

# HEREDITY OF THE LINSEED NUMBER OF BOLLS PER SQUARE METER

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## ABSTRACT

In comparison with majority of other crops, studies regarding heredity of many linseed (*Linum usitatissimum* L.) metric traits, including number of bolls per square meter, are lacking or they are very rare. The purpose of this study was to estimate the genetic mechanism controlling the number of bolls per square meter. The results were achieved at the Research Institute for Cereals and Industrial Crops-Fundulea (R.I.C.I.C.), Romania, on the basis of the tests performed in flax nursery on 66  $F_1$  linseed hybrids (released by a  $p(p-1)/2$  diallel cross among twelve linseed genotypes) and their parents, in 1995. Simple phenotypic correlation coefficients between number of bolls per square meter and plant height, thousand seed weight (TSW), seed yield, oil content and oil yield respectively showed that this traits was significant connected with all other analyzed traits, excepting TSW. Both additive and dominance effects were involved in the genetic control of this trait, dominance being however prevalent. The gene or the group of dominant genes controlling the number of bolls per square meter operate after an "over dominant" type genetic mechanism, dominance being unidirectional and dominant alleles having an increasing effect on this trait. Heritability coefficients for linseed number of bolls per square meter, in narrow sense, had a quite high level, confirming that this trait is transmitted relatively uniformly into the progeny.

**Key words:** linseed number of bolls per square meter, genetic control, *Linum usitatissimum* L., parent-offspring regression, simple phenotypic correlation.

## INTRODUCTION

Linseed (*Linum usitatissimum* L.) is one of the most valuable industrial crops. Few crops can match its capacity to supply raw material for so many uses beginning with manufacture of paints, varnish, linoleum, oil cloth printer ink, soap, pharmaceutical products and so on, to the human and animal consumption (Poehhman, 1966; Hoffman et al., 1970; Turner, 1978 etc.).

Knowledge of factors that affect number of bolls (fruits, capsules) per square meter may be useful in understanding genetic mechanism of linseed yield because of the obvious relationship of this trait with seed yield (Dybing, 1988; Dybing and Grady, 1994). Investigations regarding the genetic control of number of bolls per plant were made along the time by Joshi et al., 1961; Saxena, 1962; Dalal and Gill, 1965; Anand and Murty, 1969; Badwal et al., 1970; Rao and Singh, 1984 and so on, but there is no paper about

genetic control of number of bolls per square meter.

This study was aimed to contribute to cover the lack of data concerning the genetic control of this trait.

## MATERIALS AND METHODS

Twelve linseed genotypes (9 lines and 3 varieties), well differentiated for their origin, number of bolls per square meter (NBSM), plant height, thousand seed weight (TSW), seed yield, oil content and oil yield were used as parents in 1994 to obtain 66  $F_0$  direct hybrids, in a  $p(p-1)/2$  diallel cross (Table 1).

In 1995,  $F_1$  generation together with the twelve parents were tested into a micro-trial experiment (four replicate completely randomized blocks design), each elementary plot consisting in three rows (1,5 m length, 0,21 m distance between rows), mechanically drilled with a Seedmatic machine (Wintersteiger, Austria).

Recording of NBSM (in thousands) was made by counting all capsules on the middle row of each plot (central part of one meter of this row) and then by adjusting to one square meter.

These data were subjected to a chain of statistical analysis such as: simple phenotypic correlation coefficients among NBSM and plant height, TSW, seed yield, oil content and oil yield, block variance analysis (Ceapoiu, 1968);  $1/2$  diallel table variance analysis (Walters and Morton, 1978); covariance ( $W_r$ ) and variance ( $V_r$ ) graphical analysis (Jinks and Hayman, 1953; Hayman, 1954); evaluation of components of genetic variation (Jinks, 1954; Hayman, 1954; Mather and Jinks, 1974); assessing of the theoretical parents with maximum number of dominant and recessive genes (Joshi et al., 1961); correlation between mean parent NBSM and corresponding sum of covariance and variance (Mather and Jinks, 1974) and finally mid parent- $F_1$  hybrid offspring regression (Simmonds, 1979).

Table 1. Characterization of twelve linseed parental genotypes (R.I.C.I.C. Fundulea, 1995)

Parent	Origin	Trait					
		Number of bolls/m <sup>2</sup>	Plants length (cm)	TSW (g)	Seed yield (t/ha)	Oil content (%)	Oil yield (t/ha)
L - 6529 - 90	Romania	4.40	49.25	6.20	2.30	47.20	1.09
L - 5506 - 90	Romania	4.26	62.50	7.00	2.08	42.60	0.89
L - 3060 - 91	Romania	5.24	60.75	7.80	2.54	47.60	1.21
L - 8254 - 91	Romania	3.14	50.75	7.00	2.18	44.68	0.98
L - 6106 - 93	Romania	4.24	55.50	7.50	2.30	49.53	1.14
L - 5115 - 92	Romania	4.60	68.50	6.40	2.02	41.78	0.84
L - 4222 - 92	Romania	4.36	59.25	7.10	2.16	44.70	0.97
L - 4272 - 92	Romania	5.67	70.25	7.00	2.80	46.58	0.86
L - 5312 - 92	Romania	5.34	50.90	7.10	2.40	46.08	1.11
C.I. Nos. 1432	India	2.28	35.50	4.80	1.48	40.23	0.60
Crista B - 15	Germany	2.10	35.25	8.10	1.51	41.40	0.62
NP (RR)	India	2.21	29.25	8.30	1.55	40.83	0.63
Mean		3.99	53.14	7.03	2.11	44.43	0.91
L.S.D. 5%		0.55	2.05	0.08	0.22	0.24	0.11

## RESULTS AND DISCUSSIONS

Simple phenotypic correlation coefficients between NBSM and plant height, TSW, seed yield, oil content and oil yield respectively, showed that this trait was significantly connected (from  $P < 0.05$  for oil content to  $P < 0.001$  for seed yield and plant height) with all other analyzed traits, excepting TSW (Table 2).

These data confirmed the close relationship between this trait and seed yield, pointed out by Dybing (1988, 1994).

Mean NBSM of the twelve parental genotypes and their 66  $F_1$  direct hybrids showed that best parents for this trait were Romanian linseed lines: L-4272-92, L-5312-92 and L-3060-91 while the worst the foreign varieties:

Crista B-15, NP (RR) and C.I. Nos. 1432 (Table 3).

