.

Table 2. Descriptive statistics for the period of bean formation and the duration of flowering for 84 common bean accessions

Bean formation		Duration of flowering	
Mean	52.63	Mean	22.48
SE	0.30	SE	0.42
Med	52.50	Med	23.00
Mo	55.00	Mo	26.00
SD	2.79	SD	3.81
S^2	7.80	S^2	14.49
R	13.00	R	21.00
Min.	46.00	Min.	14.00
Max.	59.00	Max.	35.00
CV%	5.31	CV%	6.93
Count	84.00	Count	84.00

The mean value for flowering duration is 22.48 days with a standard deviation of 3.81 days and a range of 21 days. The mode (26 days) is higher than the median (23 days). However, the range of values is relatively wide with minimum of 14 (69846 - Germany) and maximum 35 days (cultivar - Trakya). The coefficient of variation remains within the limits of low variability. This indicates, that despite the visible differences, the relative variability in relation to the mean is moderate and the trait is more stable than it appears based on absolute values. A similar pattern was observed for the length of the vegetation period.

Differences in vegetation periods are important for breeding evaluation, as they allow the identification of genotypes with shorter or longer flowering duration, as well as forms that transition earlier or later into reproductive development.

The traits determining productivity included in this study are: 100-seed weight; seed weight per plant; seed length, width, thickness, perimeter, and area. The descriptive statistics are presented in several tables.

The first one (Table 3) includes the traits seed weight per plant and 100-seed weight. The mean seed weight per plant is 8.39 g, with a median of 7.81 g. The lowest value is 4.46 g (A8E0458 - Momchilovgrad), while the maximum reaches 17.61 g (69846 - Germany), resulting in a substantial range of 13.15 g. The coefficient of variation is 31.77%, indicating high variability. This shows that seed weight per plant is a highly variable trait within the studied group.

Table 3. Descriptive statistic of the seed mass from plant (SeedMass) and 100 seeds weight (TSW). The traits are measured, using digital scale with precision 0.01g

SeedMass		**TSW**	
Mean	8.39	Mean	27.72
SE	0.29	SE	0.73
Med	7.81	Med	27.09
Mo	5.85	Mo	#N/A
SD	2.67	SD	6.66
S^2	7.10	S^2	44.32
R	13.15	R	30.42
Min.	4.46	Min.	15.12
Max.	17.61	Max.	45.54
CV%	31.77	CV%	24.02
Count	84	Count	84

The mean value of TSW is 27.72 g. The minimum is 15.12 g (91201017 - Portugal) and the maximum reaches 45.54 g (cultivar - Skitya), resulting in a large range of 30.42 g. The standard deviation is 24.02%. This is a key indicator of productivity and technological suitability and the high variation highlights the presence of substantial differences. This confirms that the collection is represented by those with lower and those with higher mass per 100 seeds, from which we can conclude the presence of small-seeded and large-seeded genotypes.

In relation to seed size, the statistical indicators, concerning the biometric traits, especifically seed length, width, and thickness are presented in table 4. The results show average variation for all three traits and a considerable range among the studied samples.

The descriptive statistics indicate that the mean seed length is 11.51 mm, with a median of 11.50 mm, practically identical to the mean. The minimum value is 8.03 mm (B0E0048 - Dimitrovgrad) and the maximum is 14.77 mm (C1E0049 - Mezek), resulting in a range of 6.74 mm. The standard deviation is 1.38 mm and the CV% = 11.96, indicating a transition from low to average variability.

The mean seed width is 6.47 mm, with a median of 6.46 mm, again nearly identical. The minimum value is 4.84 mm (91201151 - France) and the maximum is 8.11 mm (C0E0320 - v. Selcha), giving a range of 3.26 mm. The standard deviation is 0.76 mm, and the CV% = 11.72 which also corresponds to medium variability.

The mean value for seed thickness is 4.80 mm, with a median of 4.78 mm, very close to the mean. The minimum value is 3.78 mm (91201017 - Portugal) and the maximum is 6.21 mm (cultivar - Skitya), resulting in a range of 2.44 mm. The standard deviation is 0.54 mm, and the CV% = 11.16. Notably, this trait has the lowest coefficient of variation among the seed size parameters examined so far.

