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THE VARIABILITY OF PROTEIN CONTENT IN SOYBEAN *GLYCINE MAX* (L. MERR.) GENOTYPES IN A.R.D.S. TURDA COLLECTION

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Abstract: *The soybean protein is the only complete and available source of vegetable protein. The protein content of grains is a polygenic asset controlled by additive gene action; it ranges depending on the genotype, precocity and environmental conditions; thus, early varieties have higher protein content (35-45%) than the late varieties (30-40%). Early wild varieties are with 5-7% richer in proteins, serving as a source of germplasm for the improvement of protein content. The identification and selection of combinations in transgressive positive segregate generations demonstrated that it is possible to improve this objective. By the artificial induction of mutations have been identified forms high in protein. The objective of this work was the study of the soybean genotypes variability in ARDS Turda germplasm collection regarding the protein content, entirely and grouped according to some morpho-physiological characters. The research has conducted at Agricultural Research and Development Station Turda, in the experimental field of the Leguminous Breeding Laboratory, between the years 2007-2010. It has been studied the soybean germplasm collection from ARDS Turda, that includes 38 lines and native varieties (15.8%) and 202 lines and foreign varieties (84.2%). For the determination of protein and oil content, 50g of grains were weighed for each sample, then were crushed with laboratory mill; the flour resulted was examined using NIR analyzer, Dickey-John brand, INSTALAB 600 type. The statistics index that best characterize the variability of protein content are the arithmetic mean, the standard deviation, the amplitude of variation, the coefficient of variation. The highest protein content registered to the soybean genotypes with shorter vegetation period, with violet flowers and brown pubescence. The genotypes notice for their high protein content and that can be use as sources of germplasm in the breeding processes were disposed between the average protein content and the upper limit of the string variation (42.3% and 47.2%).*

Key words: *soybean genotypes, protein content, the color of flowers, the color of pubescence, the vegetation period, variability, statistical parameters.*

INTRODUCTION

Soybean is the most important source of vegetable protein known by humanity (33-49%); it is also one of the most inexpensive and handy protein sources available, especially in developing countries. Therefore, it is very important in protein deficit remedy resulted from food diets (IDRISA et. all, 2010). The soybean protein is the only complete and available source of vegetable protein. Due to the numerous roles that it plays in the organism, this can be consider the most important macronutrient for the human body, capable to satisfy daily demand protein for kids, adults and people with special diets like vegetarians or those with lactose intolerance.

The vegetarians appreciate for a long time the soybean products for their high protein content, as well as for their quality and digestibility. The digestibility of protein has been defined as the proportion of ingested protein that has been absorbed. The true digestibility of soybean proteins is 97%, comparable to others high quality proteins such as milk, meat and eggs, that ranges between 94 - 97%. Other plant proteins have lower digestibility (SOLAE, 2009).

The improvement of soybean protein content is a primary goal of breeding programs. The researchers from the University of Missouri used the germplasm from Nepal as well as an exotic improvement source of the protein and amino acids content from soybean varieties. It is encouraging that the level of amino acids in proteins is variable in nature, offering the possibility of changing it without a structural and functional major impact on the plants (KRISHNAN et al., 2006).

The grain protein content is a polygenic asset controlled by the additive gene action. The protein content varies with the genotype, precocity and environmental conditions. Thus, the early varieties have a higher protein content (35-45%) compared to the late varieties (30-40%). Early wild varieties are rich in proteins with 5-7%, serving as a source of germplasm for the protein content improvement. The identification and selection of combinations in transgressive positive segregate generations demonstrated that it is possible to improve this objective. By the artificial induction of mutations have been identified high protein forms (GIOSAN et al., 1986).

The results of WILCOX and GUODONG (1995) revealed that, the soybean genotypes with indefinite growth represented a better source selection, combining high yields with high protein content.

The objective of this work was the study of the soybean genotypes variability in ARDS Turda germplasm collection regarding the protein content, entirely and grouped according to some morpho-physiological characters (the color of flowers, the color of pubescence, the vegetation period).

