

Research Article



Comparison of Old and Local Varieties *Phaseolus vulgaris* L. in the Variability of Some Morphological Characters of Seeds

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Many growers and family farmers in the countryside still conserved original and culinary important old and local crop varieties. These varieties are the basis of the food security of the rural population. Under the conditions of Slovakia, the common bean (*Phaseolus vulgaris* L.) has always been an important legume crop, evidenced by the hundreds of old and local varieties still grown nowadays. The research focused on determining the economic value of a selected collection of old and local varieties of common beans widespread in Slovakia for selected morphological characters of seeds for their classification, cataloguing, and long-term preservation. We determined morphometric parameters of seeds for all specimens the range for the length of seeds 12.08–17.66 mm (V% of 4.65–12.21), width of seeds 7.19–10.19 mm (V% of 3.88–8.62), thickness of seeds 5.22–7.85 mm (V% of 4.94–9.33), length of hilum 2.13–2.63 mm (V% of 5.51–19.00), width of hilum 0.89–1.55 mm (V% of 7.78–29.35), weight of 50 seeds 19.73–38.74 (V% of 21.71), length/width shape index 1.39–2.03 (V% 4.30–16.20), width/thickness shape index 1.15–1.80 (V% 4.36–13.46). The obtained results document the importance of preserving evaluated old and local varieties in gene banks and as on farm production for our cultural heritage and biological genetic diversity.

Keywords: Common bean, genetic resources, morphometric analysis, variability

Introducion

The legume (Fabaceae Lindl.) family is the second most important family among crop plants after Poaceae Barnhart (Lewis et al., 2005) and contains five *Phaseolus* species that are cultivated worldwide for the commercial production of beans. Common beans (*Phaseolus vulgaris* L.), belong to the Fabaceae family and are part of the genus *Phaseolus* L. (Freytag & Debouck, 2002) with an estimated origin approximately 6–8 million years ago (Delgado-Salinas et al., 2006), now comprised ~90 species (OECD, 2016).

While the genus *Phaseolus* was defined by Linnaeus (1753), a revised definition came at the international legume conference held in Kew, England, in August

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1978, set forth by independent researchers (Maréchal et al., 1978). Different authors have since used and validated this definition of the genus (Freytag and Debouck, 2002; Delgado-Salinas et al., 2006).

The genus is monophyletic and naturally distributed in mild temperate to warm regions (mostly frost-free during the growing period) of the New World. Beans originate from Southern America and were discovered and brought to the Old World by Columbus (Bitochhi et al., 2012).

Common synonyms are French bean, haricot bean, salad bean, snap bean, string bean, frijoles (Spanish), feijão and feijoeiro (Portuguese for the seed and the plant, respectively), and mharagwe (Swahili) (Gepts and Debouck, 1991; Wortmann, 2006; Loko et al., 2018b).

Phaseolus vulgaris has an 85% share in worldwide bean production, followed by *P. lunatus, P. coccineus, P. acutifolius*, and *P. dumosus* (Mir et al., 2020). In fact, it is the most economically important bean species and agricultural crop after cereals, with an annual global dry yield of more than 8,741 kg·ha⁻¹ over 33 million ha (FAO, 2019).

Phaseolus vulgaris is the most consumed leguminous pulse in the world and is a major dietary staple and source of protein in Africa and Latin America (Mamidi et al., 2013). Bean seed is rich in protein contents, fibre, polyphenols, flavonoids, carotenoids, saponins, oligosaccharides, condensed tannins, lectins, trypsin inhibitors, and phytic acid which are the most important phytochemicals responsible for antioxidant biological activities and preventive against cardiovascular or chronic degenerative (Hayat et al., 2014; Suárez et al., 2023). Also, it is the source of essential vitamins (A, B₁₂, and C), minerals, and dietary fibre, which make it an excellent component of human nutrition (Akond et al., 2011; Philipo et al., 2020; Jan et al., 2021; Alcázar-Valle et al., 2021).

Under the conditions of Slovakia, the common bean has always been an important legume, which is evidenced by the hundreds of local and old varieties that are still grown by many producers nowadays. Our study aimed to evaluate the collection of old and local varieties for selected morphological characters of seeds for their classification, cataloguing, and long-term preservation.