The moderate variability in all seed dimensions confirms the presence of diversity among the genotypes.

Table 4. Descriptive statistic of the seed length, width, and thickness, using digital clipper with data transfer cable

SeedLength		SeedWidth		SeedThickness	
Mean	11.51	Mean	6.47	Mean	4.80
SE	0.15	SE	0.08	SE	0.06
Med	11.50	Med	6.46	Med	4.78
Mo	11.24	Mo	6.29	Mo	4.68
SD	1.38	SD	0.76	SD	0.54
S^2	1.89	S^2	0.57	S^2	0.29
R	6.74	R	3.26	R	2.44
Min.	8.03	Min.	4.84	Min.	3.78
Max.	14.77	Max.	8.11	Max.	6.21
CV%	11.96	CV%	11.72	CV%	11.16
Count	84	Count	84	Count	84

The descriptive statistics for the morphometric traits seed area and seed perimeter, using Marvin seed analyzer, are presented in Table 5.

The mean seed area is 86.83 mm², with a slightly higher median (90.73 mm²), suggesting a slight shift toward larger values. The minimum area is 17.59 mm² (C4E0002 - Karavelovo) and the maximum reaches 136.52 mm² (91201170 - Mexico), resulting in a very large range of 118.93 mm². The standard deviation is 27.57 mm² and the CV% = 31.75, indicating high variability. Seed area reflects the overall size of the measured seed surface and such high variability is fully expected, given the substantial differences in TSW.

Table 5. Descriptive statistic of the seed perimeter mm (Perimeter) and seed area mm² (Area) morphometry, using Marvin seed analyser

Perimeter		Area	
Mean	45.95	Mean	86.83
SE	0.99	SE	3.01
Med	42.90	Med	90,73
Mo	#N/A	Mo	#N/A
SD	9.03	SD	27.57
S^2	81.56	S^2	760.22
R	41.99	R	118.93
Min.	32.71	Min.	17.59
Max.	74.70	Max.	136.52
CV%	19.66	CV%	31.75
Count	84.00	Count	84

The mean seed perimeter is 45.95 mm, with a median of 42.90 mm. The minimum value is 32.71 mm (91201141 - Germany) and the maximum reaches 74.70 mm (C4E0001 - v. Karavelovo), resulting in a significant range of 41.99 mm. The standard deviation is 9.03 mm and the coefficient of variation (CV% = 19.66) places this trait at the boundary between medium and high variability, according to the applied scale. This indicates that the perimeter is more variable than the linear dimensions (length, width, thickness), yet more stable than the TSW, SeedMass and seed area. This intermediate level of variability may reflect differences in seed shape which are not fully captured by individual linear measurements.

Based on the traits examined so far, the samples were classified into four cluster groups using cluster analysis, according to Ward's method

(Figure 3), which is widely recommended for multivariate quantitative data and is considered one of the most robust agglomerative algorithms (Murtagh and Legendre, 2023).

A table summarizing the variation of the indicators for each cluster, including the mean values and CV%, was prepared (Table 6). The clustering was performed, using all recorded quantitative traits, and the resulting structure represents the overall multivariate relationships among the samples.

Table 6. The mean values and the variation coefficient (CV%) in the brackets of the vegetation periods and the productivity traits for four cluster groups for 84 common bean accessions

Traits	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Veg.	76.19 (3.70%)	85.59 (4.17%)	73.15 (4.21%)	75.87 (5.37%)
M/F	33.48 (3.52%)	38.53 (8.95%)	33.62 (3.75%)	35.74 (11.94%)
B/F	53.29 (3.73%)	54.24 (4.59%)	49.23 (3.23%)	52.48 (5.63%)
D/F	24.45 (14.66%)	22.94 (17.80%)	19.54 (14.11%)	21.13 (13.56%)
WSP	8.33 (32.79%)	10.26 (32.11%)	7.30 (18.53%)	7.70 (25.38%)
TSW	32.26 (20.89%)	27.00 (13.34%)	29.43 (6.19%)	21.15 (19.88%)
S/L	12.32 (11.69%)	11.44 (8.88%)	11.38 (5.47%)	10.55 (11.43%)
S/W	6.64 (8.34%)	6.60 (8.78%)	7.34 (4.51%)	5.64 (8.37%)
S/T	4.92 (6.86%)	4.67 (6.72%)	5.61 (4.87%)	4.28 (7.79%)
Area	83.36 (38.46%)	85.18 (34.03%)	107.25 (11.75%)	81.18 (26.71%)
Per.	50.77 (19.47%)	47.90 (20.39%)	42.11 (3.49%)	40.16 (12.30%)