Mean NBSM of many hybrid combinations overpassed the value registered for their best parent, although there were  $F_1$  generation values intermediate between the two parents (Table 3).

Block variance analysis for NBSM showed significant ( $P < 0.05$ ) genotypic differences concerning this trait, demonstrating the high variability of this trait among genotypes (Table 4).

The 1/2 diallel table variance analysis of this trait, which represented the first step of the decomposition of total genetic variance, showed that both additive ( $g_i$ ) and dominance ( $l_i$ ,  $l_{ii}$  and  $l_{ixj}$ ) effects were significantly

Table 2. Phenotypic correlation coefficients among number of bolls per square meter, plants length, thousand seed weight (TSW), seed yield, oil content and oil yield of the twelve linseed parental genotypes (R.I.C.I.C. Fundulea, 1995)

Independent variable	Dependent variable				
	Plant length	TSW	Seed yield	Oil content	Oil yield
Number of bolls/m <sup>2</sup>	0.84***	0.01 <sup>NS</sup>	0.92***	0.70*	0.75**
Plant length		0.02 <sup>NS</sup>	0.77**	0.45 <sup>NS</sup>	0.52 <sup>NS</sup>
TSW			0.09 <sup>NS</sup>	0.19 <sup>NS</sup>	0.13 <sup>NS</sup>
Seed yield				0.84***	0.80**
Oil content					0.89***

NS - Non significant

\*, \*\*, \*\*\* - Significant for  $P < 0.05$ ,  $P < 0.01$  and  $P < 0.001$  respectively

Table 3. Number of bolls per square meter (thousands) of twelve linseed parental genotypes and of all their 1/2 diallel F<sub>1</sub> hybrids (R.I.C.I.C. - Fundulea, 1995)

No.	Genotype	Replication				Mean
		I	II	III	IV	
1	L-6529-90	4.62	4.49	4.41	4.09	4.40
2	L-6529-90/L-5506-91	5.17	5.06	6.55	5.98	5.69
3	L-6529-90/L-3060-91	4.43	5.10	4.41	4.57	4.63
4	L-6529-90/L-8254-91	3.93	3.86	3.81	3.66	3.82
5	L-6529-90/L-6106-93	5.43	5.13	5.11	6.09	5.44
6	L-6529-90/L-5116-92	4.6	3.63	4.33	4.01	4.14
7	L-6529-90/L-4222-92	4.67	6.07	4.77	4.85	5.09
8	L-6529-90/L-4272-92	5.30	5.55	4.78	4.17	4.95
9	L-6529-90/L-5312-92	6.30	7.14	7.05	7.30	6.95
10	L-6529-90/C.I.Nos. 1432	3.83	4.86	4.07	4.96	4.43
11	L-6529-90/Crista B-15	4.02	4.42	4.01	5.17	4.41
12	L-6529-90/L-NP (RR)	4.89	5.87	5.07	4.49	5.08
13	L-5506-91	4.78	4.07	4.20	4.00	4.26
14	L-5506-91/L-3060-91	5.52	5.47	5.40	5.70	5.52
15	L-5506-91/L-8254-91	4.87	4.22	4.15	4.58	4.46
16	L-5506-91/L-6106-93	5.83	5.83	5.39	5.87	5.73
17	L-5506-91/L-5116-92	5.40	5.31	4.92	4.75	5.10
18	L-5506-91/L-4222-92	5.52	5.49	5.07	5.64	5.43
19	L-5506-91/L-4272-92	6.57	6.05	5.21	5.88	5.93
20	L-5506-91/L-5312-92	7.28	6.10	7.37	6.09	6.71
21	L-5506-91/C.I.Nos. 1432	3.83	3.87	4.32	4.54	4.14
22	L-5506-91/Crista B-15	2.86	3.19	3.34	3.07	3.12
23	L-5506-91/L-NP (RR)	3.10	3.66	3.52	3.93	3.55
24	L-3060-91	5.31	5.37	5.90	4.39	5.24
25	L-3060-91/L-8254-91	6.01	5.63	5.89	6.53	6.02
26	L-3060-91/L-6106-93	4.82	4.09	4.14	4.51	4.39
27	L-3060-91/L-5116-92	4.09	4.64	4.32	4.46	4.38
28	L-3060-91/L-4222-92	4.52	3.88	4.47	4.13	4.25
29	L-3060-91/L-4272-92	4.61	4.01	4.40	4.57	4.40
30	L-3060-91/L-5312-92	5.19	5.59	5.40	4.90	5.27
31	L-3060-91/C.I.Nos. 1432	6.08	5.91	4.97	6.10	5.77
32	L-3060-91/Crista B-15	3.65	3.59	4.16	4.00	3.85
33	L-3060-91/L-NP (RR)	4.45	4.05	3.72	4.23	4.11
34	L-8254-91	2.85	3.45	2.94	3.31	3.14
35	L-8254-91/L-6106-93	4.67	4.34	5.43	4.69	4.78
36	L-8254-91/L-5116-92	5.16	4.29	4.14	4.46	4.51
37	L-8254-91/L-4222-92	5.18	4.62	4.81	4.39	4.75
38	L-8254-91/L-4272-92	5.92	5.87	5.71	5.16	5.67
39	L-8254-91/L-5312-92	4.86	5.29	5.56	6.01	5.43

