# A glance on the phenotypic diversity among pea (*Pisum sativum*) local genotypes in Albania

# G. Sallaku, T. Nasto and A. Balliu

Department of Horticulture and Landscape Architecture, Agricultural University of Tirana, Tirana, Albania.

#### Abstract

Twelve Albanian local pea genotypes (Cekin, BG14106, BG14005, BG25 1013, BG250906, BG13803, BG251120, BG13702, BG250805, BG14207, BG250701, BG143000) were planted during the spring of 2014 for characterization purposes. The seeds were first sown in polystyrene trays in a non heated greenhouse and after full germination twenty selected plants of each genotype were transplanted in individual single rows in open field. The phenotypic characterization was conducted according to IBGRI descriptors and significant phenotypic variation was found regarding the number of nodes up to first fertile node, days to flowering, number of seeds per pod and the weight of 100 seeds. There were several promising genotypes regarding specific traits such weight of 100 seeds (Cekin and BG 143000), and earliness (BG 14005 and BG 143000) which should be further evaluated and might be used in future breeding programs.

Keywords: growth model, days to flowering, flower's color, seed shape

## **INTRODUCTION**

Pea (*Pisum sativum* L.) belongs to the Leguminosae family, which has an important ecological advantage because it contributes to the development of low-input farming systems by fixing atmospheric nitrogen. Furthermore it serves as a 'break crop' in crop rotations which further minimizes the need for external inputs. Dry pea currently ranks second only to common bean as the most widely grown grain legume in the world. Pea seeds are rich in protein (23-25%), slowly digestible starch (50%), soluble sugars (5%), fiber, minerals and vitamins (Smýkal et al., 2012).

Grain legumes were fundamental crops at the start of the 'agricultural revolution' which facilitated the establishment of permanent settlements. Subsequently, during centuries of selection and breeding, thousands of pea cultivars were developed. Plants in agriculture have been additionally subjected to thousands of years of selection and breeding for traits desirable for cultivation or consumption by people or domesticated animals. Initially, wild plants carrying promising traits for cultivation were selected, leading eventually to locally adapted landraces that had lost many allele combinations that were disadvantageous to the farmer (e.g., dehiscent pods and thick testas) and gained useful ones such as increased seed size. Modern breeding has largely continued this process by crossing the 'best with the best' and the increase in yield and performance are still being maintained today. Unfortunately, this strong selection has narrowed the genetic diversity of cultivated germplasm (Jing et al., 2010). However, a considerable level of genetic variance among peas of diverse origin has been reported by some breeders (Umar et al., 2014).

The genetic diversity of landraces is thought to be the most valuable economic component of global agro-biodiversity and is considered of paramount importance for future world production (Singh et al., 1991). The genetic diversity of species is the outcome of cumulative mutation, recombination and selection on individuals by the environment. The characterization of landraces is the first step towards the classification of crop germplasm (Nisar et al., 2008). It allows quantification and structuring of genetic variability of the germplasm which is of great importance for pre breeding, and the conservation of genetic diversity and variability (Pereira et al., 2009).

The aim of this study was the characterization of several local pea genotypes in



Albania based on their phenotypic traits, in order to identify the most promising ones for the most valuable traits.

### MATERIALS AND METHODS

The experiment was conducted in the spring 2014 in the experimental farm of Agricultural University of Tirana, Albania (41°21'35" N, 19°46'28" E). For that purpose, twelve different local accessions of pea (*Pisum sativum*), were included in the experiment: (1) Cekin, (2) BG14106, (3) BG14005, (4) BG25 1013, (5) BG250906, (6) BG13803, (7) BG251120, (8) BG13702, (9) BG250805, (10) BG14207, (11) BG250701, (12) BG143000.

The seeds of selected genotypes were first sown in pyramidal polypropylene trays in a non heated greenhouse and then, after the first true leaves were appeared 20 healthy plants of each genotype were transplanted in open field, in individual single rows. The planting distances were 60×15 cm. Common local production practices applied during the growing season; no chemical fertilization was supplied and no chemicals were used against potential diseases or pests.

