

# GENETIC CONTROL OF THE NUMBER OF NODES PER STEM IN MILLET (*Panicum miliaceum* L.)

Mihai Pricop\*

## ABSTRACT

The number of nodes per stem in millet has a special contribution to plant growth and development, being directly, positively and significantly correlated with the number of leaves and panicles per plant, TKW, green mass, grain and protein yield. The researches performed at Agricultural Research and Development Station Podu-Iloaiei pointed out an average variability for this trait. Hybridological analyses showed that the trait value was not influenced by environmental conditions, being determined by genotype and controlled by the presence of 4.4 dominant genes, with partial dominance effect, although the additivity effects have the highest percentage into the total genetic variance. The established heredity coefficients show that this trait has a high transmission to the offsprings and could be used into transgressive selection.

**Key words:** additivity effects, genetic control, millet, number of nodes per stem

## INTRODUCTION

Millet growing (*Panicum miliaceum* L.), contemporary with that of wheat, lost from its importance and area at the same time with the extension of maize, buckwheat and potato, being recorded in many countries, as a sporadic crop (Pricop, 1997).

After 1980, in Romania, as a necessity of successive crop development, the millet was reconsidered as a crop plant and the releasing of productive cultivars, qualitatively superior, which reach maturation under successive crop conditions, has started (Pricop and Pricop, 1997; Pricop, 1997).

The number of nodes per stem has a special contribution to plant growth and development, being directly, positively and significantly correlated with many other productivity traits.

The aim of this paper was to perform a complete study regarding the heredity of the number of nodes per stem and to identify the cultivars able to produce, by hybridization, superior genotypes for grain yield.

## MATERIAL AND METHODS

The biological material, consisting of seven millet genotypes, different as precocity and botanical variety (Pricop and Pricop, 1998; Pricop, 1998) and 21 hybrid combinations obtained by direct diallel hybridization, was tested in experiments, performed in randomized blocks and three repetitions on a medium leached cambic chernozem.

In order to establish the correlations between the number of nodes per stem and other 14 traits, five cultivars, tested under principal and successive cropping conditions, were used.

With a view to establish the heredity of nodes number per stem the following analyses were performed: ANOVA for all cultivars (Ceapoiu, 1968); table's half diallel variance analyses (Walters and Morton, 1978); estimation of components of both genetic variance and heritability coefficients in narrow and large sense (Jinks, 1954; Hayman, 1954; Mather and Jinks, 1974); determination of theoretical genetic parents with a maximum number of dominant and recessive genes (Joshi et al., 1961) as well as the sum of adequate variance and covariance (Mather and Jinks, 1974).

The study was performed at ARDS Podu-Iloaiei during 1991-1995, with differentiated years from climatic viewpoint but favourable to millet crop. The crop technology of millet for seed was used.

## RESULTS AND DISCUSSION

The study of correlations between the number of nodes per stem and other 14 millet traits shows the existence of some positive and significant statistical relationships which depend on both genotype and cropping type (Table 1). Thus, in the principal cropping the number of nodes per

\* Agricultural Research and Development Station (A.R.D.S.), Podu-Iloaiei, Iasi County, Romania

stem is positively and very significantly correlated with: number of branches per plant (Iantarnoe-414, Turghai, Tall Down); plant height (Minerva); number of panicles per plant (Minerva, Turghai); number of branches per panicle (Minerva);

genotype purposely developed for a cropping type (Turghai).