No.	Genotype	Replication				Mean
		I	II	III	IV	
40	L-8254-91/C.I.Nos. 1432	2.06	2.21	2.17	2.11	2.14
41	L-8254-91/Crista B-15	2.44	2.66	2.49	2.30	2.47
42	L-8254-91/L-NP (RR)	2.67	2.27	2.37	2.36	2.42
43	L-6106-93	4.14	4.77	3.69	4.35	4.24
44	L-6106-93/L-5116-92	5.30	6.24	5.86	5.28	5.67
45	L-6106-93/L-4222-92	4.83	5.85	5.59	5.60	5.47
46	L-6106-93/L-4272-92	4.25	4.11	5.11	4.82	4.57
47	L-6106-93/L-5312-92	4.45	4.80	4.23	4.46	4.49
48	L-6106-93/C.I.Nos. 1432	5.01	4.15	5.60	4.48	4.81
49	L-6106-93/Crista B-15	4.33	4.23	3.81	4.64	4.25
50	L-6106-93/L- NP (RR)	3.87	4.20	4.00	4.11	4.05
51	L-5116-92	4.89	4.36	4.61	4.55	4.60
52	L-5116-92/L-4222-92	4.12	3.86	4.06	4.14	4.05
53	L-5116-92/L-4272-92	6.73	5.85	7.20	5.87	6.41
54	L-5116-92/L-5312-92	6.30	7.31	7.45	6.81	6.97
55	L-5116-92/C.I.Nos. 1432	3.24	2.95	3.00	3.56	3.19
56	L-5116-92/Crista B-15	3.06	2.59	2.56	2.43	2.66
57	L-5116-92/L- NP (RR)	3.15	3.50	3.73	4.05	3.61
58	L-4222-92	4.49	4.40	3.87	4.69	4.36
59	L-4222-92/L-4272-92	4.14	4.59	5.35	4.77	4.71
60	L-4222-92/L-5312-92	6.30	5.62	6.24	5.77	5.98
61	L-4222-92/C.I.Nos. 1432	4.08	4.34	4.38	4.79	4.40
62	L-4222-92/Crista B-15	4.67	5.60	5.01	4.77	5.01
63	L-4222-92/L- NP (RR)	3.21	3.16	3.65	3.88	3.48
64	L-4272-92	5.96	5.46	5.11	6.16	5.67
65	L-4272-92/L-5312-92	5.89	5.27	5.78	5.97	5.73
66	L-4272-92/C.I.Nos. 1432	5.17	5.02	4.86	5.59	5.16
67	L-4272-92/Crista B-15	3.78	4.10	4.34	4.14	4.09
68	L-4272-92/L- NP (RR)	4.82	4.73	4.90	5.35	4.95
69	L-5312-92	5.04	5.96	4.91	5.45	5.34
70	L-5312-92/C.I.Nos. 1432	4.88	4.42	5.17	4.39	4.72
71	L-5312-92/Crista B-15	4.82	5.64	5.46	4.88	5.20
72	L-5312-92/L-NP (RR)	3.39	3.71	4.04	4.49	3.91
73	C.I.Nos. 1432	2.40	2.62	1.87	2.23	2.28
74	C.I.Nos. 1432/Crista B-15	2.52	2.64	2.13	2.35	2.41
75	C.I.Nos. 1432/L-NP (RR)	2.59	2.73	2.10	2.42	2.46
76	Crista B-15	2.06	2.20	2.01	2.12	2.10
77	Crista B-15/L-NP (RR)	2.70	2.55	2.68	2.64	2.64
78	NP (RR)	2.17	2.36	2.03	2.28	2.21

General mean 4.51  
L.S.D. 5% 0.08  
Coefficient of variation 8.73%

involved in the genetic control of NBSM (Table 5). These data highlighted, also, that the effects of dominance were prevalent in the heredity of this trait, as compared to additive ones (sum of variances of all dominance effects were more than two time higher than that estimated for additivity).

Table 4. Block variance analysis for linseed number of bolls per square meter (R.I.C.I.C. - Fundulea, 1995)

Source of variation	SS	DF	s <sup>2</sup>	F
Blocks	0.14	3	0.05	
Genotypes	409.84	77	5.32	34.41***
Error	35.73	231	0.15	
Total	445.71	311	-	

\*\*\* - Significant for P<0.001

Data from table 5 suggested also that dominance of NBSM was unidirectional (1 component significant for P<0.001); the favorable and unfavorable alleles involved in this trait were asymmetric distributed among the twelve parents (li component significant for P<0.001); and finally, in case of this set of parents some hybrids with specific unexpected reaction (lixj significant for P<0.001) were produced.

Table 5. 1/2 diallel table variance analysis linseed number of bolls per square meter (R.I.C.I.C. - Fundulea, 1995)

Source of variation	SS	DF	s <sup>2</sup>	F
Additive contribution of i genotype (gi)	69.75	11	6.34	40.99***
Mean deviation due to dominance (l)	15.33	1	15.33	90.09***
Dominance deviation due to i genotype (li)	8.33	11	0.73	4.90***
Dominance deviation due to ixj cross (li x j)	129.62	54	2.40	15.52***
Error	35.73	231	0.15	-

\*\*\* - Significant for P<0.001

Analysis of both the values of additive (gi) and dominance (li) effects at each parent level revealed that the parent genotypes L-4272-92, L-5312-92 and L-3060-91 had the best positive additive effects for this trait while parents L-5312-92 and L-5506-91 had the best positive dominance effects (Table 6).

The best positive specific reaction (the better hybrid combination) for NBSM were L-3060-92/C.I. Nos 1432, L-3060-92/L-8254-91, L-5116-92 / L-5312-92, L-4222-92 / Crista B-15, L-5116-92 / L-4272-92, L-6529-90 /

NP(RR) (Table 7).

Table 6. Additive effects (gi), dominance deviation (li) and mean dominance deviation (l) of the twelve linseed parental genotypes for number of bolls/m<sup>2</sup> (R.I.C.I.C. - Fundulea, 1995)

Parental genotype	gi	li
L-6529-90	0.208±0.009	0.193±0.012
L-5506-91	0.134±0.009	0.342±0.012
L-3060-91	0.628±0.009	-0.432±0.012
L-8254-91	-0.425±0.009	0.009±0.012
L-6106-93	0.125±0.009	0.153±0.012
L-5116-92	0.308±0.009	-0.301±0.012
L-4222-92	0.188±0.009	-0.013±0.012
L-4272-92	0.843±0.009	-0.248±0.012
L-5312-92	0.677±0.009	0.397±0.012
C.I.Nos. 1432	-0.853±0.009	0.154±0.012
Crista B-15	-0.945±0.009	-0.106±0.012
NP (RR)	-0.888±0.009	-0.148±0.012
I = 0.614 ± 0.004		

Because the covariance and variance differences (Wr-Vr) of the arrays with a common parent, for linseed NBSM, is expected to be constant if an additive-dominance model with independent gene distribution is adequate to explain the genetic control of this trait (see Mather and Jinks, 1974), first step of graphical analysis of covariance (Wr) and variance (Vr) was the variance analysis of covariance-variance differences. The lack of significance of arrays differences (Wr-Vr) suggested that this model was appropriate to explain this trait heredity of NBSM (Table 8). These data were also confirmed by the graphical analysis of covariance (Wr) and variance (Vr) for this trait, the value of the regression line slope (b=1.035±0.011) non-significant different from 1.00.

