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Quantitative genetic analysis of storage proteins in soybean

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ABSTRACT - *A population of 95 RILs in generation F_9, from a cross of BARC-8 and Garimpo, provided the plant material studied. This population was grown at two sites: Viçosa and São Gotardo, both in the State of Minas Gerais, Brazil. Environmental factors are involved in the regulation of the expression of the evaluated traits at both sites, since the interaction RIL x site was significant. The heritability of protein content was high at both sites as well as in the joint analysis. Heritabilities of the other evaluated traits were also high at both sites. However, the heritabilities of these traits were lower in the joint analyses, due to the effect of the interaction RIL x site. 11S protein and total storage protein (11S+7S) had a positive and high correlation with the total protein content, while 7S protein presented a low correlation to the total protein content.*

Key words: Heritability, storage proteins, soybean, genotypic correlations.

INTRODUCTION

Soybean seeds contain more protein than any other commercially used plant species. Approximately 40% of the soybean seed dry weight is proteins and 20% oil. Historically, soybean was genetically improved in order to increase the productivity and oil content of the grain. Lately, soybean breeding programs have focused on the development of more productive varieties, with high protein contents.

Currently, soybean meal is the main by-product of the crush industries in Brazil, most of which is assigned for exportation. The protein content in the hulls has influence on its commercial value, which makes the development of productive varieties with high protein content desirable. Two storage proteins, β-conglycinin and glycinin, make up around 70% of the storage proteins in soybean. In general, the amount of glycinin is higher (Moreira et al. 1979, Coates et al. 1985).

Glycinin (11S) contains three to four more times cysteine and methionine than β-conglycinin (7S) (Koshiyama 1968, Coates et al. 1985, Harada et al. 1989). The amount of the two proteins can vary in the different soybean seeds, depending on the genetic constitution of the seed and the environment where they are grown. Natural genetic variations occur in the composition of the subunits in the two main

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storage proteins in soybean. These variations may be due to regulation mechanisms of the gene expression that encode these subunits. Knowledge on these mechanisms could therefore be used to increase the storage protein type selectively for specific purposes (Yaklich et al. 1999). Research into the genetic manipulation of these two proteins is being applied with the aim of increasing the levels of essential amino acids in the formulas of livestock feed as well as for human consumption (Kwanyuen et al. 1997).

The heritability estimates, expected selection gains, and the correlations of the selected traits are extremely important to align and plan breeding programs. Erickson et al. (1981) estimated the heritability for protein content in a population originated from four pairs of interspecific bi-parental crosses (*Glycine max* x *G. soybean*). To calculate the narrow-sense heritability, was used the regression of the F_3 family means on F_2 plants; for the broad-sense heritability, the variance components of the F_3 family means were used for the calculation. The narrow-sense heritability estimate for the protein content was 27% and, in the broad-sense, 78%, based on 100 F_3 families evaluated at two sites.

Wilcox (1998) conducted a recurrent selection program to increase the protein content in seeds in two soybean populations. The environmental variance was obtained through the variability of protein contents among plants of the variety (Century) used as control. The genotypic variance was estimated as a result from the difference between the phenotypic and the environmental variance. Estimates of heritability were calculated at each cycle of recurrent selection. They varied from 55 to 89% between the first and the seventh cycle, while the variability of the protein content increased along with the number of recurrent selection cycles.

According to Hanson and Weber (1963) the estimate of the heritability coefficient reaches two basic objectives of genetic improvement: firstly, it demonstrates the relative easiness or difficulty with which the different traits are selected in a particular improvement scheme, and secondly it allows estimates the expected progress with selection. For Cruz and Regazzi (1997) knowledge on the correlation among traits is of great importance for plant breeding, especially if any of the evaluated traits present low heritability and/or there are problems with measurement and identification.