MATERIAL AND METHODS

The research was conducted at Agricultural Research and Development Station Turda, in the experimental field of the Leguminous Breeding Laboratory. It has been studied the soybean germplasm collection from ARDS Turda. It includes varieties and lines from the breeding centers in the country and abroad because of the biological material exchanges. The material resulted from their own breeding program was represented by lines that have not been validated as variety but presents interest due to a character that stands out and can be used in breeding programs to improve it; 38 indigenous lines and varieties (15.8%) and 202 foreign lines and varieties (84.2%) represented the genotypes studied within the collection. Genotypes are mostly from Europe (Romania, Hungary, Russia, Germany, France, Belgium, Netherlands, Serbia, Bosnia Herzegovina and Croatia), follow by the America's countries (Canada, USA) and Asia (China, Japan). Generally, in the collection genotypes were represented all major ecological areas of soybean cultivation. The diversity of genotypes collection gives it a wide ecological variability.

For the determination of protein and oil content, 50g of grains were weighed for each sample, then were crushed with laboratory mill; the flour resulted was examined using NIR analyzer, Dickey-John brand, INSTALAB 600 type.

The statistics index that best characterizes the variability of protein content, are the arithmetic mean, the standard deviation, the amplitude of variation, the coefficient of variation.

In the studied cases can observe the phenotypic variability of characters, which includes the genetic variability, due mostly to genotypes and a percentage of other nature variability, such as the interaction with microclimate conditions, as well as the determination errors. The results for amplitude variation of analyzed characters are representing in diagrams and histograms.

RESULTS AND DISCUSSION

Taking into account the protein content of all 240-soybean genotypes can observe that the amplitude of variation ranged from 38.1% to 47.2%, with an average of 42.3% and the standard deviation was 1.7%, indicating that most of the genotypes grouped around the average, confirmed by the value of the variance (2.9).

The value of variation coefficient (4.03%) indicated a low variability of protein content in the collection (table 1).

Table 1

Study on protein content in soybean genotypes from the collection (Turda, 2009)

Statistical parameter	Protein content (%)
Mean	42.26
Standard Error	0.1100
Standard Deviation	1.7034
Sample Variance	2.9015
The coefficient of variation,%	4.03
Kurtosis	0.1142
Skew ness	0.2338
Range	9.1
Minimum	38.1
Maximum	47.2
Count	240
Confidence Level (95.0%)	0.2166

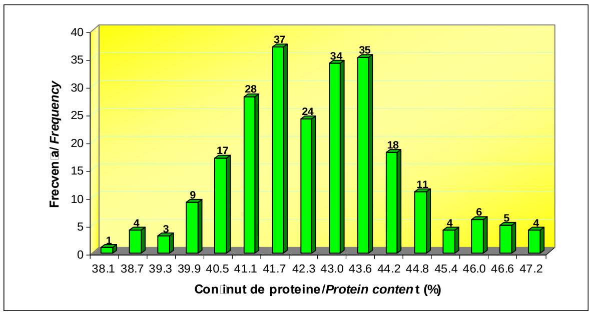


Figure 1. Frequency distribution of genotypes in the soybean collection according to their protein content (Turda, 2009)

Table 2

Soybean genotypes remarked for protein content (Turda, 2009)

Nr. Crt.	Genotype	Protein content (%)	Oil content (%)	Vegetation period (days)	Color	
					Flowers	Pubescence
1	PEKING	47.2	17.7	132	violet	brown
2	STRENGS WEIHENSTEPHANER	46.7	17.8	133	violet	brown
3	BERNESS GHESHECHTE	46.7	17.9	135	violet	brown
4	P.I. 295952 (Salut 216)	46.2	16.7	136	violet	brown
5	P.I. 132204(No. D. 5)	46.1	17.5	137	violet	brown
6	P 73-2	46.0	18.1	138	violet	brown
7	P.I. 153266 (Poppelsdorf)	46.0	18.0	137	violet	brown
8	F.C. 89065-2	46.0	16.7	138	violet	brown
9	P.I. 189859 (LIGHT BROWN)	45.8	17.8	139	violet	brown
10	P.I. 153281(N 22)	45.8	17.6	136	violet	brown
11	NOVOSADSKA NR. 3	45.7	17.3	136	white	brown
12	P.I. 153315 (Maguisard)	45.6	18.2	136	white	grey
13	HARDOME	45.4	17.6	138	violet	grey
14	F.C. 30683	45.4	18.2	136	violet	brown
15	P.I. 295947 (Amurskaja 57)	45.3	18.2	137	violet	brown
16	P.I. 303650 (Sys li zia)	45.0	18.8	140	violet	brown
17	P.I. 290131 (LOCALE 11)	44.9	18.7	136	violet	grey
18	GOLDSOY	44.8	18.4	134	violet	grey
19	P.I. 189906 (Halton)	44.7	18.8	137	violet	brown
20	P.I. 153213 (B-16)	44.7	18.1	139	violet	brown