Material and methodology

Biological material

Seeds *P. vulgaris* were taken from fields in September and October 2023 and analysed in the morphometric laboratory at the Institute of Plant and Environmental Sciences in Nitra (Slovakia).

Morphometric analysis

The total number of evaluated genotypes was 10 (PHV-01, PHV-02, PHV-03, PHV-04, PHV-07, PHV-10, PHV-11, PHV-12, PHV-15, PHV-17).

They were evaluated the following characters: seeds:

O 15 seeds were evaluated from each genotype (n = 15);

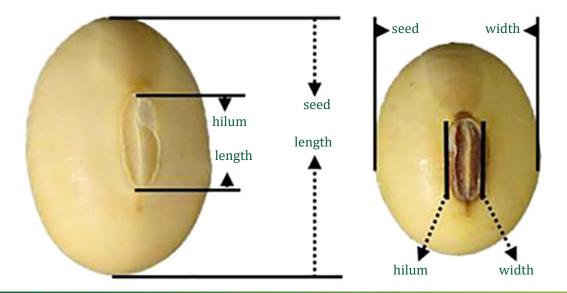


Figure 1 Illustration of measuring process: the length, width, and thickness of the seeds, hilum length and hilum width Source: Zhao et al., 2021

The weights were determined by digital scale (Kern ADB-A01S05, Germany; KERN DS – type D-72336, Kern and Sohn GmbH, Germany), accurate to 0.01 g. Seeds were measured by a digital calliper (METRICA 111 – 012, Czech Republic) accurate to 0.02 mm.

Image analysis:

• Seeds: the shape of seeds,

• seeds: the colour of seeds.

Images were obtained using the stereomicroscope ZEISS SteREO Discovery.V20 (MicroImaging GmbH 37081 Göttingen, Germany), and Fuji FinePix S 7000 and Panasonic DMC FZ50 digital cameras.

Statistical analysis

It was evaluated the variability of each character using descriptive statistics. For the characteristics it was used the basic descriptors of variability: average, minimum measured value, maximum measured value, and the coefficient of variation (%). The degree of variability was determined by the coefficient of variation values. The given parameter is independent of the unit of the evaluated character. Theoretically, they can acquire different values (Stehlíková, 1998). We used analysis of variance (ANOVA) in the program STATISTICA 1.10 to determine the dependence between individual characters. Dependences between characters were evaluated by linear correlation analysis according to Pearson.

Results and discussion

Evaluation and identification of genotypes based on morphological traits are important for the detection and selection of individuals that are suitable genetic material for hybridization and breeding program of new varieties, which contributes to the global conservation of biological diversity (Grygorieva et al., 2017, 2018; Arteaga et al., 2019; Brindza et al., 2019; Fatrcová-Šramková et al., 2019; Horčinová Sedláčková et al., 2021, 2022).

Beans may vary in colour, from uniformly white, grey, greenish, orange, pink, reddish, burgundy, light brown, dark brown, purple, dark black-violet, or bi-coloured, such as striped or mottled on a white or brown background. Results have shown high variability of shapes and colours of *Phaseolus vulgaris* in our collections.

The colorimetric properties of a common bean landrace are directly related to its chemical composition and may be related to its functional properties as well. This is why it is important to have methods that allow the colour analysis to study the potential relationships between colorimetric and chemical properties. Furthermore, this would also allow the comparison of similarities and differences among landraces (Morales Reyes et al., 2021).

In our collections of genotypes, the seeds are categorized as, oval, elliptical, elongated, flattened elongated, kidney, and parabolic seeds are the most represented (Figure 2), which is in accordance with the literature data.

Loko et al. (2018a) distinguished the shapes of local bean seeds as oval, cuboid, kidney, and markedly truncated shapes. In colouring dominated brown-red and cuboid shapes in the common bean collection of the central region of Benin Republic (Loko et al., 2018a). Kara et al. (2013) classified common been cultivars, according to their size and shape, as oblongus, ellipticus, subcompressus, and compressus. Varieties from the Western Himalayas are circular, elliptic, cuboidal, kidney, and circular to elliptical, as reported by Jan et al. (2021). Stoilova et al. (2013) described the shape of the common bean from Portugal as kidney, cuboid, and oval with white, red, brown, brownish, or bicolour colours and from Bulgaria as kidney and cuboid shapes with white, bicolour, and brownish colours.

