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PHENOTYPIC DIVERSITY OF COMMON BEAN (*Phaseolus vulgaris* L.) GERMPLASM, A POTENTIAL CROP FOR ENSURING FOOD SECURITY

Diana BATÎR RUSU[1], Danela MURARIU[1], Domnica Daniela PLĂCINTĂ[1], Cristian TUDOSE[2], Elena Liliana CHELARIU[3], Oana MÎRZAN[4], Margareta NAIE[4]

[1]Suceava Genebank, 17, 1 Mai Blvd, 720224, Suceava, Romania
[2]"Alexandru Ioan Cuza" University of Iași, 11 Carol I Blvd, 700506, Iasi, Romania
[3]"Ion Ionescu de la Brad" Iasi University of Life Sciences, 3 Mihail Sadoveanu Alley, Iasi, Romania
[4]Agricultural Research Development Station Secuieni, 377 Main Street, 617415, Neamț County, Romania

Corresponding author email: danela.murariu@svgenebank.ro

Abstract

Bean crop is of great economic interest, being among the most used grain legumes in human nutrition. Also, it can use like organic crop, with great ecological plasticity, cultivated from the plains to high altitudes, also being a good precursor for other crops, leaving the soil rich in nitrogen. Therefore, we must give priority to the phenotypic characterization of local bean germplasm to provide breeders with valuable genetic sources, useful in creating of productive advanced cultivars, resistant to adverse environmental factors, to ensure food security. The objective of this study was to evaluate variability of morpho-physiological and agronomic traits of some common bean landraces (Phaseolus vulgaris L.), well adapted to pedoclimatic conditions from different regions sites of the country, conditioned by the genetic factors of the species. These populations could be used in prebreeding programs to improve some morpho-physiological characteristics very useful for future new creations. We must give priority to the phenotypic characterization of local bean germplasm to provide breeders with valuable genetic sources, useful in creating of productive advanced cultivars, to ensure food security.

***Key words**: common bean landraces, variability, variation, phenophasic, morphological and agronomic traits.*

INTRODUCTION

Phaseolus vulgaris L. (common bean), a traditional grain legume in Romania is the most important cultivated species of the genus. Is one of the most remarkable crops for its seed nutritional value, as it has a high protein content and is considered to be one of the main sources of protein in the human diet (Abdollahi et al., 2016). It was introduced to our country at the beginning of the 17th century, and until 1989, it was cultivated on large areas (168,000 ha) (Bîlteanu, 1989). It has a high economic interest, being among the most used legumes in human nutrition. In general, seeds are used for their high content of digestible proteins rich in essential amino acids, but pods are also used; and sometimes young shoots are used as a salad.

There are several varieties, classified according to the shape of the grain: *compressus, oblongus, ellipticus, sphaericus*, according to the type of growth: nanus (small type), vulgaris (climbing type) and various intermediate biotypes between varieties (Musango et al., 2016). Within the varieties, there are different types differentiated by color as follows, unicolor (white, black, brown, beige, etc.), punctatus (dotted), maculatus (spotted), variegatus (motley) and zebrinus (striped) (Muntean, 1995; Ciofu R. et al., 2003; Stoilova, et al., 2005; Abdollahi et al., 2016).

The objective of this study was to evaluate the variability of morpho-physiological and agronomic traits of some common bean landraces (*Phaseolus vulgaris* L.), well adapted to pedoclimatic conditions from different regions sites of the country, conditioned by the genetic factors of the species. All these local landraces were collected from local farmers, who prefer and grow them in their gardens due to the multiple uses in food and the adaptation to biotic and abiotic stress factors, in the context of current climate changes (Stoilova et al., 2013; Szilagyi et al., 2011).

The study was carried out at the Suceava Genebank, during period 2016-2018 and included 122 bean local varieties. Morpho-physiological and agronomic traits were evaluated during the growing season according to bean descriptors edited by ECP/GR. The investigations carried out showed differences between the populations for all the analyzed traits. All the local bean varieties collected showed high variability, representing potentially valuable genetic resources for breeders of this species.

