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ESTIMATION OF GERMINATION POSSIBILITIES OF SOME PEAS STORAGES ACCESSIONS AND THE EVALUATION OF SOME QUALITATIVE INDICATORS ON ALBANIAN PLANT GENE BANK

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Abstract

The study of seeds stored in the gene bank includes 12 different genotypes of peas (*Pisum sativum*). The study was conducted at the testing laboratory of Albanian gene bank on the sample of 100 seeds, placed in 4 repetitions, for two years (2010-2011). The study analyzed descriptors: the energy and power of germination, plant coloring antocyanins (presence or not) and color of the floral sheets. Assessment of life skills of peas seeds stored in the collection of genus *Pisum* is done in accordance of ISTA standards. Results represent different levels of germination ability. The variance analysis indicates the existence of differences between pea forms validated indicators analyzed in the study. Comparisons between their average values of each indicator obtain in the study, using Student test (for t = 2.17881 and α = 0.05) express differences between and within genotypes proved to $P_{0.05}$ and $P_{0.01}$ levels of probability. Results with cluster method rank the genotypes of pea's distances in several distinct groups among them. It is evident a strong positive correlative (0.8971) between the germination energy and power of peas seeds. Results are with interest for evaluation and characterization of peas in the gene bank.

Key words: accessions, gene bank, life skills, collection, descriptors.

Introduction

Genetic resources of forages and legumes have a major contribution to the growth of agricultural food products and livestock nutritional base. Nowadays, the preservation of genetic resources is considered a necessity for human society. Gene banks offer the main means to store plant genetic resources (FAO-IPGRI, 1994). The seeds of pea accessions contained in gene bank are a vital and irreplaceable resource, a heritage which must be conserved to provide future needed genetic pool and useful plant materials to be used by farmers and plant breeders. The collection of pea genetic resources in the Genetic Bank of Albania, meets partially the needs and objectives of an improvement pea program. Therefore, exploration, collection, identification and viability testing of pea collected seeds are the first steps to accept genetic materials into the gene bank. Agro-bio-morphological evaluation in the field is also essential not only for the preliminary evaluation of germplasm but also for the future usage value of

genetic materials stored in gene-bank (Hong & Ellis, 1996). Besides collecting and preservation of local forms and new varieties (wild species less) maintenance of a collection lies in assessing the early time of life skills to their seed accessions stored in the genetic bank and obtain registration information into a usable database. A good database of information on genetic material in long-term preservation, also leads to increased use by farmers germplasm of pea plants and improvers. In this context, testing and evaluation of life skills of plant genetic resources and documenting the results obtained are considered an integral part of preserving plant genetic resources conserved in gene bank (Engels & Visser, 2003; Painting *et al.*, 1993).To recognize and enhance the value of using genetic material of pea, which are stored in the Genetic Bank of Albania, for the present and future, needs testing and study of the life skills sometime accessions of pea seeds, identification of different forms of pea and inclusion of data obtained in the system of recording and genetic bank computerization (Painting *et al.*, 1993). For this reason the study was conducted life skills (power of germination) of some forms of pea stored in gene bank. The purpose of this study is to assess life skills of pea seeds of *Pisum* genus and genetic diversity analysis of native peas germplasm stored in the collection of genetic bank. It is interest to study the recognition of different forms of pea with a lack or limited information, to meet modern standards of pea germplasm database and increase the possibilities of using these forms from the farmers and further programs of genetic improvement him.

Materials and Methods

In the study of life skills of seeds of peas that were stored in the genetic bank includes 12 different genotypes of *Pisum* genus.The study was conducted at the laboratory testing of genetic seed bank on the sample of 100 seeds, placed in 4 recurrences for two consecutive years (2010-2011) (Table 1). During the tests were conducted surveys, assessments, measurement, and analysis of various, photo assessment indicators in the study received.

