UDC: 635.651:575.21(497.7)
Original scientific paper

THE EVULATION OF PHENOTYPIC VARATION OF NATIVE POPULATIONS OF THE BEAN IN MACEDONIA

Xhezair Idrizi, Xhabir Abdullahi, Gafur Xhabiri, Durim Alija

University of Tetova
Email: xhezair.idrizi@unite.edu.mk

Abstract

The genetic variation is a raw material for the improvement of plants and one of the important components of every ecosystem or agricultural system generator (Pham 2000). Using this we can come to the development of lines, hybrids, the improvement of population, the development of synthetic cultivars with high frequency of desirable genes for yield, quality and resistant towards environmental stresses. As much as diversified is the spectrum of genetic variation, the higher is the frequency of desirable genes manipulation in the genetic backgrounds of the new appearance of plants. (Saavedra, 2002). The genetic plant variation can be accounted in the phenotypic and molecular level using different methods and techniques (Wouw 1999, Kearsey 2000). The amount of phenotypic variation is important not only in using breeding programme for the improvement or development of new genetic make-up of plants, but also for better understanding the role of flora in a practical and useful environment. Practically, the evaluation of phenotypic variation is simpler than the evaluation of molecular variation. Even if the morphological variation is highly influenced by the environmental conditions, it doesn't give a clear scene of the real genetic variation that exists among and between different genotypes of a population, and morphologic markers are used for the characterization of germplasm. For identification of genetic variation are used different methods. All of them are based on the differentiation of polymorphisms that exist between different genotypes. Either these polymorphisms might be qualitative or quantitative. Usually the phenotypic plant variation is assessed to rank and weigh or quantify phenotypic differences that exist between individuals of a population, between and among species. Through the estimation of phenotypic variation, genotypes are classified in different groups in order to facilitate the planning of crossing among plants in a breeding programme. The need of genetic diversity is increasing as is the need for food. It is also essential for a sustainable development of agriculture which adapts according to the environmental alternation, and continuous functioning of biosphere regarding mankind survival. As the other plants, existence of genetic variation in the bean is an important component for a successful programme application for genetic development that aim the improvement for characters as the number of beans per pod, protein content, resistance to drought and other environmental stresses. This study aims to identify genetic diversity of native bean populations using morphological polymorphisms, as well as their relation will be determined through the different statistical analysis, creating the possibility of estimation of their evolutive and philogenesys history.
The Pollog area is opulent with genetic bean resources. Its geographic position, climate and the landscape have enabled this zone the cultivation of autochthon plants a long time ago, not only for genetic development but also for the cultivation of different agricultural plants. Owing to good and edaphically climate as well as the microclimate and habitat of this zone, the genetic variation can be easily detected by local farmers. In this study, the most important is the evaluation of genetic variation between the local varieties for agronomic traits. The target of this study generally is based on the evaluation of the collected populations in the field conditions.

Keywords **:** phenotypic variation, hybrids, geographic position, environmental stresses

1. Plant material and methods

As a plant material of this research are used 22 autochthon populations of bean with an early, secondary and dilatory cycle, collected in Pollog area, generally in the villages and suburbs of Tetova, Skopje and Gostivar (fig.1). As we can see in the figure below, most of the population (63.6%) are collected in the areas of Tetova.

The research for the realization of this study is focused on the evaluation of the autochthonous population of beans in field conditions. The region where the collection is conducted is approximately 450-500m above sea level. The air average temperature in the Pollog's area is 11.3°C.