Cluster 1 group 31 samples with a medium-early vegetation period (76.19 days; CV% = 3.70). The flowering duration is relatively long (24.45 days), showing moderate variability (CV% = 14.66). In terms of productivity, this cluster is characterized by a relatively high seed weight per plant (8.33 g; CV% = 32.79) and the highest values for TSW (32.26 g; CV% = 20.89). These are productive, medium-early forms with high seed weight, making them suitable for use in breeding programs aimed at developing high-yielding common bean cultivars.

Cluster 2 includes 17 forms with the longest vegetation period of 85.59 days (CV% = 4.17), as well as the longest period to flowering of 38.53 days (CV% = 8.95). Regarding seed weight per plant, the mean value (10.26 g) in this cluster is the highest among all clusters, suggesting that this may be attributed to genetic differences and that later-maturing forms tend to exhibit higher seed weight per plant.

Cluster 3 groups 13 genotypes characterized by the earliest mass flowering (33.62 days; CV% = 3.75), the shortest flowering duration (19.54 days; CV% = 14.11), and a vegetation period of 73.15 days. The seed perimeter, measured using the Marvin seed analyzer, has a mean value of 42.11 mm and low variability (CV% = 3.49). This cluster also contains the accessions with the largest seed area (107.25 mm²) (also measured with the Marvin analyzer), with the trait showing moderate variability (CV% = 11.75) and represented by very uniform values of all clusters. This cluster includes the samples with the most stable values across all clusters for the following traits: TSW (CV% = 6.18), seed weight per plant (CV% = 18.53), and seed dimensions (length CV% = 5.47; width CV% = 4.51; thickness CV% = 4.87). This is a cluster with very low internal variability in morphometric traits. Additionally, the short vegetation periods highlight these samples as suitable donors for breeding programs, aimed at developing early-maturing common bean varieties.

Cluster 4 groups 23 samples, including forms with mostly medium-early vegetation period (75.87 days; CV% = 5.36) and the lowest seed perimeter values (40.16 mm; CV% = 12.30). The most stable traits within this cluster are the seed dimensions (length CV% = 11.43; width CV% = 8.37; thickness CV% = 7.79).

These results demonstrate that the morphometric characteristics of the seeds play a primary role in differentiating the genotypes, whereas the phenological traits further refine the separation by capturing differences in the duration of the developmental periods.

The Marvin Seed Analyzer data on RGB, HSL and I-Max colour parameters should be considered. The colour analysis separates the genotypes into four distinguishable groups, using Ward's hierarchical clustering method (Figure 4). The resulting clusters show high internal consistency and a clear distinction between light, medium-dark, mottled, and dark seeds. Table 7 presents the mean values and the coefficient of variation for each cluster.