This study is part of the soybean quality breeding program developed at the Instituto de Biotecnologia Aplicada à Agropecuária - BIOAGRO/UFV, which aims at the development of productive varieties with high protein content and the following objectives: (i) estimation of the heritability of the total protein concentration in soybean, evaluated by the modified Kjeldahl method; (ii) estimation of the heritability of the soybean storage protein concentration and of its respective subunits, evaluated by polyacrylamide gel electrophoresis in denaturing condition (SDS-PAGE) together with densitometry, (iii) estimation of the genotypic correlations to each one of these traits, and (iv) evaluation of the interaction genotype x environment for these traits.

MATERIAL AND METHODS

Plant material

The population of 95 RILs (Recombinant Inbred Lines) was obtained from the cross between two contrasting parents for protein contents: line BARC-8 (genotype with a high protein content, around 50%) obtained at the Beltsville Agricultural Experimental Station – USDA, Beltsville, MA, USA and the commercial variety Garimpo (genotype with normal protein content, around 36%). The female parent was BARC-8. The RILs were obtained by the SSD (single seed descent) method from F_2 generation. Lines from F_9 generation provided the plant material used in his study. These RILs were planted at two sites: Viçosa and São Gotardo, both in the State of Minas Gerais. The experiments were installed in a randomized complete block design in three replications.

Protein Analysis

Analysis of the total protein content

The seed protein content of each family was determined collecting a representative seed sample from all plants in the plot. This determination was realized by the modified Kjeldahl method, according to the Instituto Adolfo Lutz (1985), which requires a minimum of three hundred milligrams (about 10 seeds) of ground soybean. After the digestion of the material with sulphuric acid, 30% hydrogen peroxide was added in the digestion phase; thereafter, the mixture was heated for 30 more minutes. During the distillation phase, the released ammonium was collected in a 4% boric acid solution. The nitrogen content was obtained by the ammonium titration with 0.05% chloridric acid. The percentage of total protein was calculated multiplying the nitrogen content by the factor 6.25. Protein contents were expressed in percentage, based on dry matter (sample dried for 24 hours at 105 ^{o}C).

Analysis of the 11S and 7S protein concentrations and their respective subunits

The storage proteins glycinin (11S) and β-conglycinin (7S) were extracted from the RILs with saline phosphate buffer

(sodium phosphate buffer 0.05 M, pH 7.6; NaCl 0.4 M; β-mercaptoethanol 0.28%). Approximately 50 mg of ground soybean and 1.5 mL of the extraction buffer were used in 1.5 mL tubes. After 45 minutes in an ultra-sound bath, the tubes were centrifuged for 15 minutes at 14.000 rpm in a microcentrifuge. Two aliquots, one of 800 μL (set aside for a posterior analysis) and another of 30 μL were withdrawn from the supernatant. Fifteen μL of the sample buffer 3X (TRIS 0.1875 M; SDS 6.9%; glycerol 30%; pH 6.8), 10 μL of bromophenol blue 0.05%, and 10 μL of β-mercaptoethanol were added to the aliquot of 30 μL. Thereafter, the tubes were placed in water bath at 100 °C for 3 minutes and 25 μL of the solution was applied in a 12.5% polyacrilamide gel. An initial run was carried out at 60 volts, for about 1.0 h, when the current was raised to 80 Volts, until the end of the step (~5h), which was defined as 30 minutes after the appearance of the dye on the bottom of the gel. After the run, the gels were immersed in dye solution (1.5 g of Coomassie Brilliant Blue G, 90 mL acetic acid, 450 mL methanol, and 460 mL water) for 12 hours and afterwards in bleaching solution (75 mL acetic acid, 250 mL methanol, and 675 mL water) for 24 hours. After bleaching, the gels were stored in 10% glycerol solution until the densitometry analysis.