The graphical analysis of covariance and variance suggested also some other important aspects of the heritability of NBSM. The linseed NBSM had an "over-dominant" type of genetic control (a = -0.346; D<H1); the parents with the highest number of dominant genes were L-6106-93, L-3060-91, L-4222-92 and L-4272-92; the parents with the highest number of recessive genes were L-8254-91, C.I. Nos. 1432 and L-5115-92; none of the parents was too near from the theoretical parents with maximum number of dominant or recessive genes (Figure 1).

The next stage of this study was the estimation of the components of genetic variation,

D,  $H_1$ ,  $H_2$ , F,  $h^2$  and E, of their proportional values with genetic significance and of the

Significance of both D (which estimates the additive effects) and  $H_1$ ,  $H_2$  and  $h^2$  param-

Table 7. Dominance deviation due to  $i \times j$  cross ( $i, j$ ) for linseed number of bolls per square meter (R.I.C.I.C. - Fundulea, 1995)

No.	Female genotype	Male genotype										
		2	3	4	5	6	7	8	9	10	11	12
1	L-6529-90	0.213	-0.571	-0.771	0.160	-0.866	-0.087	-0.647	0.873	0.128	0.453	1.114
2	L-5506-91	x	0.249	-0.206	0.375	0.012	0.178	0.255	0.560	-0.237	-0.912	-0.488
3	L-3060-91	x	x	1.633	-0.686	-0.427	-0.723	-0.996	-0.601	1.667	0.102	0.351
4	L-8254-91	x	x	x	0.319	0.321	0.390	0.884	0.172	-1.348	-0.663	-0.732
5	L-6106-93	x	x	x	x	0.784	0.163	-0.902	-1.468	0.630	0.423	0.202
6	L-5116-92	x	x	x	x	x	-0.738	1.209	1.287	-0.720	-0.898	0.036
7	L-4222-92	x	x	x	x	x	x	-0.659	0.133	0.321	1.286	-0.265
8	L-4272-92	x	x	x	x	x	x	x	-0.542	0.663	-0.056	0.790
9	L-5312-92	x	x	x	x	x	x	x	x	-0.259	0.576	-0.731
10	C.I.Nos. 1432	x	x	x	x	x	x	x	x	x	-0.441	-0.405
11	Crista B-15	x	x	x	x	x	x	x	x	x	x	0.128
12	NP (RR)	x	x	x	x	x	x	x	x	x	x	x

var. ( $li \times j$ ) = 0.032

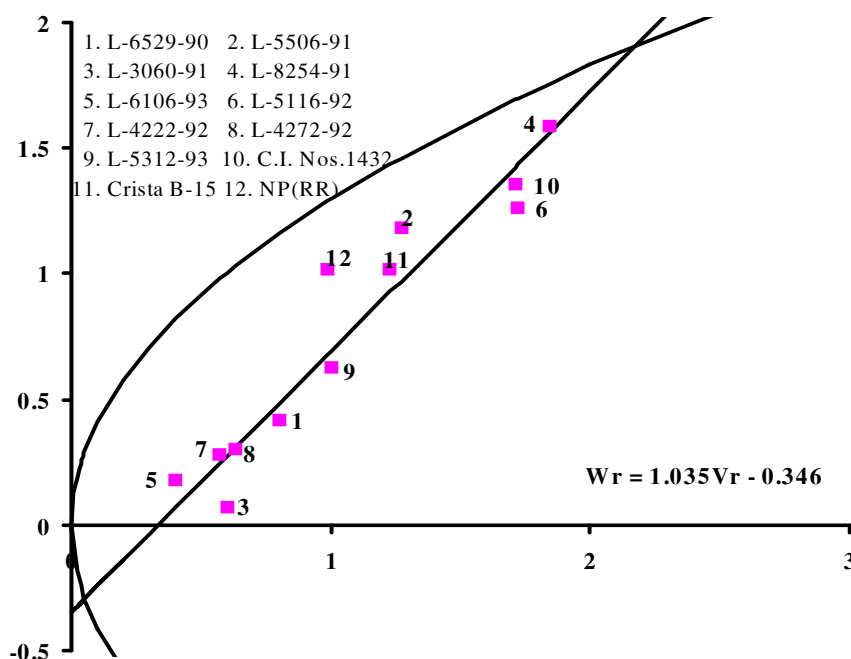


Figure 1. Covariance ( $W_r$ ) and variance ( $V_r$ ) graphical analysis for linseed number of bolls/m<sup>2</sup> (RICIC Fundulea, 1995)

heritability coefficients (in broad and narrow sense) for this trait (Table 9).

Table 8. Variance analysis of covariance - variance differences ( $W_r - V_r$ ) for linseed number of bolls/m<sup>2</sup> (R.I.C.I.C. - Fundulea, 1995)

Source of variation	SS	DF	$s^2$	F
Blocks	0.253	3	0.084	
Arrays ( $W_r - V_r$ )	1.181	11	0.107	2.101 <sup>NS</sup>
Error	1.686	33	0.051	
Total	3.120	47	-	

N.S. - Non significant

ters (for dominance effects) confirmed that in the genetic control of the linseed NBSM the both types of effects, but dominance being however prevalent, were involved.

F value was not significantly different from zero, showing that an almost similar number of dominant and recessive alleles was present among the twelve linseed genotypes.

The proportional values ( $H_1D$ )<sup>1/2</sup> or  $V_r/W_r$  (which estimate the mean dominance ratio) having a value larger than 1.00 (1.274 or 1.395)

confirmed the graphical analysis results ("over-dominance" type of dominance).