The average results of the number of nodes per stem (Table 2) at those 28 tested genotypes (seven parents and 21 F<sub>1</sub> hybrids) pointed out an

Table 1. Correlations between the number of nodes per stem and other millet traits

Number of nodes per stem	Type of cropping	„Population”	Minerva	Iantarnoe-414	Turghai	Tall Dawn
Number of tillers	CP	-0.15	0.22	0.80**	0.54**	0.50**
	CS	0.19	0.01	-0.11	-0.25	0.12
Plant height	CP	0.30	0.46**	-0.45°	0.16	0.43*
	CS	0.41*	0.06	0.44*	-0.14	0.30
Number of panicles per plant	CP	0.29	0.38**	0.08	0.66**	0.16
	CS	0.53*	-0.03	0.21	-0.37°	0.18
Panicle length	CP	-0.06	-0.45°	-0.38°	0.21	0.31
	CS	0.10	-0.36°	0.34	0.21	-0.32
Number of branches per panicle	CP	-0.64°°	0.46**	-0.40°	0.14	0.37*
	CS	-0.52°°	0.09	0.07	-0.32	0.43*
Number of floral buds per branches	CP	-0.23	-0.30	0.63**	0.23	0.34
	CS	-0.12	-0.04	0.37*	-0.40°	0.11
Number of grains per branches	CP	-0.24	-0.31	0.64**	0.64**	0.36*
	CS	-0.14	-0.06	0.33	-0.48°°	0.20
Number of grains per panicle	CP	-0.36°	-0.30	0.39*	0.62**	0.44*
	CS	-0.30	-0.06	0.17	-0.48°°	0.10
TKW	CP	0.39*	0.08	0.04	-0.20	-0.24
	CS	0.07	-0.28	0.11	-0.34	-0.10
Grain weight per panicle (g)	CP	-0.33	-0.30	0.63**	0.61**	0.35
	CS	-0.26	-0.05	0.25	-0.41°	0.11
Grain weight per plant (g)	CP	-0.27	-0.30	0.63**	0.60**	0.32
	CS	-0.02	-0.06	0.34	-0.49°°	0.09
Grain yield (t/ha)	CP	-0.02	0.07	0.16	-0.32	0.18
	CS	-0.11	-0.08	-0.56°°	-0.34	0.41*
Fodder yield expressed as dry matter (t/ha)	CP	0.11	-0.14	0.01	-0.25	0.04
	CS	0.09	0.20	-0.15	-0.32	0.09
Protein yield (t/ha)	CP	0.10	0.03	-0.07	-0.14	-0.26
	CS	0.11	-0.05	0.03	-0.12	-0.19

CP = principal cropping; CS = successive cropping

LSD 5 % = 0.36; LSD 1 % = 0.46

number of grains per one branch (Iantarnoe-414, Turghai); number of grains per panicle (Turghai); grain weight per panicle and plant (Iantarnoe-414, Turghai).

Under successive cropping, there are positive and significant correlations between this trait and: plant height (Iantarnoe-414); number of flower buds per one branch of panicle (Iantarnoe-414) and grain yield (Tall Down).

The correlations studied under these two cropping conditions seem to be significantly antagonistic in some cases, primarily due to the

obvious phenotypical variability, showing that this trait ranged between 4.73 (Iantarnoe-414) and 7.61 (Pop. Lovrin Rosu x Pop. Socodor-1).

The simple analysis of variance emphasized the fact that the differences between these genotypes were significant. The study of variance of half diallel table by decomposing the total genetic variance into its components for the additivity effects ( $g_i$ ) and dominance ones ( $l_i$  = average deviation due to dominance,  $l_i$  = dominance deviation due to genotype, and  $l_{ij}$  = dominance deviation due to crossing  $i \times j$ ) of genes involved in the number of nodes per stem heredity, being distinctly significant, demonstrates that have an in-

portant role in genetic control of this trait (Table 3).

Data of this table show that the genes with dominance effect have a prevalent role in manifestation of this trait, while the gene additivity effects control about ¼ from the trait manifestation.