The phenotypic characterization was conducted according to IBGRI descriptors for several traits including: days to flowering (no. of days from sowing to the stage when 10% of plants flowering), flower colour, 100 seeds' weight, shape of seed (sferical, ovoid, cylindrical, rhomboid, triangular, irregular), seed – black colour of hilum (absent, present), seed – color of testa (redish-brown, brown, brownish-green), growth type (determinant, indeterminant), number of nodes up to and including first fertile node, maximum number of flowers per node, pod – degree of curvature (absent or very weak, weak, medium, strong, very strong), pod – type of curvature (concave, converse), pod-number of ovules, pest and disease sensitivity.

The best genotypes of each individual trait were identified and recommended for further evaluation (Table 1). The respective dendrograms, calculated as hierarchical cluster of a multivariate dataset based on dissimilarities, were performed for 'days to flowering' and 'weight of 100 seeds' with the help of the on-line Free Statistics Software (Wessa, 2014). Based on that, groups of genotypes with similar characteristics were identified.

Range	Accessions of best performance
6.8-31	Cekin, BG143000, BG14005, BG 13803
7-27	BG 14005, BG 143000, BG 250906, BG 13803
1-2	BG 250906, BG 13803, BG 14106
4-8	BG 14207, BG 250805, BG 250701, BG 143000, Cekin
	Range   6.8-31   7-27   1-2   4-8

Table 1. List of pea genotypes with the best performance for some of evaluated traits.

### **RESULTS AND DISCUSSION**

For most of analyzed traits, the phenotypic variation of characterized genotypes was broad. In a very high frequency (83,3%), Albanian local genotypes of *Pisum sativum* were indeterminate (Table 2), and mostly characterized by a good growth vigor. The only determinant genotypes were BG 251013 and BG 250906.

Since earliness is a highly important trait, the identification of early genotypes was a priority. Considering that the earliness of a certain pea genotype will be determined by the combination of several traits (number of nodes up to first fertile node, the flowering time and length of maturity period of settled pods) attention was paid to identify the best genotypes of each above traits. Indeed, the number of leaves up to first fertile node was largely different, varying from 7 to 27. BG 14005 had the smallest number of nodes up to first fertile node, followed by BG 143000. Despite that, the earliest flowering genotype was BG 143000 (number 12 in the dendrogram) which set flowers 70 days after sowing, followed by BG13803 (6; 71 days) and BG14005 (3; 73 days) (Figure 1). The latest flowering genotypes were BG251013 (93 days after sowing) and BG14207 (91 days after sowing), represented by numbers 4 and 10 in the respective dendrogram of flowering time (Figure 1).

Traits	f	Percentage
Seed – black colour of hilum		
Absent	10	83.3
Present	2	16.7
Shape of seed		
Spherical	8	66.7
Irregular	4	33.3
Seed – color of testa		
Reddish brown	0	0
Brown	4	33.3
Brownish green	8	66.7
Seed – Violet or pink spots on testa		
Absent	7	58
Faint	0	0
Intense	5	42
Growth model		
Indeterminate	10	83.3
Determinant	2	16.7
Flower color		
White	2	16.7
Purple	10	83.3
Pod – degree of curvature		
Absent	1	8
Weak	11	92
Pod – type of curvature		
Concave	12	100
Convex	0	0
Stipule – type of development		
Rudimentary	0	0
Well developed	12	100

Table 2. The distribution frequency (f) of several qualitative traits of pea genotypes.



Figure 1. The dendrogram of 'days to flowering' trait of local pea genotypes.



BG14207 and BG13702 were the genotypes with the longest vegetation period, continuing to grow and flower also during the hot days of summer when the rest of genotypes were completely dry. Because of that, they should be considered as potential genotypes in dry agriculture.

The weight of 100 seeds ranged from 6.8 to 31 g. 'Cekin' (1) had the highest weight of 100 seeds (31 g), followed by BG 143000 (12) with 25.2 g 100 seeds<sup>-1</sup>. The lowest seed weight was found in BG 250906 (5) with 6.8 g 100 seeds<sup>-1</sup>. Both them, along with BG14106 (2), BG14005 (3) and BG13803 (6) were all included in the same group of dendrogram (Figure 2). The rest of genotypes with smaller seeds were also grouped together in another branch.



Figure 2. The dendrogram of 'weight of 100 seeds' trait of local pea genotypes.