Table 9. Components of the genetic variation for linseed number of bolls per square meter (R.I.C.I.C. - Fundulea, 1995)

Component	Values
a) Genetic parameter:	
D	1.524±0.030
H <sub>1</sub>	2.471±0.060
H <sub>2</sub>	2.306±0.050
F	-0.016±0.068
h <sup>2</sup>	1.462±0.034
E	0.155±0.033
b) Proportional values:	
(H <sub>1</sub> /D) <sup>1/2</sup>	1.247
V <sub>r</sub> /W <sub>r</sub>	0.395
H <sub>2</sub> /4H <sub>1</sub>	0.234
$\frac{(4DH_1)^{1/2}+F}{(4DH_1)^{1/2}-F}$	0.992
$\frac{1}{2}F$	
$[D(H_1-H_2)]^{1/2}$	0.016
h <sup>2</sup> /H <sub>2</sub>	0.634
c) Heredity coefficients:	
- in narrow sense	0.538
- in broad sense	0.902

The ratio  $[(4DH_1)^{1/2}+F]/[(4DH_1)^{1/2}-F]$ , which estimates the total number of dominant and recessive genes among parents, had value very close to 1.00, suggesting a symmetric distribution of these kinds of genes among the twelve linseed genotypes.

The same fact was spotlighted also by the H<sub>2</sub>/4H<sub>1</sub> ratio, which assesses the relative partition of the dominant and recessive genes among parents. H<sub>2</sub>/4H<sub>1</sub> ratio value, very close to its maximum theoretical value of 0.25 (occurring when these genes have the same frequency = 0.5 at all loci) showed the equality of dominant and recessive genes.

The ratio  $1/2 F/[D(H_1-H_2)]^{1/2}$ , which had a value very close to zero, showed that dominance was not consistent over all loci.

From the h<sup>2</sup>/H<sub>2</sub> ratio, the NBSM seemed to be controlled by one gene or one group of dominant genes (Table 9).

Linseed NBSM had a relatively good level of heredity, the heredity coefficients obtained by variance decomposition being between 0.54 in narrow sense and 0.99 in broad sense (Table 9).

Comparison among the sum of covariance and variance of the hybrid arrays with a common parent (W<sub>r</sub>+V<sub>r</sub>) with values of the theo-

retical parents with a maximum number of dominant (W<sub>r</sub>' + V<sub>r</sub>' = -0.24) or recessive (W<sub>r</sub>" + V<sub>r</sub>" = 4.37) genes, suggested that none of the twelve linseed parental genotypes was close to the latter ones (Table 10).

The highest dominant genes number among these parents belong to L-6106-93, L-3060-92, L-4222-92 and L-4272-92 genotypes. The dominance order of these parents was L-6106-93, L-3060-91, L-4222-92, L-6529-90, L-5312-92, NP(RR), L-5506-91, L-5116-92, C.I. Nos. 1432, Crista B-15 and L-8254-91 (Table 10).

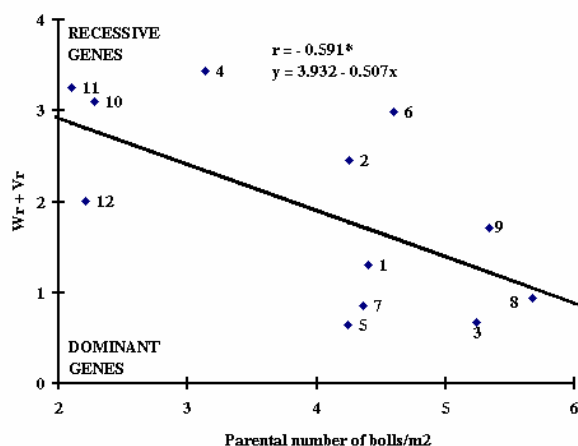
Table 10. Mean parental number of bolls per square meter (Y<sub>r</sub>), sum of covariance and variance of the arrays with one common parent (W<sub>r</sub> + V<sub>r</sub>), values of the theoretical parents with a maximum number of dominant (W<sub>r</sub>' + V<sub>r</sub>') and recessive (W<sub>r</sub>" + V<sub>r</sub>") genes and order of dominance for linseed number of bolls per square meter (R.I.C.I.C. - Fundulea, 1995)

Parental genotype	Y <sub>r</sub> (thousands)	W <sub>r</sub> + V <sub>r</sub>	W <sub>r</sub> ' + V <sub>r</sub> '	W <sub>r</sub> " + V <sub>r</sub> "
L-6529-90	4.40	1.31		
L-5506-91	4.26	2.46		
L-3060-91	5.24	0.68		
L-8254-91	3.14	3.45		4.37
L-6106-93	4.24	0.65	-0.24	
L-5116-92	4.60	2.99		
L-4222-92	4.36	0.85		
L-4272-92	5.67	0.94		
L-5312-92	5.34	1.71		
C.I.Nos. 1432	2.28	3.08		
Crista B-15	2.10	3.25		
NP (RR)	2.21	2.01		
Order of Dominance:	L-6106-93, L-3060-91, L-4222-92, L-4272-92, L-6529-90, L-5312-92, NP (RR), L-5506-91, L-5116-92, C.I.Nos. 1432, Crista B-15, L-8254-91			

Correlation between mean parent NBSM and sum of covariance and variance of the hybrids arrays having a common parent (W<sub>r</sub>+V<sub>r</sub>) had a negative and significant (P<0.05) value (-0.59), meaning that dominance of this trait was unidirectional and that dominant alleles involved in its heredity had an increasing effect on NBSM (Figure 2).

Finally, the mid parent - F<sub>1</sub> hybrid offspring regression (which offers a better evaluation of the narrow sense heritability than classical methods of variance partition - see Simmonds, 1979) suggested that NBSM

might have had a higher level of heritability than when estimated by variance decomposition (Figure 3).



\* Significant for  $P < 0.05$

- |              |              |                    |
|--------------|--------------|--------------------|
| 1. L 6529-90 | 5. L 5116-93 | 9. L 5312-93       |
| 2. L 5506-90 | 6. L 5116-92 | 10. C.I. Nos. 1432 |
| 3. L 3060-91 | 7. L 4222-92 | 11. Crista B-15    |
| 4. L 8254-91 | 8. L 4272-92 | 12. NP (RR)        |

Figure 2. Correlation between mean parental number of bolls/m<sup>2</sup> and sum of covariance and variance of hybrid.

## CONCLUSIONS

Due to the strong relationship between the linseed NBSM and seed yield ( $r=0.92^{***}$ ), genetic study of this trait have an wide interest for all linseed breeders.

This study showed that both additive and dominance effects of the genes which are involved in the genetic control of NBSM were present, but dominance was more important and prevalent.