In all analyses, the same standard sample was used (BARC-8), which was extracted, applied on the gel, and quantified together with the other samples. This sample, called extraction standard, was added to the analyses to correct possible differences of extraction and electrophoresis conditions between one analysis and another. The densitometric analysis was realized on the Personal Densitometer SI Molecular Dynamics set, which belongs to the Núcleo de Biologia Aplicada da Embrapa Milho e Sorgo, Sete Lagoas, MG. Software Image Quant for the integration of the volume occupied by the gel band was used in the determination of the percentage of each subunit , , and of the 7S protein and acids and basics polypeptides of the 11S storage proteins present in the gels in relation to the total protein of each gel lane (Figure 1). The apparent optical density (OD) of each protein was obtained by the subtraction of the mean OD of the background from the total OD of the protein bands. The subunits of the storage proteins were identified based on electrophoretic mobility (Fontes et al. 1984, Yaklich 2001). In order to transform the values of the subunit percentages after the densitometry analyses into protein percentage in 100 mg, the 800 aliquots that had been set aside after the extraction were used to quantify the total protein by the modified Kjeldahl method.

Normality tests

The asymmetry, kurtosis, and Lilliefors tests were performed.

Joint variance analysis

The following model was applied for the joint variance analysis

$$Y_{ijk} = \mu + g_i + a_j + (ga)_{ij} + (b/a)_{jk} + e_{ijk}$$

where

μ = general mean;

g_i = random effect of the ith genotype (RIL) (i = 1, 2 ,..., g); G_i ~NID (0, σ^2_g);

a_j = random effect of the jth environment (j= 1, 2 ,..., a); A_j ~NID (0, σ^2_a);

$(ga)_{ij}$ = random effect of the interaction of the ith genotype with the jth environment; GA_{ij} ~NID (0, σ^2_{ga});

$(b/a)_{jk}$ = random effect of the kth block within the jth environment (k= 1, 2 ,..., b); b/a_{jk} ~NID (0, $\sigma^2_{b/a}$);

e_{ijk} = random error, $e_{ijk} \approx$NID $(0, \sigma^2)$.

Genotypic correlation

The genotypic correlation was estimated according to Cruz and Regazzi (1997). All statistical analyses of this paper were run on the software Genes (Cruz 2001).

RESULTS AND DISCUSSION

The densitometry analysis of storage proteins subunits was realized on the 12.5% polyacrilamide gels (Figure 1). Except for protein concentration in Viçosa, all other traits (total protein concentration in São Gotardo, the storage proteins 7S and 11S, as well as their respective subunits) presented an approximately normal distribution (P<0.01). This fact indicates the existence of continuous variation and the possibility that several genes are involved in the control of these traits in soybean. Since these traits are being evaluated

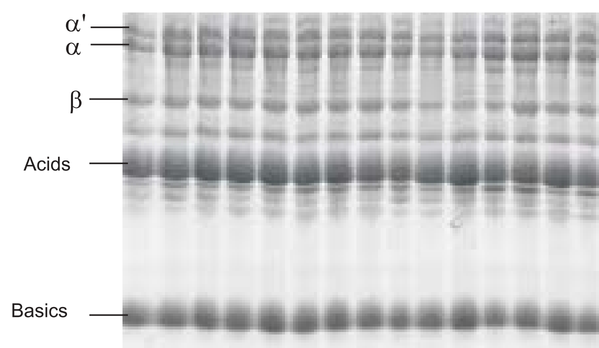

Figure 1. Denaturing polyacrilamide gel (SDS-PAGE) of some RILs used in his study. The subunits of β-conglycinin (7S) are α', α, and β, and the subunits of glycinin (11S) are the acidic and basic subunits

for genetic mapping, if QTLs related to the total protein content obtained in Viçosa are detected, they should be analyzed with some precaution, since the estimation method of QTLs presumes that the trait must present a normal distribution. Yet by the Lilliefors, asymmetry, and kurtosis tests, it is concluded that this trait does not follow a normal distribution (Table 1). However, it must be observed that the degree of asymmetry (0.8565) and kurtosis (4.1105) are not as high as of the trait 11S+7S, for example, whose Lilliefors test was not significant.

The means of almost all obtained protein concentrations were greater in the experiment running in São Gotardo (Table 1). This fact might be due to the environmental effects as temperature, soil, altitude etc., which can be influencing the protein content of the soybean grown at this location, in this case, the combination of these effects contributed to increase the protein content. This indicates a simple predominant interaction, which is not disadvantageous for the selection of the best genotypes at both sites.