Table 1. Analysis of plant materials in study of viability of seed of peas

ID	Genotypes	ID	Genotypes	ID	Genotypes
B2	greenfast6000	B7	Carmanovi	B18	WBH1601
B4	coronation	B8	conv.spa.Rusi	B25	nr.5 R.SH
B6	con.val.kopusine	B9	pa emer Rusi	B29	nr.10 R.SH
B6	liliputi	B11	5002-zalsirai	B30	nr.11 R.SH

The indicators analyzed in the study were: germination energy, the power of germination, plant hue - anthocyanins (presence or not) and colorful floral sheets. Assessment of life skills of pea seeds stored in the collection of genus *Pisum* posted by ISTA standards. Results represent different levels of seed viability.

Processing of data for all test environments (locations x years) was made by calculating the average statistics (MSTAT), the analysis of variance with ANOVA, evaluating the distance between genotypes with hierarchical technique Cluster, Ward method (Milligan, 1980).

Productive ability of a plant depends peas set of factors affecting the production (Salillari, 1988), study therefore, to see the effects of interactions of all analyzed indicators were assessed correlative connections between them. Variance calculations, genetic distances and multiple correlation coefficients were made with the program SAS 2009.

Results and Discussion

Results of the study for the analysis of variance and values of the indicators analyzed are summarized in Tables 2 and 3.

Variance analysis indicates the existence of differences between forms of pea validated indicators analyzed in the study. This is confirmed by the actual values for the indicators F^{ve} analyzed, which have resulted in high test levels of probability (Table 2).

Table 2. Analysis of variance for the indicators for energy and power germination of *Pisum* genus

Source Traits	Sum of Squares (df=11)	Error (df= 12)	C. Total (df = 23)	Mean Square Genotypes	Mean square Error	F Ratio	Prob >F
Germin – energy	16805.750	1910.750	18716.500	1527.80	159.23	9.5949	0.000 2
Germin – ability	8744.3021	1210.312	9954.6146	794.937	100.85	7.8816	0.000 5

The value of F' factic to verify for $P_{0.05}$ (*) and for $P_{0.01}$ (**)

Comparisons between their average values of each indicator to obtain the study, using student test (for t = 2.17881 and α = 0.05) express differences between and within genotypes proved to P0.05 and P0.01 levels of probability. Confirmed the presence of differences of averages of indicators has ordered the pea genotypes at different levels, which are expressed by means of letters (a, b, c, etc.). Averages with same letter are not differences between them proved to P0.05 level of probability (Table 3).

Table 3. Comparisons energy averaging indicators - viability and levels of the order of the pea genotypes under analysis with the Student test (t = 2.17881, α = 0.05)

Germination energy			Germination ability		
Genotypes	Mean	level	Genotypes	Mean	level
B30	96.750000	a	B30	97.750000	a
B11	88.000000	ab	B18	93.625000	a
B6	85.500000	ab	B11	92.250000	a
B9	83.000000	abc	B9	91.500000	a
B4	82.500000	abc	B4	87.750000	a
B2	79.000000	abc	B6	85.500000	a
B5	72.500000	abcd	B7	83.500000	a
B7	67.500000	bcd	B2	79.000000	ab
B18	56.500000	cd	B5	76.000000	ab
B8	46.000000	d	B8	59.000000	bc
B29	15.000000	e	B29	48.250000	cd
B25	13.750000	e	B25	34.125000	d

Levels not connected by same letter are significantly different

Distance analysis

To analyze the presence or not of differences between forms of peas, evaluation became genetic distances between genotypes, using Cluster-Ward hierarchical method (PGR Forum, 2003). Analysis and results of all indicators rank genotype distances of peas in three distinct groups among forms (Fig. 1). This presented with features consistent and well distinct from the other genotypes B7 and B18 involved in the first cluster, genotypes B4, B11 and B30 involved in second cluster of genotypes B25 and B29 and the third cluster

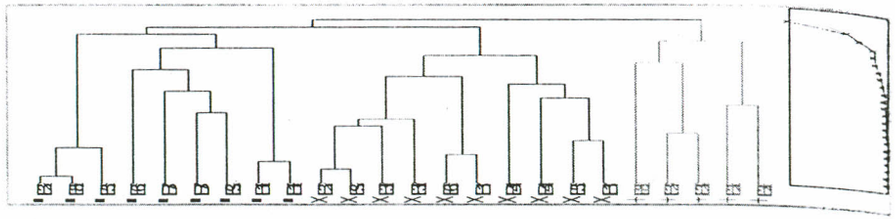

Figure 1. Dendrograma the appearance of distance and clusters of pea genotypes

Genotypes B2, B5, B6 and B9 in the cluster also included the first and second display changes in the results analyzed in two stages: energy and power of germination. This can be explained by the state not fully genotypic stabilized of these forms of peas.

