Evaluation of selected traits in grasspea (*Lathyrus sativus* L.) genetic resources.

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Introduction

Grass pea (*Lathyrus sativus* L.) is one of the most important species of the *Lathyrus* genus. It has two subspecies [(8)]: spp. *asiaticus* Zalk., which has small, coloured seeds, occurring mainly in the continental part of Asia and Africa and spp. *europaeus* Zalk. with large seeds, occurring predominantly in Central Europe and European Russia. According to Vavilov [(8)] its genetic centre is in the Mediterranean region. It is utilised for nutritional, fodder and technical purposes. It is undemanding to grow and so has been cultivated predominantly in dry and warm regions of Southern Europe, North Africa and Asia Minor [(5)]. It is less widespread in Central Europe.

Under the leadership of ECP/GR (European Cooperative Programme for Crop Genetic Resources Network) the European database of grass pea was established in 1985. Its holder has been IBAES in Pau, France. The database consists of approximately 4000 grass pea accessions [(2)]. The largest collections of grass pea genetic resources are in India (Raipur, 2659 genotypes), in Syria (ICARDA, 1560 genotypes) and in France (University of Pau, 1807 genotypes) [(1)].

In Slovakia grass pea has not been grown on a large area, and nowadays is only grown in the south. In the Research Institute of Plant Production (RIPP) in Pieštany, Slovakia the grass pea genetic resources have been maintained since 1994, when grass pea landraces were obtained by collecting expeditions. Within the National Programme for Cultural Plant Genetic Resources Preservation in Slovakia the collection has been expanding, mainly with further domestic landraces, comprising a valuable national resource. At present the grass pea collection is composed of 49 genotypes, mainly of domestic origin.

The objectives of this study were to:

- Evaluate the selected biological and economic traits and characters of 35 grass pea genetic resources.
- Select those with interesting characteristics to be used in breeding.
- Find correlations of individual traits, and to characterise the set from the point of all traits.

Materials and methods

During 1998 and 1999 years a set of 35 grass pea genetic resources, comprising 34 of Slovak (SVK) and 1 of Syrian (SYR) origin, was evaluated in a maize growing area at RIPP Pieštany. The trial was sown in plots with a harvest area of 10 m^2 (6.25 x 1.6 m). Distance between rows was 0.4 m. During the vegetative period the genetic resources were evaluated with morphological, phenological, biological and economic parameters using relevant descriptors for *Lathyrus* spp.

In mechanical analyses values of the following traits were measured in 20 plant samples:

- Time to maturity (sowing date to harvest) (d).
- Plant height (mm).
- Height of setting the first pod (mm).
- Plant dry weight (g).
- Number of pods per plant.
- Number of seeds per plant.
- Weight of seeds per plant (g).
- 1000 seeds weight (or TGW) (g).
- Yield ($t.ha^{-1}$).
- Resistance to lodging, on 1 (low) to 9 (high resistance) point scale.
- State of the stand, on 1 (low leaf area index) to 9 (high) point scale.
- Resistance to the fungus *Fusarium oxysporum*, on 1 (low resistance) to 9 (high) point scale
- Protein content was measured by CSN-2000 analyser.

The data were evaluated by variance analysis (ANOVA) and correlation coefficients between tested traits and characteristics were calculated. For the purpose of classification of the 13-dimensional structure two multivariate techniques were used: a principal component analysis [(7)] and a cluster analysis [(6)] with Ward's method. Because different scales were used for the descriptors, data were first standardised as recommended [(3)]. All analyses were carried out using the Statgraphic v.7.0. and the SPSS v.8.1. package.

Results

The results of variance analysis showed that the year contributed highly significantly to variability in most traits. The effect of genotype was highly significant only for TGW and significant for the height of the first pod. The effect of the year was not recorded in the other traits (Table 1). All genotypes mentioned are of Slovak (SVK) origin unless specifically designated Syrian (SYR).

Table 1. Mean values and ranges of the set of measured traits, and F ratios of the effect of genotype and years from ANOVA.