The analyses of variance at each site (Tables 2) pointed out that the experimental precision was high for the total protein content, in the experiment in Viçosa as well as in São Gotardo, as the variation coefficients illustrate (3.10% in Viçosa and 2.64% in São Gotardo). The traits storage proteins 7S and 11S and their respective subunits, and the relations 11S+7S, 11S:7S, and total protein minus storage proteins [TP-(11S+7S)] presented the highest variation coefficients, which ranged from 4.41% to 20.15% in Viçosa, and from

Table 1. Trait means, tests of Lilliefors, asymmetry, and kurtosis, for several evaluated traits in Viçosa and São Gotardo

Traits	Mean (%)	Test of Lilliefors	Symmetry	Kurtosis
		Viçosa		
T P	45.49	0.1209*	0.8565*	4.1105**
α'	1.6657	0.0779	0.3721	2.976
α	2.3133	0.0598	-0.2014	3.2192
β	1.8651	0.0607	-0.0002	2.3739
Acids	9.5848	0.0591	-0.2496	3.3076
Basics	12.1459	0.1197*	0.4132	3.2435
7S	5.8444	0.0563	-0.0903	2.4924
11S	21.7307	0.0699	0.2089	3.8908
11S+7S	27.5751	0.0702	0.6037*	4.3714**
11S:7S	3.8898	0.0772	0.2914	3.26
TP-(11S+7S)	17.917	0.0898	-0.0454	7.4825**
		São Gotardo		
T P	46.79	0.0711	0.1701	3.1494
α'	1.8994	0.0817	0.3929	3.1323
α	3.2611	0.0808	0.1547	2.3661
β	2.0389	0.0696	-0.0305	3.1882
Acidics	10.4586	0.1112*	0.4743	3.319
Basics	11.4685	0.0586	0.138	4.1551*
7S	7.2984	0.0981	0.3101	3.1169
11S	21.9271	0.0796	0.3745	3.9864*
11S+7S	29.2255	0.0589	0.1366	3.2143
11S:7S	3.0992	0.1063	0.7779*	4.5446*
TP-(11S+7S)	17.5672	0.1117*	0.4186	2.6305

*, ** significant at $P<0.05$ and $P<0.01$, respectively

Table 2. Summary of the variance analysis for 11 evaluated traits in the experiments in Viçosa and São Gotardo and estimates of the genetic variance (σ_g^2), the heritability (h^2), and the variation coefficient (VC)

Sources of variation	df	Mean Squares										
		TP	α'	α	β	Acids	Basics	7S	11S	11S+7S	11S:7S	TP(11S+7S)
		Viçosa										
Blocks	2	66.7720	0.0125	1.1142	0.3263	14.4773	17.2097	0.8667	10.4385	6.0644	1.1478	90.8649
RILs	94	22.3617**	0.5076**	1.1488**	0.5623**	11.7362**	9.1916**	3.0769**	25.5745**	27.3436**	2.3727**	19.2339**
Error	188	1.9935	0.1127	0.1866	0.1206	1.5608	4.3324	0.5681	5.8737	6.2792	0.4731	6.0019
σ_g^2		6.7893	0.1316	0.3207	0.1472	3.3918	1.6197	0.8362	6.5669	7.0215	0.6332	13.6535
$\hat{h}^2$ %		91.0851	77.787	83.7534	78.5598	86.7012	52.8657	81.5355	77.0331	77.0359	80.0599	68.7951
VC %		3.1036	20.1586	18.6730	18.6592	13.0640	17.1370	12.9063	11.1640	9.0959	17.6864	4.4107
		São Gotardo										
Blocks	2	2.7703	0.4161	1.8694	2.2187	20.0921	25.5331	2.0032	20.1848	12.0409	1.9419	6.9085
RILs	94	19.2721**	0.4079**	0.9013**	0.4118**	7.4156**	7.5692**	2.8520**	13.3894**	14.5994**	0.9206**	2.2759**
Error	188	1.5329	0.1106	0.2903	0.0860	2.6950	2.9267	0.7886	2.0621	2.3161	0.2426	3.0725
σ_g^2		5.9131	0.0991	0.2037	0.1086	1.5735	1.5475	0.6878	3.7758	4.0944	0.2260	1.3067
$\hat{h}^2$ %		92.0458	72.8885	67.7928	79.1072	63.6569	61.3336	72.3496	84.599	84.1356	73.653	56.0612
VC %		2.6459	16.6409	16.5212	14.3869	15.6968	14.9171	12.1674	6.5489	5.2074	15.8909	9.9779