The genotypes noticed for their high protein content and used as germplasm sources in the breeding processes arranged between the average protein content and the upper limit of the string variation (42.3% and 47.2%) (Figure 1).

In table 2 are represent the first 20 soybean genotypes with the highest protein content identified on the basis of frequency distribution genotypes from the collection. From the table, it can see that, the highest protein content registered to the soybean genotypes with shorter vegetation period, with violet flowers and brown pubescence; also, the oil content increases as the protein content decreases, confirming the antagonistic relationship between those two quality characters.

The genotypes with violet flowers were 197 and the genotypes with white flowers were 43. Accounting the protein content according to the color of flowers remarks that, in the case of the violet flowers genotypes, the average protein content was 42.3%, and in the case of white flowers, the average protein content was 42.1%, the differences between groups being insignificant.

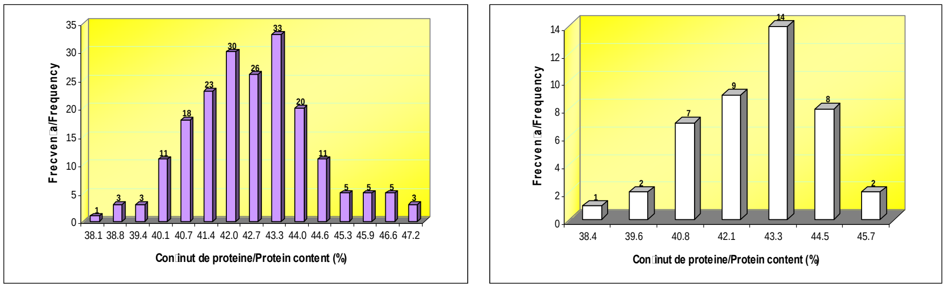
The variation limits of genotypes with violet flowers were between 38.1% and 47.2%, and the variation limits of genotypes with white flowers were between 38.4% and 45.7%; it noticed that, the genotypes with violet flowers recorded higher values of protein content than the genotypes with white flowers (Table 3).

The standard deviation, with small values obtained in both cases, revealed a group of string variation values around the mean.

Table 3

Study on protein content in soybean genotypes from the collection according to the color of flowers (Turda, 2009)

Statistical parameter	Protein content (%)	
	Violet flowers	White flowers
Mean	42.30	42.10
Standard Error	0.1234	0.2404
Standard Deviation	1.7317	1.5765
Sample Variance	2.9986	2.4853
The coefficient of variation,%	4.09	3.74
Kurtosis	0.1237	-0.0321
Skew ness	0.2493	0.0729
Range	9.1	7.3
Minimum	38.1	38.4
Maximum	47.2	45.7
Count	197	43
Confidence Level (95.0%)	0.2433	0.4852



Genotypes with violet flowers

Genotypes with white flowers

Figure 2. Frequency distribution of soybean genotypes for protein content according to the color of flowers (Turda, 2009)

The value of the coefficient of variation, a little smaller in the case of genotypes with white flowers shows a lower variability of this group for protein content. It can see, from figure 2, that the histogram of genotypes with white flowers is approaching more of the normal distribution model.

From the observations above and the values obtained for the protein content, can conclude that, in the group of genotypes with violet flowers recorded higher values of this character than in the group of genotypes with white flowers.