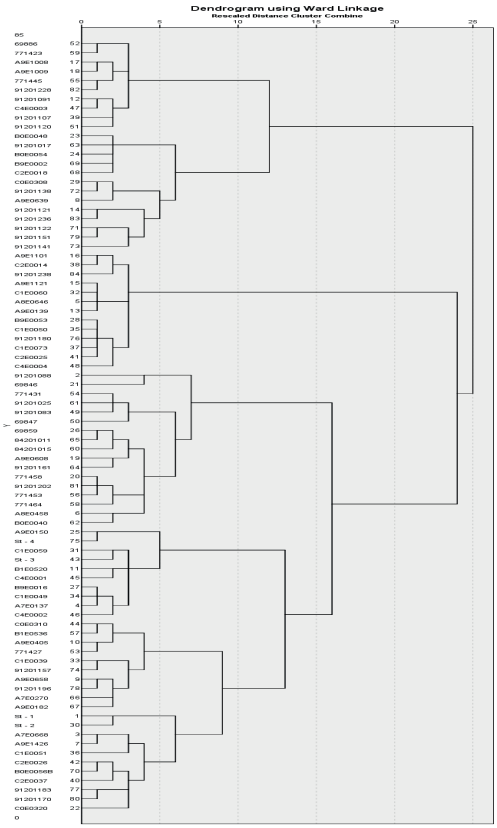

Figure 3. Cluster analysis of the vegetation periods and the productivity traits for 84 common bean accessions

Table 7. The mean values and the variation coefficient (CV%) in the brackets of the I-Max, RBG and HSL colour parameters

Traits	Cluster 1	Cluster 2	Cluster 3	Cluster 4
I-Max	246.11 (1.92%)	226.76 (2.63%)	218.31 (2.36%)	218.87 (3.18%)
Red	229.02 (3.24%)	222.71 (1.25%)	151.40 (19.37%)	72.10 (53.81%)
Green	218.87 (4.78%)	213.89 (1.51%)	110.89 (21.61%)	59.27 (60.94%)
Blue	185.77 (6.71%)	181.93 (3.22%)	84.46 (23.39%)	57.57 (52.75%)
Hue	47.35 (7.81%)	47.77 (4.93%)	29.25 (38.36%)	237.99 (25.17%)
Saturation	0.5798 (10.41%)	0.4475 (9.46%)	0.3633 (16.34%)	0.2118 (75.00%)
Lightness	0.8141 (4.71%)	0.7940 (1.90%)	0.4613 (20.18%)	0.2500 (52.09%)

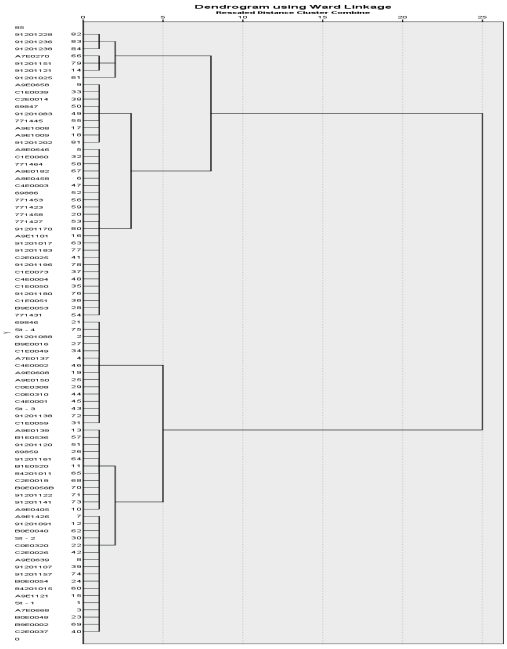

Figure 4. Cluster analisys (Wards linkage) of I-Max, RGB and HSL color parameters

Cluster 1 groups 29 samples. It is characterized by the highest I-Max values (246.11; CV% = 1.92). The RGB components are also high - Red 229.02 (CV% = 3.24), Green 218.87 (CV% = 4.78), and Blue 185.77 (CV% = 6.71). Lightness is high (0.8141; CV% = 4.71), confirming that the seeds in this cluster are the lightest among all groups. The colour types represented in this cluster, based on comparison with the visual assessment of the seeds, include: white seeds (Figure 5 - C2E0026 - Sveta Petka); white seeds with slightly darker shades or the presence of spots (Figure 6 - 91201122 - Germany); and white seeds with a secondary colour concentrated around the hilum (Figure 7 - C2E0018 - Velingrad).

Cluster 2 groups 14 accessions and includes seeds with relatively high brightness, although lower than that observed in Cluster 1. The I-Max value is 226.76 (CV% = 2.63), indicating stable but moderate intensity. The RGB values are high and highly consistent: Red 222.71 (CV% = 1.25), Green 213.89 (CV% = 1.51), and Blue 181.93 (CV% = 3.22). The Hue value is 47.77 (CV% = 4.93), almost identical to that of Cluster 1, suggesting a similar colour tone. Lightness is 0.7940 (CV% = 1.90), indicating light-coloured seeds, though not as bright as those in Cluster 1.