**: significant at P<0.01, by the F test.

5.21% to 16.64% in São Gotardo. There was significant genetic variability among the RILs for all evaluated traits in both environments.

Studies of QTL mapping are based on the possibility to find molecular markers connected to a trait of interest, whose presence or absence determine significant variation in the mean of these traits. Therefore, the existence of genetic variability, as observed in these assays, confers to this population a great potential for future molecular studies.

The joint variance analysis (Table 3) indicated that environmental factors are involved in the regulation of the gene expression of the evaluated traits in Viçosa and São Gotardo, since the interaction RILs x sites was significant (P<0.01). There was also a significant effect of the RILs and sites for all traits (P<0.01), with exception of the environment effect for the traits 11S and TP-(11S+7S), which were not significant.

It is assumed that any plant under breeding the interactions genotype x environment is present. The relative magnitude of these interactions gives the breeder a strategy of choosing genotypes of broad or restricted adaptation to specific environments (Vencovsky and Barriga 1992). The same assumption can be used for the identification of site-specific QTLs or QTLs of broad expression.

In maize seven agronomical traits, including grain yield, were measured in the same population in six different environments in the United States (Stuber et al. 1992). QTLs detected in one site were, frequently, detected in other site, suggesting a small interaction QTLs x sites. A study with tomato evaluated a segregant population in three different environments (Paterson et al. 1991). Forty-eight percent of the QTLs were detected in at least two and the other 52% in only one environment. The QTLs that showed greater effects in one environment were also the most likely to be detected in another. The most similar sites, in relation to climate and agricultural practices, were those with more QTLs in common, in agreement with the lowest effect of the interaction genotypes x environments. This study suggests that a large proportion of the QTLs, which affect a quantitative character in one environment may be active in another environment. This is particularly true for QTLs with a greater effect (Tanksley 1993). However, Paterniani (1990) shows that the environmental variations in Brazil are more drastic than in

Table 3. Summary of the joint variance analysis of the analyzed traits from the experiments in Viçosa and São Gotardo, and estimates of the genetic variance(σ_g^2), the heritability (h^2), and the variation coefficient (VC)

Sources of variation	**df**	**Mean Squares**										
		TP	α'	α	β	Acids	Basics	7S	11S	11S+7S	11S:7S	TP(11S+7S)
Blocks/sites	4	34.7711	0.2143	1.4918	1.2725	17.2847	21.3714	1.4349	15.3116	9.0527	1.5449	48.8867
RILs (R)	94	30.7771**	0.5207**	1.0927**	0.6524**	13.3516**	8.7030**	3.5284**	25.6730**	25.2760**	2.0679**	14.1905**
Sites (S)	1	241.0033**	15.766**	127.94**	4.5185**	144.3122**	65.381**	303.01**	6.7907	400.5257**	88.89**	20.1499
RXS	94	10.8568**	0.3948**	0.9274**	0.3218**	5.8001**	8.0579**	2.4005**	13.2909**	16.6671**	1.2253**	12.0361**
Error	376	1.7632	0.1117	0.2385	0.1033	2.1279	3.6296	0.6784	3.9679	4.2977	0.3578	4.5372
σ_g^2		3.3200	0.02097	0.02255	0.0551	1.2586	0.1075	0.1879	2.0637	1.4348	0.1404	0.3591
$\hat{h}^2$ %		64.7244	24.1688	12.3809	50.6737	56.5586	7.4128	31.9655	48.23	34.0596	40.7482	15.182
VC%		2.8777	18.2403	17.5193	16.4836	14.5717	16.1355	12.5376	9.1299	7.3029	17.1199	11.9969

**: significant at P<0.01, by the F test

the United States, mainly in relation to the planting seasons, which normally present very intensive climatic variations, which suggests a greater effect of the interaction genotypes x environments. Therefore, under our conditions a lower stability of the identified QTLs is expected.