When evaluating the genotypes (Table 1), the average length of the seeds has been determined in the range of 12.08 mm (PHV-11) – 17.66 mm (PHV-04) with coefficients of variation in the interval of 4.65 (PHV-03) – 12.21 (PHV-07) %. These data demonstrate that the characters are from the low to medium degree of variability.

The average width of the seeds has been determined in the interval from 7.19 mm (PHV-12) to 10.19 mm (PHV-10). The coefficients of variation were determined in the range of 3.88 (PHV-17) to 8.62 (PHV-07) %. These data demonstrate that the characters have a low degree of variability.

We determined the average thickness of grains in the collection of beans in the range of 5.22 mm (PHV-04) – 7.85 mm (PHV-10). The values of the coefficients of variation confirm the low degree of variability 4.94% (PHV-11) – 9.33% (PHV-12). We found small differences between the collections.



Figure 2 Variability in the shape and the colour of seeds of evaluated genotypes of *Phaseolus vulgaris* L.

Kara et al. (2013) evaluated 12 Turkish genotypes of *P. vulgaris* seeds and obtained data from the main parameters as average length (9.1 ±0.5–17.8 ±1.6 mm), average width (5.98 ±0.3–10.0 ±1.0 mm), average thickness (4.6 ±0.5–6.0 ±0.6 mm) and shape index (1.55–2.12). Chhetri and Bhatta (2017) studied 12 genotypes of common beans grown in Jumla (Nepal) and determined seed length in the interval 0.76– 1.70 cm. Loko et al. (2018a) evaluated 57 genotypes of common bean and determined seed length and seed width in the range of 0.60–1.60 (1.05 ±0.03) cm and 0.31–0.73 (0.62 ±0.01) cm, respectively. Our genotypes in morphometric parameters have mainly wider range in all traits against foreign studies.

The difference between genotypes were noted in the average weight of 50 seeds in the interval from 19.73 g (PHV-12) to 38.74 g (PHV-10) with coefficient of variation V% = 21.71. The differences in the weight of tested varieties were significant, and that is in full compliance with the studies assortment of bean seeds from Egypt (Nassar et al., 2010), Bulgaria and Portugal (Stoilova et al., 2013), Benin Republic (Loko et al., 2018a), Slovenia (Sinkovič et al., 2019), Western

Table 1Morphometric parameters of seeds of old and local varieties of *Phaseolus vulgaris* L.

]	Length of g	grain (mm)			Width of grain (mm)				
	n	min	max	x	V		n	min	max	x	V
				Gei	notypes w	ith low valu	es				
PHV-11	15	11.00	13.82	12.08	6.43	PVH-12	15	6.44	8.02	7.19	5,82
PVH-03	15	12.26	14.38	13.06	4.65	PVH-03	15	6.82	8.21	7.61	5.11
				Gen	otypes w	ith high valu	ies				
PHV-01	15	14.61	19.30	16.38	7.75	PVH-04	15	8.11	10.74	9.30	7.73
PVH-04	15	16.23	20.07	17.66	6.43	PVH-10	15	9.27	11.56	10.19	5.88
		Th	ickness of	grains (m	m)			Weigh	t of 50 gra	ins (g)	
	n	min	max	x	V		n	min	max	x	v
				Gei	notypes w	ith low valu	es				
PVH-04	15	4.49	5.95	5.22	9.15	PVH-12	50	_*	_*	19.73	_*
PVH-12	15	4.79	6.76	5.53	9.33	PVH-03	50	_*	_*	22.28	_*
				Gen	otypes w	ith high valu	ies				
PVH-11	15	6.98	8.26	7.59	4.94	PVH-07	50	_*	_*	32.86	_*
PVH-10	15	7.01	8.81	7.85	8.11	PVH-10	50	_*	_*	38.74	_*
_			Length/w	width ratio			Width/thickness ratio				
	n	min	max	х	V		n	min	max	х	V
				Gei	10types w	ith low valu	es				
PHV-11	15	1.27	1,54	1.39	5.90	PHV-11	15	1.05	1.23	1.15	4.36
PHV-10	15	1.25	1.67	1.44	7.93	PHV-07	15	1.08	1.28	1.17	4.86
				Ger	otypes w	ith high valu	ies				
PVH-12	15	1.71	2.29	1.99	8.74	PVH-12	15	1.07	1.53	1.31	8.98
PVH-01	15	1.85	2.39	2.03	7.70	PVH-04	15	1.41	2.38	1.80	13.46
_		I	Length of h	ilum (mm)			Widt	h of hilum	(mm)	
	n	min	max	х	V		n	min	max	х	V
				Gei	notypes w	ith low valu	es				
PVH-11	15	1.09	2.55	2.13	19.00	PVH-04	15	0.70	1.14	0.89	15.10
	15	1.98	2.36	2.17	5.52	PVH-01	15	0.76	1.86	0.94	29.35
PVH-03											
PVH-03				Ger	notypes w	ith high valu	ues				
PVH-03 PVH-07	15	2.06	2.96	Ger 2.60	notypes w 13.35	ith high valu PVH-07	ues 15	1.04	1.53	1.30	12.61