Figure 5. Accession C2E0026 - Sveta Petka



Figure 6. Accession 91201122 – Germany



Figure 7. Accession C2E0018 - Vrelingrad

All samples are characterized by white coloration, but they can be described as: pure white, white with a slightly grayish tint, or white with lower saturation. This cluster represents white seeds with very high colour stability and minimal variability.

Cluster 3 is represented by 33 genotypes and is the most diverse in terms of colour characteristics. It includes the widest range of colors, based on the visual assessment - brown (Figure 8 - A9E1009 - Dragoshinovo), pinto (Figure 9 - C4E0004 - v. Karavelovo), beige (Figure 10 - 771427 - Chile), gray (Figure 11 - C2E0025 - Velingrad), brown-white on half of the seed (Figure 12 - 771445 - France), etc. The high variability of the RGB and Hue parameters confirms that this is the cluster with the greatest internal colour diversity.



Figure 8. Accession A9E1009 – Dragoshinovo



Figure 9. Accession C4E0004 - v. Karavelovo

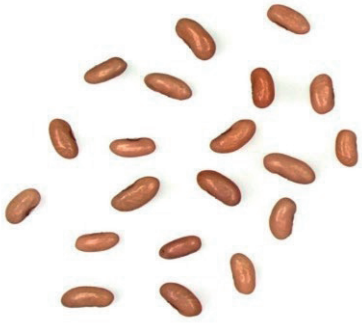

Figure 10. Accession 771427 - Chile

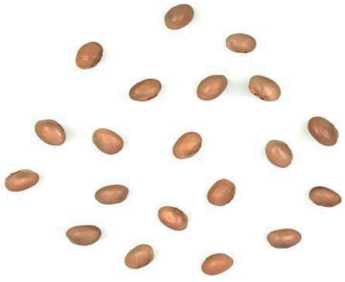

Figure 11. Accession C2E0025 - Velingrad



Figure 12. Accession 771445 - France

Cluster 4 is represented by 7 samples with the darkest seed coloration. The I-Max value is 218.87 (CV% = 3.18), similar to that of Cluster 3. The RGB values are substantially lower: Red 72.10 (CV% = 53.81), Green 59.27 (CV% = 60.94), and Blue 57.57 (CV% = 52.75). Hue is exceptionally high at 237.99 (CV% = 25.17). Saturation is the lowest among all clusters (0.2118; CV% = 75.00), indicating an almost complete lack of color saturation. Lightness (0.2500; CV% = 52.09) is the lowest value across all clusters. This cluster includes black (Figure 13 - 91201151 - France), red (Figure 14 - 91201025 - Portugal), black-white on half of the seed (Figure 15 - 91201151 - France), and accession which include different color of seeds (Figure 16 - A7E0270 - v. Mikrevo).

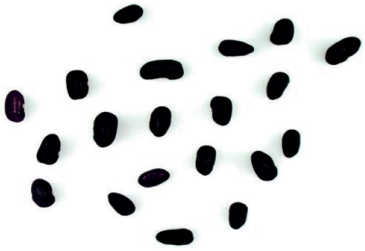

Figure 13. Accession 91201238 – Türkiye

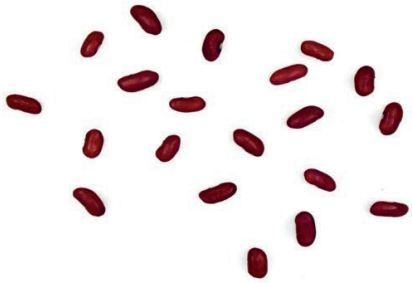

Figure 14. Accession 91201925 – Portugal



Figure 15. Accession 91201151 - France



Figure 16. Accession A7E0270 - Mikrevo

The colour parameters measured, using the Marvin Seed Analyzer, enabled a reliable and precise grouping of the samples into four clearly differentiated clusters. These clusters reflect the actual visual differences among the genotypes and may provide valuable information for breeding, variety identification, and phenotypic characterization. Seed colour may prove to be a highly informative trait that can be used both for morphological classification and for genetic and breeding purposes.