The dominant genes had an unidirectional effect, were asymmetric distributed among parents and produced some hybrids with unexpected specific reaction.

Linseed NBSM was controlled by a genetic mechanism of "over-dominant" type, dominant alleles having generally an increasing effect on it.

The total number of dominant and recessive genes controlling NBSM had almost an equal frequency, dominance being not consistent over all loci, among the twelve linseed parents.

It seems that in the heredity of this trait (for this specific set of genitors) one gene or one group of dominant genes was involved.

Data showed also that linseed NBSM had

bridged array with a common parent ( $W_r + V_r$ ) for linseed number of bolls/m<sup>2</sup> (RICIC Fundulea, 1995)

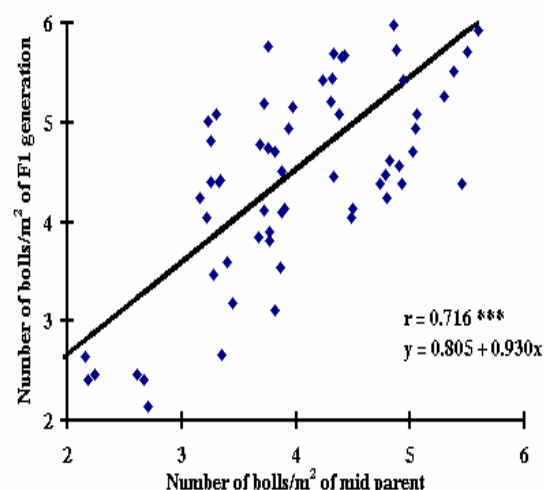


Figure 3. Mid parent – F<sub>1</sub> hybrid of spring regression for linseed number of bolls/m<sup>2</sup> (RICIC Fundulea, 1995)

a relative good (according to variance partition) or very good (according to parent-offspring regression) level of heredity.

Because none of the twelve linseed genotypes used in this cross program was close to the theoretical parent with maximum number of dominant or recessive genes for this trait, probability to obtain superior segregates by using this biological material is relatively low, additionally germplasm seeking being necessary.

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**Table 1. Characterization of twelve linseed parental genotypes (R.I.C.I.C. Fundulea, 1995)**

Parent	Origin	Trait					
		Number of bolls/m <sup>2</sup>	Plants length (cm)	TSW (g)	Seed yield (t/ha)	Oil content (%)	Oil yield (t/ha)
L - 6529 - 90	Romania	4.40	49.25	6.20	2.30	47.20	1.09
L - 5506 - 90	Romania	4.26	62.50	7.00	2.08	42.60	0.89
L - 3060 - 91	Romania	5.24	60.75	7.80	2.54	47.60	1.21
L - 8254 - 91	Romania	3.14	50.75	7.00	2.18	44.68	0.98
L - 6106 - 93	Romania	4.24	55.50	7.50	2.30	49.53	1.14
L - 5115 - 92	Romania	4.60	68.50	6.40	2.02	41.78	0.84
L - 4222 - 92	Romania	4.36	59.25	7.10	2.16	44.70	0.97
L - 4272 - 92	Romania	5.67	70.25	7.00	2.80	46.58	0.86
L - 5312 - 92	Romania	5.34	50.90	7.10	2.40	46.08	1.11
C.I. Nos. 1432	India	2.28	35.50	4.80	1.48	40.23	0.60
Crista B - 15	Germany	2.10	35.25	8.10	1.51	41.40	0.62
NP (RR)	India	2.21	29.25	8.30	1.55	40.83	0.63
Mean		3.99	53.14	7.03	2.11	44.43	0.91
L.S.D. 5%		0.55	2.05	0.08	0.22	0.24	0.11

**Table 2. Phenotypic correlation coefficients among number of bolls per square meter, plants length, thousand seed weight (TSW), seed yield, oil content and oil yield of the twelve linseed parental genotypes**

R.I.C.I.C. Fundulea, 1995

Independent variable	Dependent variable				
	Plant length	TSW	Seed yield	Oil content	Oil yield
Number of bolls/m <sup>2</sup>	0.84***	0.01 <sup>NS</sup>	0.92***	0.70*	0.75**
Plant length		0.02 <sup>NS</sup>	0.77**	0.45 <sup>NS</sup>	0.52 <sup>NS</sup>
TSW			0.09 <sup>NS</sup>	0.19 <sup>NS</sup>	0.13 <sup>NS</sup>
Seed yield				0.84***	0.80**
Oil content					0.89***

NS - Non significant

\*, \*\*, \*\*\* - Significant for P&lt;0.05, P&lt;0.01 and P&lt;0.001 respectively

**Table 3. Number of bolls per square meter (thousands) of twelve linseed parental genotypes and of all their 1/2 diallel F1 hybrids (R.I.C.I.C. - Fundulea, 1995)**