The heritability of the trait protein concentration obtained by variance components was high at both sites (91.08% in Viçosa and 92.04% in São Gotardo) and also in the joint analysis (64.62%). This means that the greatest part of the observed variation is due to genetic causes and also reflects the experimental accuracy.

In previous studies we also obtained high heritability values for protein content, using variance components, in several crosses with parents contrasting for protein content (data not shown). The heritabilities of the other evaluated traits also ranged from medium to high at both sites (from 52.86% to 86.70% in Viçosa and from 56.86% to 84.60% in São Gotardo) (Table 2). However, the heritabilities of these traits in the joint analysis were smaller, varying from 7.41% to 56.56%, due to the effect of the interaction genotype x environment (Table 3). This indicates that the selection applied for these traits must be realized specificaly for each environment, and in the end, the cultivar to be recommended must be specific for similar environments.

The genotypic correlations are shown in Table 4. The results in the two environments were similar. The subunits α', α, and β concentrations had a positive correlation with 7S protein content (0.6538; 0.8431; 0.5207, respectively, in Viçosa and 0.7783; 0.8943; 0.5485 in São Gotardo). This result was expected, since these subunits are components of this protein. Likewise, the acid and basic subunits concentrations of 11S protein presented a positive and high correlation with this protein content (0.8835; 0.7351, respectively, in Viçosa, and 0.7799, 0.7756 in São Gotardo). The 11S protein and total storage protein (11S+7S) presented correlations of 0.6427 and 0.6807, respectively, to the total protein content in Viçosa, and of 0.9173 and 0.8841 in São Gotardo. Similar results were found by Kwanyuen et al. (1997). Kwanyuen et al. (1997) studied 45 selected soybean accessions from USDA Soybean Germplasm Collection, and determined that about 45% of the protein variations among the studied accessions were attributed to changes in the 11S protein content. Essentially, no correlation was found between the levels of 7S and total protein. Previous studies analyzing two high protein near isogenic lines derived from CAC-1 and UFVTN 105 (also derived from CAC-1, but with normal protein content) found that the increase of the protein content of the NILs was accompanied mainly by the increase in the amount of 11S protein. The sum of 11S+7S content increased when the protein content increased, however, the individual quantification shows that this increase only occurred in 11S protein, while 7S was even reduced (data not shown).

Total protein content minus storage proteins [TP-(11S+7S)] presented negative correlations to all the evaluated traits, except for total protein content from the experiment of Viçosa in which the correlation was 0.3818. In the experiment of São Gotardo TP-(11S+7S) presented positive and high correlations to total protein content and 11S:7S ratio, being these values 0.5622 and 0.5938, respectively.

Table 4. Estimates of the genotypic correlations among the 11 evaluated traits in the analysis of Viçosa (higher) and São Gotardo (lower, and in brackets)