The landraces (common and dwarf beans) which was studied in this paper, is grown only in peasant gardens, microfarm because it is preferred by the rural population due to the quality of pods, long harvest period and production far superior to large grain beans.

The main objective of this study was to analyze variability of morphological descriptors and variation of the main agronomic traits of locally adapted varieties from different regions sites of the country, conditioned by the genetic factors of the species. Also, the aim of this study was to use agro-morphological traits to assess the genetic diversity and relatedness among 122 *Phaseolus vulgaris* L. accessions collected from different eco-geographical areas.

We must give priority to the phenotypic characterization of local bean germplasm to provide breeders with valuable genetic sources, useful in creating of productive advanced cultivars, to ensure food security (Boros et al., 2014).

Finally, possessing a good knowledge of the available genetic diversity will permit not only a good management of the bean germplasm, but also facilitate its valorization (Dutta et al., 2016; Bareke, 2019). These results represent the starting point from which the genetic diversity of our collection was assessed, thereby making it possible to optimize new breeding strategies for planning future breeding programs to individuate specific traits useful in the environment (Scarano et al., 2014; Guidoti, et al., 2018).

MATERIALS AND METHODS

In the present study, both morphological and phenotypical characterization were employed to highlight bean germplasm diversity and to determine the genetic relationships between 122 bean accessions obtained from different regions.

The study for the assessment of phenotypic variability of *Phaseolus vulgaris* L. genotypes, for different morphological and agronomic traits was conducted in the experimental field of the Suceava Gene Bank.

The biological material used in this study consisted of a total of 122 populations belonging to the species *Phaseolus vulgaris* L., collected from regions with different ecological conditions (Table 1). The experimental design and field management was laid out in blocks, with length row of 2 m, and the distance between rows of 70 cm on a cernoziomoid soil (3-5% humus).

During the growing period, data related to phenology, morphological and agronomic.

Table 1. Origin of bean local landraces analyzed

Collecting counties	No. of samples	Collecting counties	No. of samples
Constanța	1	Cluj	2
Suceava	24	Vaslui	2
Dolj	4	Mehedinți	2
Alba	15	Argeș	2
Iași	18	Caraș Severin	2
Hunedoara	4	Bistrița Năsăud	5
Brașov	9	Arad	2
Neamț	8	Maramureș	2
Vâlcea	3	Covasna	2
Vrancea	3	Satu Mare	2
Bihor	5	Bacău	5

traits were characterized in accordance with the IPGRI descriptor list (2009). Data on analyzed traits were collected from ten sample plants from each plot, selected randomly. In order to highlight the landraces variability, the following morpho-physiological descriptors were determined in the field and in the lab:

- Biometric descriptors (Leaf length, Pod length, No. of days from emergence to flowering, No. of days from flowering to maturity, No. of days from emergence to maturity);
- IPGRI descriptors by using codes (growth type, color of the flower banner, color of the fins, color of the immature pod, cross section through the pod, curvature of the immature pod, color of the ripe pod, presence of fibers on the pod, seed shape, seed size, presence of stripes/spots on the seeds, no. of colors on the seeds, base color of the seed, secondary color of the seed, distribution of the secondary color of the seed).

All analyses were conducted using SPSS 20 and GraphPad Prism 9.4.

The following estimators were calculated for biometric descriptors mentioned: average (x), variation amplitude (min.-max.), standard deviation (ѣ) and F-ANOVA test (p/0.05), presented in tables and dendrograms by statistical analysis techniques such as: one-way ANOVA and Hierarchical Cluster Analysis.

RESULTS AND DISCUSSIONS

The following estimators were calculated for biometric descriptors: average (x), amplitude of variation, variance (s2) and coefficients of variation (s %) (Fowler J.and Cohen L., 1990). The two morphological descriptors (leaf length and pod length) and the 3 physiological ones (no. of days from emergence to flowering, no. of days from flowering to maturity and no. of days from emergence to maturity.) are presented in Table 2. The interpretation of the results is based on the determination of the coefficient of variation, as an expression of the diversity of the studied biological material. From the Table 2, a large coefficient of variation it is observed for the descriptors: pod length and no. of days from flowering to maturity. Mean values of the coefficient of variation were recorded for the descriptor leaf length and minimum values were recorded for the descriptors: no. of days from emergence to flowering and no. of days from emergence to maturity. Table 2 also shows that the bean sample with the shortest vegetation period coming from Fundulea, Călărași (SVGB-2447) and the latest comes from Brodina, Suceava (SVGB-2286).