The highest temperatures are recorded in August (average temp. of air is 22.2°C), and the lowest temperature is recorded in January (with average temp. of air 0.3°C). The average amount of rainfall in Pollog area is 700-1000 mm per annum, but the most of the rainfalls are in autumn and winter seasons and less in summer time. The soil is of deep subsoil, full of nutrient, as well as necessary microelements for normal growth and breeding of the bean crop. The trials are conducted in the plots of the Xhepçishte village (Pollog area). Precautions of the vegetables are done being based on the cultivation technology of this plant.
For the estimation of the genetic diversity existing between and within the collected autochthon bean populations are used several descriptors (Villa 2006, Hazekamp 2000), taking into account: the sowing date; the number of days until sprout, the leaf color in three stages of growth; the leaf shape; the leaf durability; the stem diameter; the stem length; the stem shape; the vegetable type; the number of days until flowering; the flowering duration; the number of flowers per plant; the color of flowers; the size of the flower bud; the shape of the pod; the thickness of the pod; the pod width; the length of the pod; the color of the (immature) pod; the color of the mature pod; the number of the days while harvest maturity; the number of days while physiological maturity; the droop of the pod; the number of the pods per plant; the number of the beans in pod; the beak shape of the pod; the beak length in mm; the position and orientation of the pod's beak. As morphological characteristics of the seed evaluated are: the shape of the seed; the color of the seed peel (film); the brightness of the seed peel; the weight of 1000 seeds; the length of the seed in mm; the width of the seed in mm; the thickness of the seed in mm and the ratio length: width. For every character, measurements are made in 10 plants within the variant and the average is computed, which is used not only to estimate the differentiation among the populations, but also for statistical analysing genetic variation models.

The elaboration of data for the identification of the variation source for each feature is made one-way variance analysis. The analysis of data is based on the scheme of the complete random block, using some different statistical softwares for elaboration of data in order to specify and alleviate their interpretation (Sobral 2000).

2. Results and discussion

According to the autochthonous populations of the white bean in Pollog area it comes to a conclusion that the populations differ a lot from each other in many characters with agronomical importance. It is thought that huge roles have played the factors of the external ambient of the microclimatic zones in which place they are cultivated, as well as the selections of the farmers living in the local areas. The areas in where these populations are cultivated have different climatic and edifice amplitudes as well as in some ways they are isolated from each other throughout geographical barriers. As these populations are specific for particular areas, their exchange or transferral to other growing areas of this territory did not happen or it happened but in a small amount that were unable to cause big recasts in genetic vectors of the phenotypic variation.

The evaluation of the phenotypic polymorphisms for plant and grains descriptors. Considering the phenotypic polymorphisms, it is possible to make the differentiation of the autochthonous bean populations (Toll, 1995). As a result of the variance analysis, it proves that there are genetic differences confirmed by statistical way for plant's characters (Tab. 1) among the bean populations.

Tab.1 The variation analysis for plant's features.

Variation source	Square sum	Degree's at large	Square average	Score F.	Table F.
The populations	1579.91	12	131.66	1.93	1.89
The features	190004.1	6	31667.35	392.40	2.23
Lapse	5010.59	72	67.90		
sum	197394.6	90			

Also for the kernel descriptors ensues a genetic variation confirmed by statistical way, offering more chances for the breeders of this plant, to manipulate slightly and successfully the characters of the plant, which are very important for the cultivating aspect as well as refining.

Tab.2 The variation analysis for grains characteristics

Variation source	Square sum	Degree's at large	Square average	Score F.	Table F.
The populations	321306	12	26775.48	2.04	1.87
The features	5608137	7	801162.4	61.18	2.12
Lapse	1099923	84	13094.32		
Sum	7029365	103			

Also there are observed a lot of phenotypic distinctions for the characters separately taken. The characters with the bigger variations (tab.1), such as the number of the kernels per plant, the weight of 1000 kernels, the product and the number of pods create more chances for the breeders of this plant to create different or mediatorial ways of markets of the new genetic off-springs. But other characters such as the stem diameter, the number of the flowers per plant, the thickness of the seed, doesn't show a big breeding potential, apart from the aspect that such characters do not show any special interest for plant's breeders.
One of the characters, which represents one of the objectives of the breeding programme of the bean for the improvement of the product's components, is the number of the kernels per pod (Swami Nathan 2002, Li, etc., 1998). According to elaboration of the outcome data throughout the evaluation of this character from the collected populations ensues that there is no genetic difference which could be considered by the breeders. Also, for the improvement of this character, the collected populations do not show any special value from the individual point of view, therefore, the breeders have limited chances if they use as a genetic material in their programme only these populations.