Traits	α'	α	β	Acids	Basics	7S	11S	11S+7S	11S:7S	TP-(11S+7S)
TP	-0.088	0.2048	0.1893	0.5939	0.4346	0.1715	0.6427	0.6807	0.2042	0.3818
	(0.255)	(0.0949)	(-0.1343)	(0.8055)	(0.6206)	(0.008)	(0.9173)	(0.8841)	(0.5397)	(0.5622)
α'		0.4033	0.0174	-0.254	-0.0638	0.6538	-0.2142	0.0184	-0.6404	-0.1321
		(0.6821)	(0.0693)	(-0.2413)	(0.0579)	(0.7783)	(-0.1187)	(0.205)	(-0.6497)	(-0.3085)
α			0.1522	0.0622	-0.1671	0.8431	-0.0383	0.2539	-0.7087	-0.0663
			(0.2294)	(-0.2446)	(0.2168)	(0.8943)	(-0.0191)	(0.3482)	(-0.6785)	(-0.4144)
β				-0.0347	0.181	0.5207	0.0649	0.2425	-0.3926	-0.0711
				(-0.4831)	(0.2551)	(0.5485)	(-0.1486)	(0.0821)	(-0.4769)	(-0.4311)
Acids					0.3318	-0.0768	0.8835	0.8279	0.5055	-0.3077
					(0.2098)	(-0.4167)	(0.7799)	(0.5781)	(0.7375)	(0.6902)
Basics						-0.0529	0.7351	0.6927	0.3868	-0.3347
						(0.2413)	(0.7756)	(0.8437)	(0.3025)	(-0.1734)
7S							-0.0815	0.2663	-0.8577	-0.1233
							(-0.1145)	(0.2999)	(-0.8053)	(-0.5139)
11S								0.939	0.5554	-0.3873
								(0.9134)	(0.6698)	(0.3346)
11S+7S									0.2411	-0.4171
									(0.3131)	(0.1107)
11S:7S										-0.0508
										(0.5938)

In the cases of the high genetic correlations found in this work, such as 11S with total protein content, there is an expectation that QTLs analyses would indicate the existence of gene blocks controlling the expression of these traits or even the existence of pleiotropic genes.

Protein 7S, as well as their subunits and presented low correlations with the total protein content, while the correlation of subunit was near zero. The genotypic correlations between proteins 11S and 7S were close to zero at both sites.

Fehr et al. (2003) evaluated the influence of the environment on the interactions between the subunits of the 11S and 7S proteins in 14 cultivars, at eight sites in 1998, 1999, and 2000. They found that 7S protein content has a phenotypic correlation of –0.99 (P<0.01) with the ratio 11S:7S, and that 11S has a positive correlation of 0.96 with that ratio. The phenotypic correlation between the 7S and 11S proteins was –0.92 (P<0.01), indicating a strong inverse relation between these two proteins. The phenotypic correlation coefficients with the total protein content were –0.34 for 7S, 0.37 for 11S, and 0.33 for the ratio 11S:7S. These authors also observed that the 7S and 11S proteins, and the ratio 11S:7S were influenced by the environment.

Since 11S protein contains more essential amino acids (cysteine and methionine) than 7S, a greater 11S:7S ratio brings forth beneficial alterations in the food quality of soybean. The data obtained in this study will be used to map

the loci that control the expression of these traits, and identify possible molecular markers that allow an assisted selection of the trait, in combination with a phenotypic selection that has already been conducted by the Soybean Quality Improvement Program of the BIOAGRO/UFV to develop high protein content lines.

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Análise genética quantitativa do conteúdo das proteínas de reserva em soja

RESUMO - *Uma população de 95 RILs, na geração F_9, obtida do cruzamento 'BARC-8' e 'Garimpo', constituiu o material genético estudado. Esta população foi cultivada em dois locais: Viçosa e São Gotardo, ambos em MG. Fatores ambientais estão envolvidos na regulação da expressão das características avaliadas nos dois locais, pois a interação RIL x local foi significativa. A herdabilidade do teor de proteína foi alta nos dois locais e também na análise conjunta. As herdabilidades das outras características avaliadas também foram altas nos dois locais. Entretanto, as herdabilidades destas características na análise conjunta foram menores, devido ao efeito da interação genótipo x local. A proteína 11S e o total de proteína de reserva (11S+7S) apresentaram correlação positiva e alta com o conteúdo de proteína total. A proteína 7S apresentou uma correlação baixa com o conteúdo de proteína total.*

Palavras chave: Herdabilidade, proteínas de reserva, soja, correlações genotípicas.

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