Referring the pod length, it can notice a variation amplitude between 6.05 cm, accession coming from Sânpetru, Brașov (SVGB-19935) and 16.35 cm, accession coming from Călărași, Dolj (SVGB-2788).

Table 2. Amplitude of variation in biometrics descriptors recorded on the bean samples analyzed

Descriptors	Average	Maxim values	Accession name	Minim values	Accession name	Stand. dev.	Variance	Coeff. of variation
Leaf length	7.69	11.14	SVGB-2504	5.28	SVGB-12577	1.16	1.335	10.41
Pod length	10.46	16.35	SVGB-2788	6.05	SVGB-19935	2.215	4.91	21.17
No. of days from emergence to flowering	45.8	51	SVGB-19614	34	SVGB-14248 SVGB-2951 SVGB-2111 SVGB-2788	3.213	10.32	7.00
No. of days from flowering to maturity	44.62	78	SVGB-19330	32	SVGB-2453 SVGB-15410	9.47	89.70	21.22
No. of days from emergence to maturity	92.48	104	SVGB-2286	76	SVGB-2447	7.094	50.33	7.67

To highlighting the links between the type of growth and the analyzed biometric descriptors (Table 3), it was calculated the F factor ANOVA which presented high values, statistically differentiating function by analyzed descriptors. In the Table 3 it is noticed the significant correlations between growth type and no. of days from flowering to maturity, and the no. of days from emergence to maturity.

Table 3. Simple linear regression of the morpho-physiological descriptors investigated

Growth type	No. of days from emergence to flowering	No. of days from flowering to maturity	No. of days from emergence to maturity	Leaf length	Pod length
Is slope significantly non-zero?					
F	0.4756	6.143	6.006	1.643	0.3751
DFn, DFd	1,108	1,108	1,108	1,108	1,108
P value	0.4919	0.0147	0.0159	0.2027	0.5415
Deviation from zero?	Not Significant	Significant	Significant	Not Significant	Not Significant

To emphasize the correlations between growth type and those two physiological traits (number of the days from flowering to maturity and number of the days from emergence to maturity) it assigned the regression lines. Growth type was positively correlated to number of the days from emergence to maturity (r = 0.435***) and also was positively correlated to number of the days from flowering to maturity (r = 0.317**) (Figure 1).

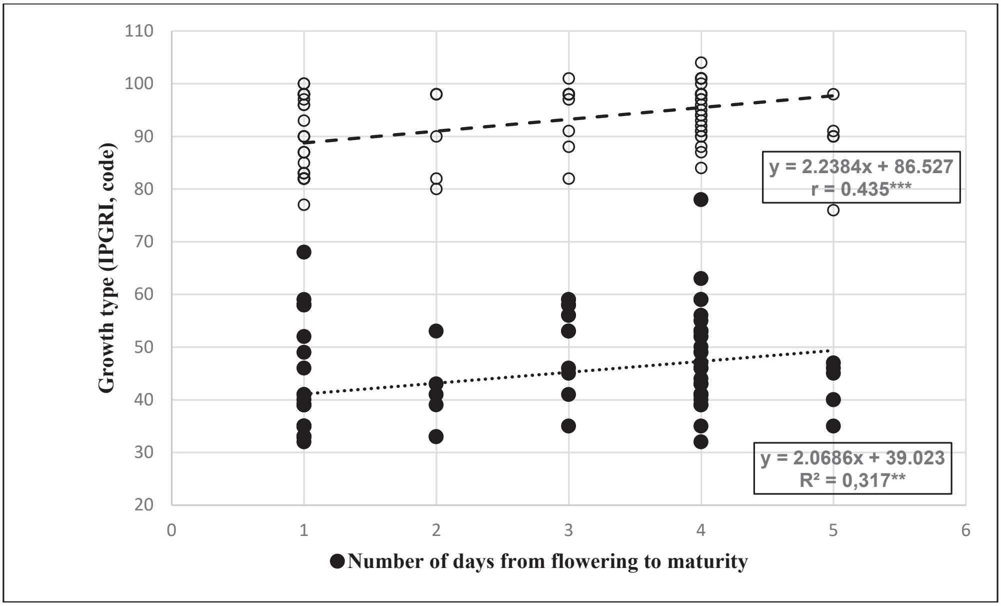

Figure 1. Relationships between growth type and the days from emergence to maturity and from flowering to maturity