Traits			F-ratio	
	Mean	Range	Genotype	Years
Time to maturity (d)	127	125 - 129	0.82	4366.93 **
Plant height (mm)	854	742 - 997	1.27	400.15 **
Height of lowest pod (mm)	242	192 - 303	1.88 *	0.02
Plant dry weight (g)	30.9	20.0 - 52.2	1.04	0.02
Number of pods per plant	27.2	17.6 - 45.1	1.14	2.03
Number of seeds per plant	53.1	33.6 - 80.9	1.10	9.91**
Weight of seeds per plant (g)	14.4	8.6 - 25.1	1.10	13.31**
1000 grain weight (g)	286	232 - 354	4.51**	15.53 **
Yield ($t.ha^{-1}$)	4.02	3.24 - 4.79	1.23	28.33 **
Resistance to lodging	4.7	3.5 - 6.0	1.78	2.25
State of stand	7.5	6.5 - 8.3	1.73	4.7*
Resistance to *Fusarium* disease	8.1	7.8 - 8.5	1.25	21.35 **
Protein concentration (%)	25.9	23.2 - 27.3	1.64	236.55 **

* significant at P<0.05, ** significant at P<0.01

The whole set had good resistance to *Fusarium oxysporum*, the average of this trait was high, 8 points according to the scale. All genotypes were resistant to the disease during the study.

PCA and cluster analysis. More detailed relationships were revealed by the principal component analysis (PCA). A principal component analysis was carried out to transform the interdependent traits into a set of independent traits as well as to reduce the dimensionality of the structure.

Results of correlation analysis showed the correlation of individual traits. Table 2 shows the matrix of correlation coefficients.

In the tested set during 1998-1999 positive strong correlation appeared between the traits, as follows:

- time to maturity and height of setting the first pod.
- plant weight and the traits: number of pods per plant, number of seeds per plant and seed weight per plant.
- number of pods per plant and the traits: number of seeds per plant, seed weight per plant and resistance to lodging.
- number of seeds per plant and the traits: seed weight per plant and yield.

Negative strong correlation appeared between the traits:

- height of setting the first pod and number of seeds per plant.
- height of setting the first pod and the traits: plant weight, number of pods per plant and seed weight.

Table 2. Selected correlation coefficients between the evaluated traits of grass pea (1998 - 1999)

		PH	LP	PW	PP	SP
Plant height	**PH**					
Height of lower pod	**LP**	0.53**				
Plant weight	**PW**	-	-0.36 *			
No. pods/plant	**PP**	-	-0.39 *	0.95**		
No. seeds/plant	**SP**	-	-0.56**	0.88 **	0.89**	
Seed weight/plant		-	-0.42 *	0.95**	0.88**	0.88**
TGW		-	0.40*	-	-	-0.26
Yield		-	-	-	0.13	0.43 **
Lodging resistance		-	-	0.37 *	0.46 **	0.34 *

* significant at P<0.05, ** significant at P<0.01

Table 3. Correlation coefficients between principal components (PC) and the set of traits.

Trait	PC1	PC2	PC3	PC4	PC5
Plant weight	0.97*	0.08	0.08	0.08	0.01
Weight of seed/plant	0.97*	-0.04	0.08	-0.04	0.11
Number of pods/plant	0.96*	0.13	-0.03	0.17	0.05
Number of seed/plant	0.93*	-0.02	-0.29	0.05	-0.43
Plant height	-0.07	0.85*	0.15	-0.09	-0.07
Resistance to *Fusarium*	0.01	0.67*	-0.06	-0.05	0.00
Resistance to lodging	0.36	0.64*	-0.15	0.33	0.19
1000 grain weight	0.04	-0.07	0.94*	-0.09	0.03
Height of the lower pod	-0.50	0.43	0.56*	0.11	-0.30
Protein concentration	0.10	0.02	0.05	0.90*	0.03
Stand	-0.07	0.02	0.47	-0.61*	0.18
Time to maturity	0.12	0.30	-0.04	-0.18	0.75*
Yield	0.20	0.30	-0.06	-0.13	-0.67*

* significant at $P<0.05$

Five principal components were obtained. Correlation coefficients between the five principal components (PC) and the set of characters are given in Table 3. Table 4 shows variance of individual components and their cumulative contribution (%) to the total variance.

As can be seen in Table 4, the five principal components explained approximately 80% of the total variance. In spite the fact that the evaluated samples did not show strong variability and clusters created by cluster analysis showed no significant differences, four small different groups can be separated (Fig. 1).

The formed groups varied mainly in plant height, height of setting the first pod and seed size. The average values of the evaluated traits in individual groups of grass pea sets are given in Table 5.