Note: n – the number of measurements; min, max – minimal and maximal measured values; \bar{x} – arithmetic mean; V – coefficient of variation (%); * – only the number of seeds was measured from each genotype

Varieties	Parameter	SL	SW	ST	HL	HW
	SL	1				
	SW	0.614	1			
PHV-01	ST	0.675	0.715	1		
	HL	0.089	0.276	0.134	1	
	HW	0.138	0.046	0.061	-0.274	1
	SL	1				
	SW	0.799	1			
PHV-02	ST	0.178	0.147	1		
	HL	-0.342	-0.182	-0.055	1	
	HW	-0.213	-0.126	-0.094	0.589	1
	SL	1				
	SW	-0.050	1			
PHV-03	ST	0.134	0.779	1		
	HL	0.072	0.327	0.051	1.000	
	HW	-0.308	-0.149	-0.241	0.208	1
	SL	1				
	SW	0.787	1			
PHV-04	ST	0.037	-0.167	1		
	HL	0.038	0.149	0.022	1	
	HW	-0.375	-0.409	-0.256	0.120	1
	SL	1				
	SW	-0.004	1			
PHV-07	ST	-0.072	0.660	1		
	HL	-0.113	-0.041	0.165	1	
	HW	-0.187	0.322	0.045	-0.085	1
	SL	1				
	SW	0.324	1			
PHV-10	ST	0.227	0.560	1		
	HL	-0.262	0.399	0.185	1	
	HW	0.061	0.339	0.208	0.118	1
	SL	1				
	SW	0.593	1			
PHV-11	ST	0.293	0.745	1		
	HL	-0.395	-0.386	-0.069	1	
	HW	-0.237	-0.433	-0.148	0.209	1
	SL	1				
	SW	0.142	1			
PHV-12	ST	0.676	0.299	1		
	HL	0.004	-0.228	-0.230	1	
	HW	0.089	0.271	0.344	-0.504	1
PHV-15	SL	1	<i></i>	0.0 1 1	0.001	-
	SW	0.838	1			
	ST	0.092	0.236	1		
	HL	0.092	-0.006	-0.024	1	
	1111	0.037	0.000	0.041	1	

Table 2Correlation between morphometric parameters of *Phaseolus vulgaris* L.

Parameter	SL	SW	ST		
		=	51	HL	HW
SL	1				
SW	0.838	1			
ST	0.092	0.236	1		
HL	0.059	-0.006	-0.024	1	
HW	-0.065	-0.117	-0.057	0.250	1
	SW ST HL	SW 0.838 ST 0.092 HL 0.059	SW0.8381ST0.0920.236HL0.059-0.006	SW0.8381ST0.0920.2361HL0.059-0.006-0.024	SW0.8381ST0.0920.2361HL0.059-0.006-0.0241

Continuation of Table 2

Notes: SL – seed length; SW – seed width; ST – seed thickness; HL – hilum length; HW – hilum width. Values in bold are significant (p < 0.05)

Himalayas (Jan et al., 2021), and Cameroon (Kouam et al., 2023).