The differences among the characterized genotypes regarding pod curvature degree, intensity of pod green color, and stipule development were not significant. All genotypes were characterized by concave pods with week curvature (92% of analyzed genotypes, Table 2). Meanwhile, the most common seed shape was regular (66.7%, Table 2). Still several genotypes (BG251013, BG251120, BG 250701, BG 143000) were characterized by irregular seed shape. Black color of helium in seeds was absent, except in BG 251013 and BG 143000.

Seed color was highly diverse among the characterized genotypes, but dominated by brownish green (66.7%, Table 2). More concisely, 'Cekin' was light brown, BG 14106 brown, BG 14005 light brown, BG 251013 dark brown with spots, BG 250906 green with brown spots, BG 13803 green with spots, BG 13702 brownish green, BG 250805 green with brown spots, BG 14207 brownish green, BG 250701 brownish green with spots and BG 143000 dark green with spots.

The differences regarding the sensitivity to Powdery mildew (*Erysiphe polygoni*) have also been detected. The most sensitive genotype was BG 14005. Meantime, BG251013, BG250906, BG13803 and BG13904 were moderately infested, while BG13904 and BG 13702 showed no sign of infestation.

#### **CONCLUSIONS**

The phenotypic variation of locally grown Albanian pea genotypes is large. There is a large diversity regarding the number of nodes up to first fertile node, number of days to flowering, number of seeds per pod and the weight of 100 seeds. There are few promising genotypes regarding specific traits such as weight of 100 seeds ('Cekin' and BG 143000), and earliness (BG 14005 and BG 143000) which might be further used in potential breeding programs.

#### ACKNOWLEDGEMENTS

This results are part of the work conducted in the framework of EUROLEGUME Project (Enhancing of legumes growing in Europe through sustainable cropping for protein supply for food and feed), founded by 7<sup>th</sup> Research Framework Programme of the European Union (FP7 Research Project No. 61378).

#### Literature cited

Ghafoor, A., Ahmad, Z., and Anwar, R. (2005). Genetic diversity in *Pisum sativum* and a strategy for indigenous biodiversity conservation. Pak. J. Bot. 37 (1), 71-77.

Jing, R., Vershinin, A., Grzebyta, J., Shaw, P., Smýkal, P., Marshall, D., Ambrose, M.J., Ellis, T.H., and Flavell, A.J. (2010). The genetic diversity and evolution of field pea (*Pisum*) studied by high throughput retrotransposon based insertion polymorphism (RBIP) marker analysis. BMC Evol. Biol. *10* (1), 44 http://dx.doi.org/ 10.1186/1471-2148-10-44. PubMed

Nisar, M., Ghafoor, A., Ahmad, H., Khan, M.R., Qureshi, A.S., Ali, H., and Islam, M. (2008). Evaluation of genetic diversity of pea germplasm through phenotypic trait analysis. Pak. J. Bot. 40 (5), 2081–2086.

Pereira, T., Coelho, C.M.M., Bogo, A., Guidolin, A.F., and Miquelluti, D.J. (2009). Diversity in common bean landraces from south Brazil. Acta Botanica Croatica *68*, 79–92.

Singh, S.P., Gepts, P., and Debouck, D.G. (1991). Races of common bean (*Phaseolus vulgaris*, Fabaceae). Econ. Bot. 45 (3), 379–396 http://dx.doi.org/10.1007/BF02887079.

Smýkal, P., Aubert, G., Burstin, J., Coyne, C.J., Ellis, N., Flavell, A.J., Ford, R., Hýbl, M., Macas, J., Neumann, P., et al. (2012). Pea (*Pisum sativum* L.) in the genomic era. Agronomy 2 (4), 74–115 http://dx.doi.org/10.3390/ agronomy2020074.

Umar, H.M.I., Ur-Rehman, Sh., Bilal, M., Naqvi, S.A., Manzoor, S.A., Ghafoor, A., Khalid, M., Iqbal, M.T., Qayyum, A., Ahmad, F., and Irshad, M.A. (2014). Evaluation of genetic diversity in pea (*Pisum sativum*) based on morphoagronomic characteristics for yield and yield associated traits. Journal of Biodiversity and Environmental Sciences 4 (5), 321–328.

Wessa, P. (2014). Free Statistics Software, Office for Research Development and Education, version 1.1.23-r7. http://www.wessa.net/.