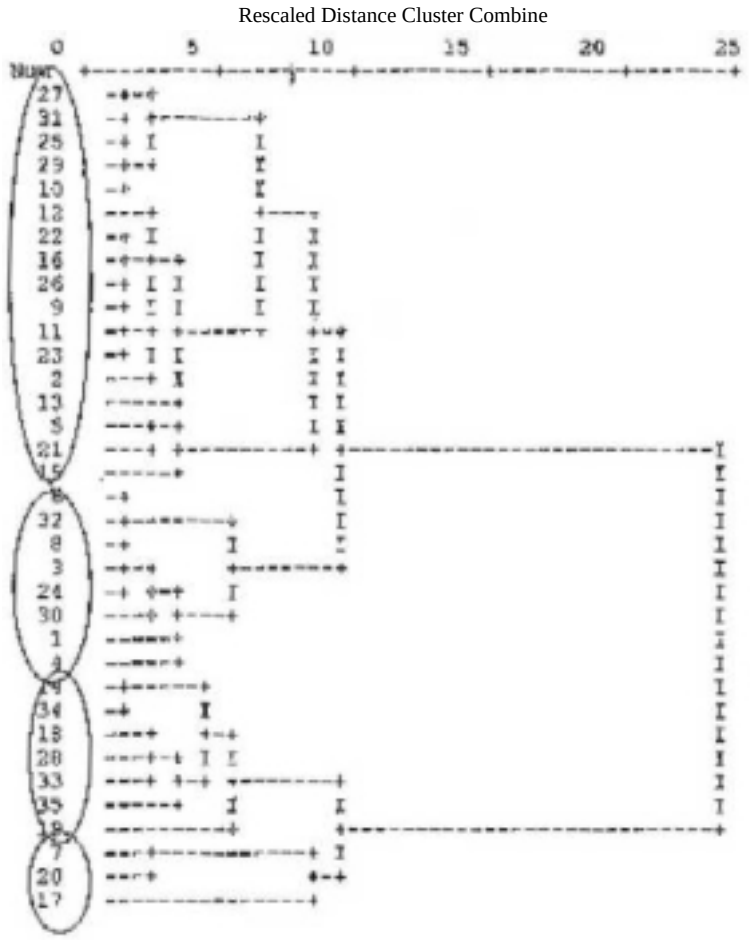
Table 4. Variance of principal components (PC) and the cumulative contribution to the total variance.

Component	Variance (%)	Cumulative variance (%)
PC1	31.5	31.5
PC2	15.1	46.6
PC3	12.0	58.6
PC4	10.8	69.5
PC5	9.1	78.6

Table 5. Means ± standard errors for plant traits of the 4 clusters (see Fig. 1).

Traits	Cluster			
	I.	**II.**	**III.**	**IV.**
Time to maturity (d)	126.88±0.24	126.88±0.35	126.57±0.43	127.0±0.58
Plant height (mm)	865±14	781±15	852±29	858±9
Height of lower pod (mm)	257±6	232±10	231±8	221±12
Plant weight (mm)	28.5±0.8	28.6±1.0	36.7±1.2	42.8±4.7
Number of pods/ plant	24.8±0.6	24.8±0.8	33.7 ±1.5	36.8±4.3
Number of seeds/ plant	47.9±1.7	50.4±1.9	66.7±3.1	70.8±7.6
Weight of seed /plant (g)	13.2±0.4	13.5±0.8	16.9±0.6	21.2±1.9
1000 seed weight (g)	294±5	282±5	263±10	313±11
Yield ($t.ha^{-1}$)	4.09±0.06	3.98±0.15	3.98±0.21	3.87±0.47
Resistance to lodging	4.8±0.2	4.0±0.2	5.4±0.2	4.7±0.4
Stand	7.6±0.1	7.4±0.1	7.0±0.1	8.0±0.2
Resistance to *Fusarium*	8.2±0.03	8.0±0.1	8.2±0.1	8.0±0.2
Protein concentration (%)	25.8±0.2	25.6±0.2	26.4±0.2	26.0±0.6

Fig. 1. Phenograph of the tested traits, created by the cluster analysis. Num denotes the individual genotypes, 35 is of Syrian origin. Clusters I to IV in order moving down the page.



Discussion

At present there is little data about this nearly "forgotten" crop. The evaluated set contained mainly landraces and one genetic resource of Syrian origin. Thus the set was quite homogenous. During a 2 year period we found that the Syrian genetic resource had the lowest value of 1000 seed weight (TGW) and the lowest yield. This is in agreement with Gáborcík [(4)] who found that TGW of Slovak genotypes was up to twice as high, with yield 1.4 times greater, than foreign genotypes. We found positive correlations among the number of pods per plant and the traits: number of seeds per plant and plant weight, which corresponds with the results of Cambell [(1)], according to his statement that seeds of high weight have set more pods per plant. Number of seeds per plant correlated with the seed yield, which again agrees with results of Cambell [(1)]. The genotype H-17 was markedly different to the others. Although it was not tall, it showed the highest values of yield, seed weight per plant, number of seeds and number of pods per plant.

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