Analysis correlative links

Seen a very strong positive correlative (r = 0.8971) between the two indicators: energy and power of germination of seeds germination of peas. The presence of this very strong positive link between the two phases of germination (red rings of compressed and stretched with the most points in their (Fig. 2) demonstrates the importance of the first phase of germination of seeds and legumes in general and the pea particular. To this stage environmental conditions must be optimal because this is the time when the expression is the potential or the energy to sprouted seeds.

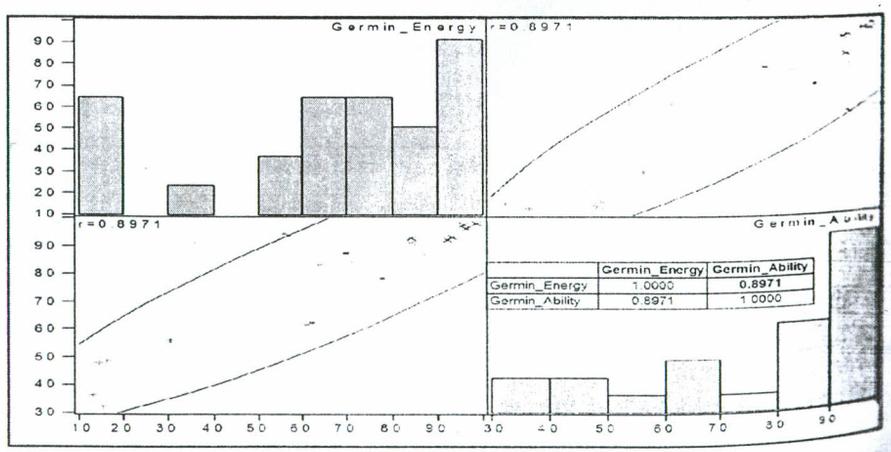

Figure 2. Scatterplot Matrix and Multivariate Correlations between Germination Energy-Ability

The study links correlative, strong positive linear and express different impacts depending on the indicators between them. The survey data for these features are consistent with studies of many other authors (Kramer. 1956).

General information on the multiple links between indicators correlative pea, "database" is a necessary recognition of its germplasm stored in gene bank. A study and attachment combination correlative, genetic distance with heritage features is the mechanism of success in implementing a program of the pea plant Wes (PGR Forum, 2003).

Study results have an interest in identifying, evaluating and characterization germplasm of the peas that are stored in the genetic bank, thus increasing the information database of genus *Pisum* and opportunities of using this information to further remedial programs pea.

Conclusions

Analysis of variance and comparisons of all the averages, the Student test (t = 2.17881 and α = 0.05), proved that between and within genotypes of pea there is a wide variability for the entirety of the studied traits.

Through the comparisons of averages, and genetic distances correlative multiple connections, the study provided important scientific information for the recognition, evaluation and characterization of 12 different genotypes of pea stored in gene bank. Analysis of student test averages with and dendrograma cluster of pea genotypes grouped into three distinct groups among them.

The study correlation very strong link between energy and power positive germinated seeds shows that it is the first phase of defining the germination energy for which environmental and testing conditions should be optimal. Study and the combination of link correlation, genetic distances with heritage features is the mechanism of success in designing and implementing an improvement program of the pea plant.

The study did assess the genetic diversity of native germplasm peas stored in the collection of genetic bank and general information that the study provides a' 'database" is necessary for its germplasm recognition.

Results of the study are of interest to meet contemporary standards of a database of genus *Pisum* germplasm increasing opportunities to use these forms to further programs of genetic improvement of pea.

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