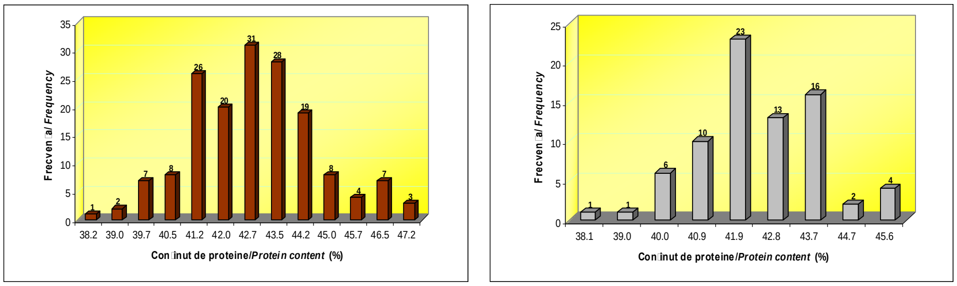
The genotypes in the collection divided depending on the color of pubescence, to determine whether this character has influence on the protein content.

From the results in table 4, it can see that, the protein content amplitude of variation ranged from 38.2% to 47.2% in the case of genotypes with brown pubescence and ranged from 38.1% to 45.6% in the case of genotypes with grey pubescence; it observed that the genotypes with higher protein content had brown pubescence.

Table 4

Study on protein content in soybean genotypes from the collection according to the color of pubescence (Turda, 2009)

Statistical parameter	Protein content (%)	
	Brown pubescence	Grey pubescence
Mean	42.44	41.88
Standard Error	0.1374	0.1740
Standard Deviation	1.7602	1.5173
Sample Variance	3.0983	2.3021
The coefficient of variation,%	4.15	3.62
Kurtosis	0.0278	0.0670
Skew ness	0.2250	0.0399
Range	9	7.5
Minimum	38.2	38.1
Maximum	47.2	45.6
Count	164	76
Confidence Level (95.0%)	0.2714	0.3467



Genotypes with brown pubescence

Genotypes with grey pubescence

Figure 3. Frequency distribution of soybean genotypes for protein content according to the color of pubescence (Turda, 2009)

The standard deviation of the average, higher at the genotypes with brown pubescence (1.76%) than in the genotypes with grey pubescence (1.52%) reveals a slightly larger deviation from the average of the protein content values in genotypes with brown pubescence than in the genotypes with grey pubescence.

The coefficient of variation is higher at genotypes with brown pubescence (4.2%) than at genotypes with grey pubescence (3.6%), but in the case of both groups indicates a low variability for the character.

The distribution of genotypes with brown pubescence is pretty much the type of normal distribution, as shown in figure 3.

In the case of genotypes with grey pubescence, the standard deviation reduced; this contraction was because the values generated strings of discontinuous variation.

The genotypes in the collection grouped, depending on the vegetation period, in three classes: 132-135 days, 136-139 days and 140-142 days.

In table 5, we note that, the majority of genotypes fit into the group with vegetative period between 136 and 139 days; the highest protein content obtained in the group of genotypes with vegetative period between 132 and 135 days (47.2%).

In the first group, the variation limits of the protein content were between 38.4% and 47.2%, with an average of 42.5%, higher than the average obtained in the group of genotypes with vegetative period between 136 and 139 days, respectively the group of genotypes with vegetative period between 140-142 days. The amplitude variation obtained in the first group was the largest of all three groups.

The reduced values of standard deviation for the three groups means grouped the genotypes around the average of the variation string, a fact confirmed by the low values of the variation coefficients (3.88%, 4.09% respectively 4.18%), meaning a low variability of protein content for all the genotypes in the collection.

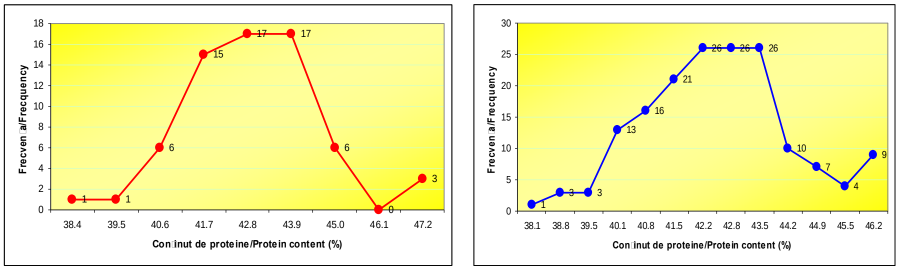
Within those three groups, a slightly larger variability for protein content found in the group of genotypes with vegetative period between 140 and 142 days.