All analyzed descriptors to those 122 local populations of *Phaseolus* were statistically classified into 4 clusters (Table 4) by the method of average linkage between groups, highlighting the similarities between members by different values of the Pearson correlation coefficients. So, it observes in dendrogram (Figure 2) their similarities, by strongly significant correlations between the color of the flower banner and color of the fins (0.777***); the base color of the seed and secondary color of the seed (0.510***); number of colors/seed and presence of streaks/spots on the seed (0.560***); number of colors/seed and distribution of secondary seed (0.777***); number of the days from emergence to maturity and number of the days from flowering to maturity (0.624***). Also there are significant correlations between presence of streaks/spots on the seed and base color of the seed (0.303*), shape of the seed and size of the seed (0.323*) and number of the days from emergence to maturity and leaf length (0.443**).

Table 4. Classification of morpho-physiological traits in clusters, by the method of average linkage between groups and Pearson correlation distance

Cluster number	Cluster membership (descriptors)	No. membership in dendogram	Cluster combined from agglomeration schedule to method average linkage between groups		Pearson correlation coefficients
			Cluster 1	Cluster 2	
1	Colour of the flower banner	7	7	8	0.777
1	Colour of the fins	8	7	10	0.206
1	Cross section through the pod	10	10	11	0.239
1	Curvature of the immature pod	11	7	12	0.100
3	Color of the ripe pod	12	2	9	0.246
2	No. of colours/seed	17	18	19	**0.510**
2	Distribution of secondary seed colour	20	17	16	**0.560**
2	Presence of streaks/spots on the seed	16	17	20	**0.777**
2	The base color of the seed	18	16	18	**0.303**
2	Secondary color of the seed	19	7	16	0.092
3	Pod length	2	1	2	0.134
3	Colour of immature pod	9	2	13	0.052
3	Shape of the seeds	14	14	15	**0.323**
3	Size of the seeds	15	14	13	0.237
3	Presence of fibers on the pods	13	2	4	0.044
3	No. of days from emergence to flowering	4	2	7	0.031
4	No. of days from emergence to maturity	5	5	6	**0.624**
4	No. of days from flowering to maturity	6	5	1	**0.443**
4	Leaf length	1	1	3	0.288
4	Growth type	3	3	4	0.053

In Dendogram using Average linkage (Figure 2) it observes the similarities of the descriptors, being grouping in 4 clusters, such as:
Cluster 1: Color of the flower banner, Color of the fins, Cross section through the pod, Curvature of the immature pod;
Cluster 2: No. of colors/seed, Distribution of secondary seed color, Presence of streaks/spots on the seed, The base color of the seed, Secondary color of the seed;
Cluster 3: Color of the ripe pod, Pod length, Color of immature pod, Shape of the seeds, Size of the seeds, Presence of fibers on the pods, No. of days from emergence to flowering;
Cluster 4: No. of days from emergence to maturity, No. of days from flowering to maturity, Leaf length, Growth type.