No.	Genotype	Replication				Mean
		I	II	III	IV	
1	L-6529-90	4.62	4.49	4.41	4.09	4.40
2	L-6529-90/L-5506-91	5.17	5.06	6.55	5.98	5.69
3	L-6529-90/L-3060-91	4.43	5.10	4.41	4.57	4.63
4	L-6529-90/L-8254-91	3.93	3.86	3.81	3.66	3.82
5	L-6529-90/L-6106-93	5.43	5.13	5.11	6.09	5.44
6	L-6529-90/L-5116-92	4.6	3.63	4.33	4.01	4.14
7	L-6529-90/L-4222-92	4.67	6.07	4.77	4.85	5.09
8	L-6529-90/L-4272-92	5.30	5.55	4.78	4.17	4.95
9	L-6529-90/L-5312-92	6.30	7.14	7.05	7.30	6.95
10	L-6529-90/C.I.Nos. 1432	3.83	4.86	4.07	4.96	4.43
11	L-6529-90/Crista B-15	4.02	4.42	4.01	5.17	4.41
12	L-6529-90/L-NP (RR)	4.89	5.87	5.07	4.49	5.08
13	L-5506-91	4.78	4.07	4.20	4.00	4.26
14	L-5506-91/L-3060-91	5.52	5.47	5.40	5.70	5.52
15	L-5506-91/L-8254-91	4.87	4.22	4.15	4.58	4.46
16	L-5506-91/L-6106-93	5.83	5.83	5.39	5.87	5.73
17	L-5506-91/L-5116-92	5.40	5.31	4.92	4.75	5.10
18	L-5506-91/L-4222-92	5.52	5.49	5.07	5.64	5.43
19	L-5506-91/L-4272-92	6.57	6.05	5.21	5.88	5.93
20	L-5506-91/L-5312-92	7.28	6.10	7.37	6.09	6.71
21	L-5506-91/C.I.Nos. 1432	3.83	3.87	4.32	4.54	4.14
22	L-5506-91/Crista B-15	2.86	3.19	3.34	3.07	3.12
23	L-5506-91/L-NP (RR)	3.10	3.66	3.52	3.93	3.55
24	L-3060-91	5.31	5.37	5.90	4.39	5.24
25	L-3060-91/L-8254-91	6.01	5.63	5.89	6.53	6.02
26	L-3060-91/L-6106-93	4.82	4.09	4.14	4.51	4.39
27	L-3060-91/L-5116-92	4.09	4.64	4.32	4.46	4.38
28	L-3060-91/L-4222-92	4.52	3.88	4.47	4.13	4.25
29	L-3060-91/L-4272-92	4.61	4.01	4.40	4.57	4.40
30	L-3060-91/L-5312-92	5.19	5.59	5.40	4.90	5.27
31	L-3060-91/C.I.Nos. 1432	6.08	5.91	4.97	6.10	5.77
32	L-3060-91/Crista B-15	3.65	3.59	4.16	4.00	3.85
33	L-3060-91/L-NP (RR)	4.45	4.05	3.72	4.23	4.11
34	L-8254-91	2.85	3.45	2.94	3.31	3.14
35	L-8254-91/L-6106-93	4.67	4.34	5.43	4.69	4.78
36	L-8254-91/L-5116-92	5.16	4.29	4.14	4.46	4.51
37	L-8254-91/L-4222-92	5.18	4.62	4.81	4.39	4.75
38	L-8254-91/L-4272-92	5.92	5.87	5.71	5.16	5.67
39	L-8254-91/L-5312-92	4.86	5.29	5.56	6.01	5.43

No.	Genotype	Replication				Mean
		I	II	III	IV	
40	L-8254-91/C.I.Nos. 1432	2.06	2.21	2.17	2.11	2.14
41	L-8254-91/Crista B-15	2.44	2.66	2.49	2.30	2.47
42	L-8254-91/L-NP (RR)	2.67	2.27	2.37	2.36	2.42
43	L-6106-93	4.14	4.77	3.69	4.35	4.24
44	L-6106-93/L-5116-92	5.30	6.24	5.86	5.28	5.67
45	L-6106-93/L-4222-92	4.83	5.85	5.59	5.60	5.47
46	L-6106-93/L-4272-92	4.25	4.11	5.11	4.82	4.57
47	L-6106-93/L-5312-92	4.45	4.80	4.23	4.46	4.49
48	L-6106-93/C.I.Nos. 1432	5.01	4.15	5.60	4.48	4.81
49	L-6106-93/Crista B-15	4.33	4.23	3.81	4.64	4.25
50	L-6106-93/L- NP (RR)	3.87	4.20	4.00	4.11	4.05
51	L-5116-92	4.89	4.36	4.61	4.55	4.60
52	L-5116-92/L-4222-92	4.12	3.86	4.06	4.14	4.05
53	L-5116-92/L-4272-92	6.73	5.85	7.20	5.87	6.41
54	L-5116-92/L-5312-92	6.30	7.31	7.45	6.81	6.97
55	L-5116-92/C.I.Nos. 1432	3.24	2.95	3.00	3.56	3.19
56	L-5116-92/Crista B-15	3.06	2.59	2.56	2.43	2.66
57	L-5116-92/L- NP (RR)	3.15	3.50	3.73	4.05	3.61
58	L-4222-92	4.49	4.40	3.87	4.69	4.36
59	L-4222-92/L-4272-92	4.14	4.59	5.35	4.77	4.71
60	L-4222-92/L-5312-92	6.30	5.62	6.24	5.77	5.98
61	L-4222-92/C.I.Nos. 1432	4.08	4.34	4.38	4.79	4.40
62	L-4222-92/Crista B-15	4.67	5.60	5.01	4.77	5.01
63	L-4222-92/L- NP (RR)	3.21	3.16	3.65	3.88	3.48
64	L-4272-92	5.96	5.46	5.11	6.16	5.67
65	L-4272-92/L-5312-92	5.89	5.27	5.78	5.97	5.73
66	L-4272-92/C.I.Nos. 1432	5.17	5.02	4.86	5.59	5.16
67	L-4272-92/Crista B-15	3.78	4.10	4.34	4.14	4.09
68	L-4272-92/L- NP (RR)	4.82	4.73	4.90	5.35	4.95
69	L-5312-92	5.04	5.96	4.91	5.45	5.34
70	L-5312-92/C.I.Nos. 1432	4.88	4.42	5.17	4.39	4.72
71	L-5312-92/Crista B-15	4.82	5.64	5.46	4.88	5.20
72	L-5312-92/L-NP (RR)	3.39	3.71	4.04	4.49	3.91
73	C.I.Nos. 1432	2.40	2.62	1.87	2.23	2.28
74	C.I.Nos. 1432/Crista B-15	2.52	2.64	2.13	2.35	2.41
75	C.I.Nos. 1432/L-NP (RR)	2.59	2.73	2.10	2.42	2.46
76	Crista B-15	2.06	2.20	2.01	2.12	2.10
77	Crista B-15/L-NP (RR)	2.70	2.55	2.68	2.64	2.64
78	NP (RR)	2.17	2.36	2.03	2.28	2.21

General mean 4.51  
L.S.D. 5% 0.08  
Coefficient of variation 8.73%

**Table 4. Block variance analysis for linseed number of bolls per square meter  
(R.I.C.I.C. - Fundulea, 1995)**

Source of variation	SS	DF	s <sup>2</sup>	F
Blocks	0.14	3	0.05	
Genotypes	409.84	77	5.32	34.41***
Error	35.73	231	0.15	
Total	445.71	311	-	