Table 3. The variations for the major characters

No	Features	Variant
1	Vegetative Cycle	93.677
2	Log's diameter	1.019
3	Number of bines per flower	1.450
4	Pod's length	4.418
5	Pod's width	7.192
6	Pod's number	618.847
7	Grain's number per pod	1.108
8	The weight of 1000 grains	34410.9
9	Grain's length	17.340
10	Seed's thickness	1.258
11	Grain's width	3.450
12	Pod's	2.994
13	The production	24975.6

Tab.4 The coefficients of the correlations for the plant's characters

Features	Veg.cycle	Log's diam	No.bine p.fl.	Stub's length	Stub,s width	Stub,s thickness	Stub,s no
Veg.cycle	1						
Log's diam	0.599	1					
Nr.of bines per Fl.	0.543	0.32	1				
Stub's length	0.756	0.46	0.390	1			
Stub,s width	0.487	0.83	0.519	0.47	1		
Stub,s thickness	0.418	0.72	0.386	0.54	0.85	1	
Stub,s no	0.298	-0.05	0.464	0.00	0.06	-0.02	1

The evaluation of the relationship between plant and seed characters. On behalf of the usage of the autochthon populations in the programs of bean breeding is the exploration of correlations between some major characters (Tab.4 and 5). In general, the correlation coefficients for plant's characters prove positively but the correlations are not so strong excepting the correlative links between pod's length and vegetative cycle, the pod's width and the diameter of the stem as well as the thickness of the pod and the log's diameter and thickness of the pod and the width of the pod. In the programs of breeding which aim the improvement of the vegetative cycle is helpfully to take into consideration the length of the pod; in order to abbreviate the vegetative cycle, we have to select the plants with short pods because the correlative linkage between these two characters is positive.

In general, the correlative relations among the seed's characters ensues weak excepting the correlative linkages between the production and weight of the 1000 kernels and the production and thickness of the seed. Even though it is not a strong linkage, it is assumed that also the linkage between the seed's thickness and length could be taken into consideration during the explorations and breeding of this crop plant. It ensues from the table 5 that if the breeders aim the production's expansion of the white bean by using in their programs for genetical improvements genetic autochthon materials of Pollog area, their program's priority or objective have to be the weight of 1000 kernels.

Tab.5 The coefficients of the correlations for the kernel's characters

The features	Nr. of grains. per plant	The weight of 1000 gr.	Length	width	thickness	Therep. Thick. /width	Produc
Nr. of grains. per plant	1						
The weight of 1000 gr.	0.61	1					
Length	0.09	0.08	1				
Width	0.07	0.21	0.18	1			
Thickness	-3	0.18	0.57	0.48	1		
Therep. Thick. /width	0.10	-0.23	-0.37	-0.20	-0.42	1	
Production	0.41	0.76	0.47	0.39	0.66	-0.36	1

4. Conclusion

Pollog area is rich in genetic variation of autochthonous white bean, which comprises a valuable genetic resource for the breeding and cultivation of this crop plant.
The greater genetic variation exists especially for quantitative characters and, mainly for the production and its components.
Most of the populations could be used as parental components in various schemes of genetic improvement, not only for the white bean cultivation with high productive capacity, but for the improvement of those that already exist in local area.

References

[1]. Hazekamp Th. (2002) The potential role of passaport data in convervation and use of plant genetic resources. In: Engles JMM, Ramanatha Rao V, Brown AHD, Jackson MT(eds.) Manging plant genetic diversity. CABI Publishing, Wallingford UK. pp,185-194
[2]. Kearsey MJ (2000) Genetic resources and plant Breeding.175-2000
[3]. Li Y.J Wang, Y Cao, W Gao, J Fang&Xizhi Lou91998) The Use of genetic resource in corp improvement: Lessions from China. Genetic Resources and corp Evulation 45:181-186
[4]. Salillari, A. Hoxha,S.2003, Gjenetika , Tiranë.
[5]. Salillari, A.Rapo,P. Hoxha, S.Demiri, H.1998 Eksperimenti shkencor; Tiranë.
[6]. Idrizi Xh.Studimi i variacionit gjenetik të popullatave të fasules të koleksionuara dhe vlerësuara nëpërmjet markerëve morfologjik" Dizertacion, 2008, Tiranë
[7]. Hoxha S.Idrizi Xh, Hoxha A.(2010):Resurset gjenetike të bimëve, Tetovë
[8]. Salillari A. Hyso M.Fasllia N. Rusinovci I.(2007): Resurset gjenetike, Tiranë.