Nassar et al. (2010) determined the specific weight of 100 seeds of common bean in Egypt conditions in the range of 32.26-34.48 (33.59 ± 0.37) g, meanwhile, in Bulgaria and Portugal, Stoilova et al. (2013) compared morphological variability of 30 common beans in different environmental conditions (15 of Portuguese and 15 of Bulgaria landraces). The authors noted 100 seeds weight in the interval 20.0-67.5 g (V% = 28.1) and 25.3-55.7 g (V% = 16.7) for Portuguese and Bulgarian landraces.

We determined the length/width ratio in the interval 1.39-2.03 and the width/thickness ratio in the range of 1.15-1.80. Sinkovič et al. (2019) evaluated 953 accessions of common *P. vulgaris* and 47 accessions of runner bean *P. coccineus* from Slovene Gene Bank and determined following parameters: lengths (13.63 ± 1.86 and 20.53 ± 2.06 mm), widths (8.22 ± 1.08 and 12.71 ± 1.17 mm), thicknesses (6.70 ± 0.94 and 8.70 ± 0.89 mm), L/W (1.08-2.64 and 1.42-1.89), W/T (0.97-2.49 and 1.27-2.17), and 100 seeds weights (51.13 ± 13.84 and 13.47 ± 3.45 g), respectively. In comparison to our experiments, authors reported lower average values in all traits for *P. vulgaris*, but wider intervals for L/W and W/T ratios (Table 1).

Sinkovič et al. (2019) classified beans according to their weight into 3 groups: low-weight seeds group included common bean accessions with 100 seed weight <35.0g (112 accessions or 12%); the medium-weight seeds group accessions with 100 seed weight measuring from 35.0 to 75.0 g (801 accessions or 84%); and the high-weight seeds group accessions with 100 seed weight >75.0 g (40 accessions or 4%).

Research of Mesoamerican an Andean types of common bean genotypes from Western Himalayas have shown results that average seed size and seed weight of Andean common bean genotypes was found more than seed size and seed weight of Mesoamerican genotypes. The average seed length, breadth, and weight of Andean genotypes was 15.3 mm, 8.04 mm, and 39 g, respectively, whereas the average seed length, breadth, and weight in Mesoamerican genotypes was 12.97 mm, 7.80 mm, and 32.90 g, respectively (Jan et al., 2021).

In Cameroon Kouam et al. (2023) evaluated 44 genotypes of *P. vulgaris* and determined seed length (0.89–2.47 cm), seed width (0.69–1.34 cm), seed height (1.22–2.53 cm) and 100 seed weight (16.42–58.6 g).

The length and width of the hilum and its shape can be important traits. The average length and width of the hilum under the study were in the range of 2.13 (PHV-11) – 2.63 (PHV-10) mm with coefficients of variation 5.51 (PHV-03) – 19.00 (PHV-11) % for length and 0.89 (PHV-04) – 1.55 (PHV-10) mm with coefficients of variation 7.78 (PHV-15) – 29.35 (PHV-01) % for width. According to coefficients of variation, we confirmed the low or high degree of variability of both characters (Table 1).

A high degree of correlation (r = 0.7-0.9) was found between seed length and seed width (PVH-02, PVH-04, PVH-15), seed width and seed thickness (PVH-03, PVH-11), seed length and hilum length (PVH-17), a moderate-high degree of correlation (r = 0.5-0.7) was found between seed length and seed width, seed length and seed thickness (PVH-01), seed width and seed thickness (PVH-07), seed length and seed thickness (PVH-12), which are reported with Table 2.

Nasar et al. (2022) studied 13 quantitative traits of plants and seeds of *P. vulgaris* and *P. coccineus* in Pakistan from six districts and according to variance components determined small and non-significant differences. The combined multivariate and univariate analyses thus indicated that most variation for traits is local.

Conclusion

Based on morphometric analysis of seeds from the collection of old and local bean varieties, we determined the range of phenotypic variability for all traits and their combinations of evaluated genotypes. We have confirmed that the evaluated collection contains very valuable and original genotypes from old and local bean varieties that can be used practically. All evaluated genotypes are potentially usable mainly for cultivation and expansion in the program of small, young, and family farms as well as for preserving all unique genotypes of our cultural heritage and biological genetic diversity.

Conflict of interest

The authors have no conflicts of interest to declare.

Ethical statement

This article doesn't contain any studies that would require an ethical statement.

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