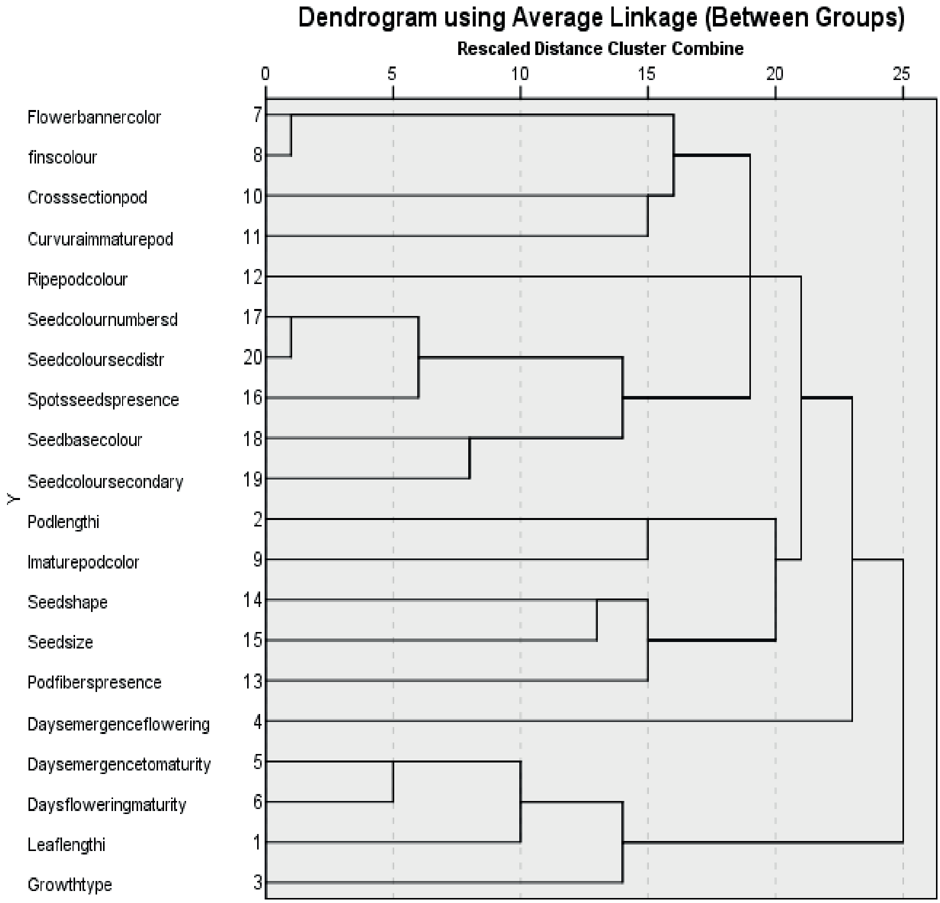

Figure 2. Hierarchical clustering of 122 common bean genotypes based on Pearson correlation using data from 20 morpho-physiological traits

The Ward Linkage dendrogram (Figure 3) built on the Euclidean distance showed the maximum distance in the third cluster (C3) represented by the following members: SVGB-14244, SVGB-14236, SVGB-2463, SVGB-2012; SVGB-15335, SVGB-2486, SVGB-14226, SVGB-2468, SVGB-244, SVGB-14247, SVGB-20313, SVGB-14239, SVGB-9059, SVGB-2457, SVGB-14648. Therefore, 13 % of the total studied members presented a high heteropgenity of the morpho-physiological traits, which could be used in the prebreeding programs to improve some morpho-physiological characteristics.