Table 5

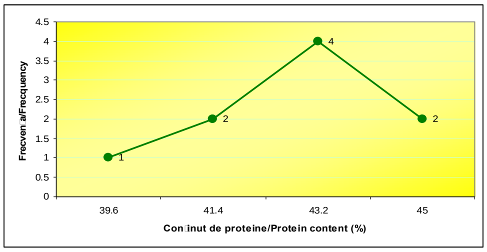
Study on protein content in soybean genotypes from the collection according to the vegetation period (Turda, 2009)

Statistical parameter	Protein content (%)		
	132-135 days	136-139 days	140-142 days
Mean	42.48	42.17	42.34
Standard Error	0.2030	0.1341	0.5898
Standard Deviation	1.6492	1.7231	1.7693
Sample Variance	2.7197	2.9690	3.1304
The coefficient of variation,%	3.88	4.09	4.18
Kurtosis	0.9993	-0.0947	-1.0059
Skew ness	0.4007	0.2134	-0.1331
Range	8.8	8.1	5.4
Minimum	38.4	38.1	39.6
Maximum	47.2	46.2	45
Count	66	165	9
Confidence Level (95.0%)	0.4054	0.2649	1.3600

The distribution of genotypes in the diagrams form showed a frequency distribution close to the normal distribution model in the case of second group of precocity, with vegetative period between 136 and 139 days (figure 4). The facts that in this group are the most genotypes (165), led to a distribution close to the ideal distribution.



(132-135 days) (136-139 days)



(140-142 days)

Figure 4. Frequency distribution of soybean genotypes for protein content according to the vegetation period (Turda, 2009)

Table 6

Soybean genotypes with the shortest and the longest vegetation period (Turda, 2009)

Nr. Crt.	Genotype	Vegetation period (days)	Protein content (%)	Oil content (%)	Color	
					Flowers	Pubescence
1	SOPRANO	132	40.7	21.4	violet	brown
2	ACME (Mt.)	132	41.3	20.1	violet	grey
3	RÎSHITA	132	42.7	19.6	violet	brown
4	RECORD SEVERIN	132	43.8	19.4	violet	grey
5	PEKING	132	47.2	17.7	violet	brown
6	CERVIN	133	41.2	20.6	violet	brown
7	DIAMANT	133	41.3	19.8	violet	brown
8	P.I. 238924 (Kirches Stamm 2008)	133	42.7	19.4	violet	grey
9	F.C. 68722	133	43.1	19.0	violet	brown
10	CLAY	133	43.6	18.6	violet	grey
…………………………						
11	AGAT	139	40.7	19.5	white	grey
12	CLUJ 330/69	140	43.1	18.5	violet	brown
13	P.I. 303650 (Sys li zia)	140	45.0	18.8	violet	brown
14	F.C. 32141 (Early Sunrise)	140	44.0	19.2	violet	grey
15	NANTO	140	43.1	19.5	violet	brown
16	SAFIR	140	41.5	20.3	violet	grey
17	FELIX	140	40.5	20.4	violet	grey
18	PAGODA	142	39.6	20.9	violet	grey
19	PODUNAVSKA	142	43.2	18.6	violet	brown
20	CRUSADER	142	41.1	19.9	violet	brown

The soybean genotypes with the shortest and the longest vegetative period are represent in table 6. Among the genotypes with the shortest vegetation period (132 days), remarks the Peking variety with the highest protein content (47.2%) from the collection and the lowest oil content (17.7%). At the opposite pole, between the soybean genotypes with the longest vegetation period (142 days) remarks the Pagoda variety, with the lowest protein content (39,6%), respectively the highest oil content (20.9%), confirming the antagonistic relationship between protein and oil content (GÂRDA, 2011).

CONCLUSIONS

The highest protein content registered to the soybean genotypes with shorter vegetation period, with violet flowers and brown pubescence. Also, the oil content increased as the protein content decreased, confirming the antagonistic relationship between this two quality characters.

Between the values obtained for the protein content, in the group of genotypes with violet flowers registered higher values of this character as in the group of genotypes with white flowers. Also, the genotypes with the highest protein content had brown pubescence.

The genotypes noted for their high protein content and used as sources of germplasm in the breeding processes arranged between the average protein content and the upper limit of the string variation (42.3% and 47.2%).

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