\*\*\* - Significant for P<0.001

**Table 5. 1/2 diallel table variance analysis linseed number of bolls per square meter  
(R.I.C.I.C. - Fundulea 1995)**

Source of variation	SS	DF	s <sup>2</sup>	F
Additive contribution of i genotype (gi)	69.75	11	6.34	40.99***
Mean deviation due to dominance (l)	15.33	1	15.33	90.09***
Dominance deviation due to i genotype (li)	8.33	11	0.73	4.90***
Dominance deviation due to ixj cross (li x j)	129.62	54	2.40	15.52***
Error	35.73	231	0.15	-

\*\*\* - Significant for P<0.001

**Table 6. Additive effects (gi), dominance deviation (li) and mean dominance deviation (l) of the twelve linseed parental genotypes for number of bolls/m<sup>2</sup>  
(R.I.C.I.C. - Fundulea, 1995)**

No.	Parental genotype	gi	li
1	L-6529-90	0.208±0.009	0.193±0.012
2	L-5506-91	0.134±0.009	0.342±0.012
3	L-3060-91	0.628±0.009	-0.432±0.012
4	L-8254-91	-0.425±0.009	0.009±0.012
5	L-6106-93	0.125±0.009	0.153±0.012
6	L-5116-92	0.308±0.009	-0.301±0.012
7	L-4222-92	0.188±0.009	-0.013±0.012
8	L-4272-92	0.843±0.009	-0.248±0.012
9	L-5312-92	0.677±0.009	0.397±0.012
10	C.I.Nos. 1432	-0.853±0.009	0.154±0.012
11	Crista B-15	-0.945±0.009	-0.106±0.012
12	NP (RR)	-0.888±0.009	-0.148±0.012
		? gi = 0	? li = 0
l = 0.614±0.004			

**Table 7. Dominance deviation due to i x j cross (li x j) for linseed number of bolls per square meter  
(R.I.C.I.C. - Fundulea, 1995)**

No.	Female genotype	Male genotype										
		2	3	4	5	6	7	8	9	10	11	12
1	L-6529-90	0.213	-0.571	-0.771	0.160	-0.866	-0.087	-0.647	0.873	0.128	0.453	1.114
2	L-5506-91	x	0.249	-0.206	0.375	0.012	0.178	0.255	0.560	-0.237	-0.912	-0.488
3	L-3060-91	x	x	1.633	-0.686	-0.427	-0.723	-0.996	-0.601	1.667	0.102	0.351
4	L-8254-91	x	x	x	0.319	0.321	0.390	0.884	0.172	-1.348	-0.663	-0.732
5	L-6106-93	x	x	x	x	0.784	0.163	-0.902	-1.468	0.630	0.423	0.202
6	L-5116-92	x	x	x	x	x	-0.738	1.209	1.287	-0.720	-0.898	0.036
7	L-4222-92	x	x	x	x	x	x	-0.659	0.133	0.321	1.286	-0.265
8	L-4272-92	x	x	x	x	x	x	x	-0.542	0.663	-0.056	0.790
9	L-5312-92	x	x	x	x	x	x	x	x	-0.259	0.576	-0.731
10	C.I.Nos. 1432	x	x	x	x	x	x	x	x	x	-0.441	-0.405
11	Crista B-15	x	x	x	x	x	x	x	x	x	x	0.128
12	NP (RR)	x	x	x	x	x	x	x	x	x	x	x

var. (li x j) = 0.032

**Table 8. Variance analysis of covariance - variance differences ( $W_r - V_r$ ) for linseed number of bolls/m<sup>2</sup> (R.I.C.I.C. - Fundulea, 1995)**

Source of variation	SS	DF	s <sup>2</sup>	F
Blocks	0.253	3	0.084	
Arrays ( $W_r - V_r$ )	1.181	11	0.107	2.101 <sup>NS</sup>
Error	1.686	33	0.051	
Total	3.120	47	-	

N.S. - Non significant

**Table 9. Components of the genetic variation for linseed number of bolls per square meter (R.I.C.I.C. - Fundulea, 1995)**

Component	Values
a) Genetic parameter:	
D	1.524±0.030
H <sub>1</sub>	2.471±0.060
H <sub>2</sub>	2.306±0.050
F	-0.016±0.068
h <sup>2</sup>	1.462±0.034
E	0.155±0.033
b) Proportional values:	
(H <sub>1</sub> /D) <sup>1/2</sup>	1.247
V <sub>r</sub> /W <sub>r</sub>	0.395
H <sub>2</sub> /4H <sub>1</sub>	0.234
$\frac{(4DH_1)^{1/2} + F}{1/2 F}$	0.992
$[D(H_1 - H_2)]^{1/2}$	0.016
h <sup>2</sup> /H <sub>2</sub>	0.634
c) Heredity coefficients:	
- in narrow sense	0.538
- in brood sense	0.902

**Table 10. Mean parental number of bolls per square meter ( $Y_r$ ), sum of covariance and variance of the arrays with one common parent ( $W_r + V_r$ ), values of the theoretical parents with a maximum number of dominant ( $W_r' + V_r'$ ) and recessive ( $W_r'' + V_r''$ ) genes and order of dominance for linseed number of bolls per square meter (R.I.C.I.C. - Fundulea, 1995)**

Parental genotype	$Y_r$ (thousands)	$W_r + V_r$	$W_r' + V_r'$	$W_r'' + V_r''$
L-6529-90	4.40	1.31		
L-5506-91	4.26	2.46		
L-3060-91	5.24	0.68		
L-8254-91	3.14	3.45		4.37

*F. POPESCU ET AL. . HEREDITY OF THE LINSEED NUMBER OF BOLLS PER SQUARE METER*

L-6106-93	4.24	0.65	-0.24
L-5116-92	4.60	2.99	
L-4222-92	4.36	0.85	
L-4272-92	5.67	0.94	
L-5312-92	5.34	1.71	
C.I.Nos. 1432	2.28	3.08	
Crista B-15	2.10	3.25	
NP (RR)	2.21	2.01	
Order of dominance:	L-6106-93, L-3060-91, L-4222-92, L-4272-92, L-6529-90, L-5312-92, NP (RR), L-5506-91, L-5116-92, C.I.Nos. 1432, Crista B-15, L-8254-91		

**Figure 1. Covariance (Wr) and variance (Vr) graphical analysis for linseed number of bolls/m<sup>2</sup> RICIC Fundulea, 1995**