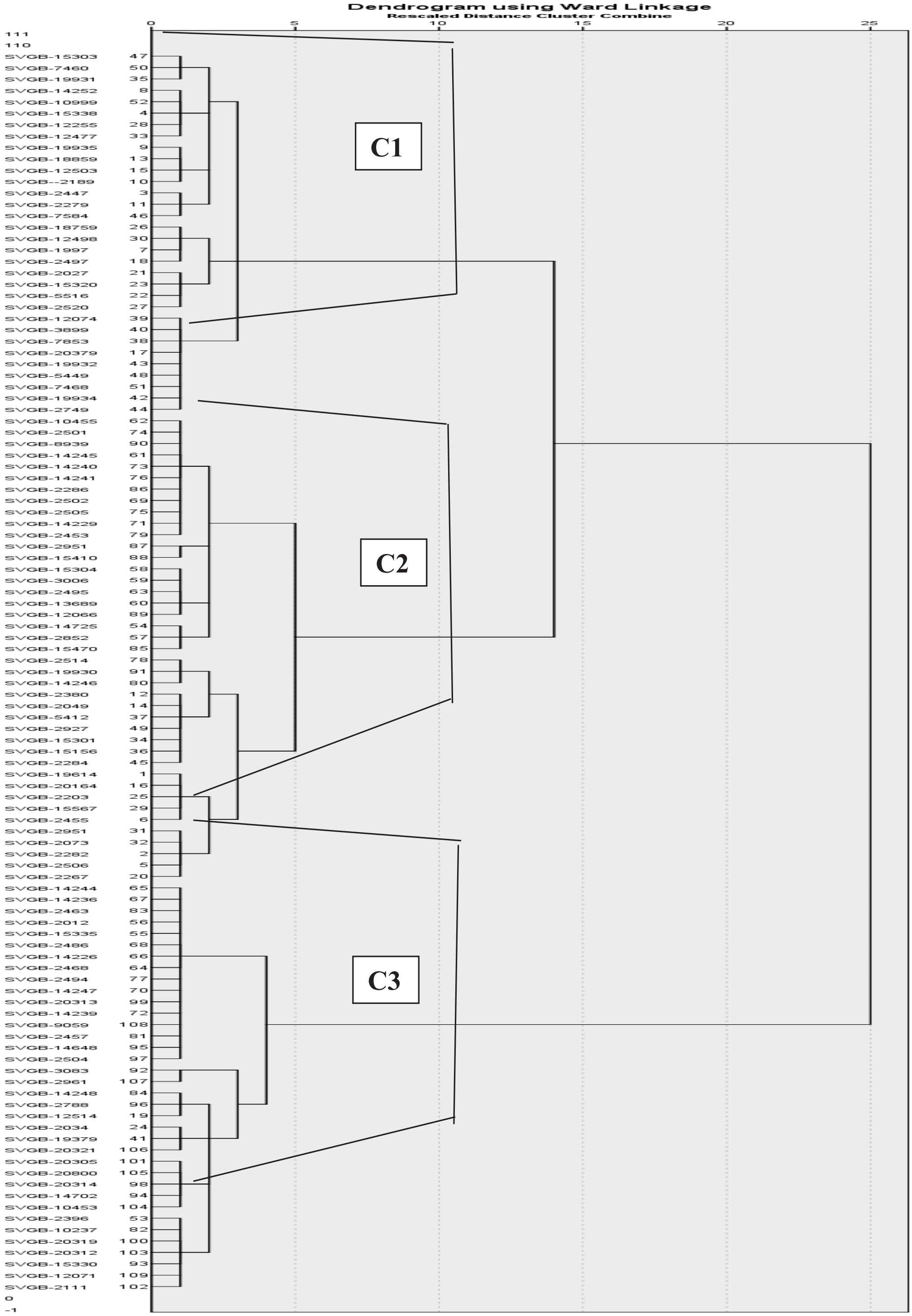

Figure 3 - Ward Dendogram based on Euclidean distance using the data from phenotypic descriptors recorded in 122 common bean populations

CONCLUSIONS

From this study it could be concluded that the bean populations represent a diversified biological material with a high variability.

The greatest variability of the studied populations was observed for the descriptors pod length, and numbers of the days from flowering to maturity.

The significant correlation coefficients were obtained between growth type and number of days from flowering to maturity, and the number of days from emergence to maturity, that mean the importance of the growth type in the obtaining of the earlier cultivars.

Concerning the Pearson correlation coefficients, it observes the strongly significant correlations between the color of the flower banner and color of the fins; the base color of the seed and secondary color of the seed; the number of colors/seed and presence of streaks/spots on the seed; the number of colors/seed and distribution of secondary seed; the number of the days from emergence to maturity and number of the days from flowering to maturity.

The Ward Linkage dendrogram built on the Euclidean distance showed the maximum heterogeneity of morpho-physiological descriptors to the following local populations: SVGB-14244, SVGB-14236, SVGB-2463, SVGB-2012; SVGB-15335, SVGB-2486, SVGB-14226, SVGB-2468, SVGB-244, SVGB-14247, SVGB-20313, SVGB-14239, SVGB-9059, SVGB-2457, SVGB-14648. These populations could be utilized in prebreeding programs to enhance specific morpho-physiological characteristics, which would prove beneficial for future breeding endeavors.

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