The correlation analysis (Table 8) reveals a clear distinction between the different groups of all measured traits and parameters. The phenological indicators show predominantly weak relationships, highlighting the relative independence of the individual developmental stages, with the exception of the strong correlation between the beginning of mass flowering and the duration of the vegetation period. Colour parameters (RGB and HSL) demonstrate the strongest relationships in the matrix, which is due to the mathematical relationship between the two-colour models, and not to biological differences. The biometric traits show both medium and weak associations: seed width and thickness are medium correlated, reflecting the stability of seed shape, whereas seed length and width show a weak relationship. The TSW is medium correlated with seed perimeter, confirming that the total seed size is a key factor for productivity.

Table 8. Correlation analysis of all 18 traits

	Veg.	M/F	B/F	D/F	I-Max	Red	Green	Blue	Hue	S.	L.	Area	P.	S/L	S/W	S/T	S/M
Veg.	1																
M/F	**0.587****	1															
B/F	**0.498***	**0.498***	1														
D/F	0.286	-0.015	**0.332***	1													
I-Max	-0.063	0.101	-0.026	-0.099	1												
Red	0.026	-0.011	0.052	0.008	0.184	1											
Green	0.054	0.015	0.086	0.066	0.158	**0.966*****	1										
Blue	0.066	0.016	0.093	0.085	0.132	**0.935*****	**0.991*****	1									
Hue	0.065	0.061	0.028	0.119	-0.115	-0.519	-0.382	-0.295	1								
S.	0.076	0.023	0.070	0.096	0.029	**0.796*****	**0.769*****	**0.746*****	-0.382	1							
L.	0.048	0.003	0.076	0.049	0.160	**0.983*****	**0.996*****	**0.984*****	-0.415	0.784	1						
Area	0.096	0.098	-0.058	0.219	-0.146	-0.108	-0.104	-0.102	0.076	0.121	-0.107	1					
P.	-0.246	-0.263	-0.279	-0.122	0.012	0.080	0.075	0.079	-0.057	-0.020	0.079	-0.403	1				
S/L	-0.116	-0.176	0.094	0.128	-0.123	-0.053	-0.033	-0.021	0.063	-0.093	-0.037	0.119	-0.148	1			
S/W	-0.035	-0.024	-0.168	0.033	0.194	0.080	0.023	0.021	-0.180	-0.068	0.049	0.089	0.045	**0.334***	1		
S/T	-0.282	-0.218	-0.353	-0.046	0.053	0.052	0.015	0.026	-0.190	-0.075	0.037	0.114	0.165	0.105	**0.679****	1	
S/M	-0.151	-0.099	-0.064	-0.046	0.068	-0.019	-0.053	-0.057	-0.007	-0.008	-0.040	-0.032	0.216	-0.209	0.024	0.110	1
TSW	-0.130	-0.128	-0.222	0.027	0.266	0.079	0.086	0.081	-0.021	0.014	0.080	0.169	**0.576****	-0.078	0.136	0.198	0.208

CONCLUSIONS

The seed perimeter is valuable trait that reflects differences in seed shape and complements linear measurements as an integrative morphometric indicator. It may reflect differences in seed shape which are not fully captured by individual linear measurements.

The 100-seed weight and seed area exhibit high variability, which identifies them as selection-relevant and highly polymorphic traits.

Cluster analyses performed on 84 common bean genotypes revealed a clearly structured phenotypic separation into four groups, differing in their morphological, biometric, phenological, and colour characteristics. The resulting clusters demonstrate both internal homogeneity and distinct differences between groups, highlighting the high level of phenotypic diversity within the studied collection.

Seed colour and the morphometric parameters from Marvin seed analyzer may prove to be highly informative traits that can be used both for morphological classification and for genetic and breeding purposes.

To identify promising groups, the study should be continued in the following experimental years. The model of common bean seed analysing, could be applied to other crops, stored in the genebank.

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