The significance of the three component types of dominance effects emphasizes:

- dominance is of partial-unidirectional type because it has the highest percentage from the total genetic variance (component 1 from table 3);
- positive and negative alleles which control this trait are relatively unequally distributed among parents (component  $l_i$  from tables 3 and 4);
- the existence of certain specific hybrids with residual dominance reaction is obvious for

Table 2. Average values of the number of nodes per stem at seven parental millet genotypes and their direct hybrids in F<sub>1</sub> generation (1994-1995)

Genotypes	Number of nodes per stem	Genotypes	Number of nodes per stem
<b>Pop. Lovrin Rosu</b> ( <i>effusum dacicum</i> , ST)	5.77°	Minerva x Iantarnoe-414	5.70°
Pop. Lovrin Rosu x Pop. Socodor -1	7.61*	Minerva x Skorospeloe-66	5.75°
Pop. Lovrin Rosu x Minerva	5.89°	Minerva x Turghai	5.90°
Pop. Lovrin Rosu x Iantarnoe-414	5.80°	Minerva x Tall Dawn	6.02
Pop. Lovrin Rosu x Skorospeloe-66	5.78°	<b>Iantarnoe-414</b> ( <i>effusum, coccineum</i> , P)	4.73°
Pop. Lovrin Rosu x Turghai	5.85°	Iantarnoe-414 x Skorospeloe-66	5.48°
Pop. Lovrin Rosu x Tall Dawn	6.12	Iantarnoe-414 x Turghai	5.60°
<b>Pop. Socodor -1</b> ( <i>effusum, flavum</i> , ST)	7.41*	Iantarnoe-414 x Tall Dawn	5.89°
Pop. Socodor-1 x Minerva	7.60*	<b>Skorospeloe-66</b> ( <i>contractum, sangvineum</i> , P)	5.25°
Pop. Socodor-1 x Iantarnoe-414	7.49*	Skorospeloe-66 x Turghai	6.00°
Pop. Socodor-1 x Skorospeloe-66	7.52*	Skorospeloe-66 x Tall Dawn	6.12
Pop. Socodor-1 x Turghai	7.58*	<b>Turghai</b> ( <i>effusum, subcoccineum</i> , SP)	5.43°
Pop. Socodor-1 x Tall Dawn	7.30*	Turghai x Tall Dawn	6.25
<b>Minerva</b> ( <i>effusum, flavum</i> , SP)	5.40°	<b>Tall Dawn</b> ( <i>compactum, astrachanicum</i> , ST)	5.57°
<b>Average = 6.17; LSD 5% = 0.17</b>			

P = precocious; SP = semi-precocious; ST = semi-late

Table 3. Analysis of variance of half diallel table

Variability source	FD	Number of nodes per stem		LSD	
		s <sup>2</sup>	F	5%	1%
<b><math>g_i</math></b>	6	2.12	192.68**	(2.29)	(3.18)
<b><math>l</math></b>	1	7.56	686.95**	(4.03)	(7.17)
<b><math>l_i</math></b>	6	0.41	37.60**	(2.29)	(3.18)
<b><math>l_j</math></b>	14	0.07	6.25**	(1.95)	(2.56)
Error	54	0.01	-		

Mathematical model (Walters si Morton, 1978) ?  $Y_{ij} = m + g_i + g_j + l + l_i + l_j$

this set of parental genotypes (component  $l_{ij}$  from tables 3 and 5).

genetic variance and heredity coefficients were estimated. As follows of this estimation, the  $g$ -

Table 4. Additivity effects of parental genotypes ( $g_i$ ) and deviations of supplementary dominance due to genotype ( $l_i$ )

Genotypes	$g_i$	$l_i$
Pop. Lovrin Rosu	0.058	-0.263
Pop. Socodor-1	0.880	0.525
Minerva	-0.126	-0.116
Iantarnoe-414	-0.459	0.037
Skorospeloe-66	-0.201	-0.083
Turghai	-0.111	-0.067
Tall Dawn	-0.041	-0.033
?	0	0

LSD ( $g_i, l_i$ ) = 0.001

Table 5. Dominance deviation  $l_{ij}$  due to crossing  $i \times j$  (genotype)

Genotypes	?	2	3	4	5	6	7
	?						
Pop. Lovrin Rosu	1	0.06	-0.01	0.08	-0.08	-0.11	0.05
Pop. Socodor-1	2		0.09	0.16	0.05	0.01	-0.37
Minerva	3			0.02	-0.07	-0.02	-0.01
Iantarnoe-414	4				-0.16	-0.14	0.04
Skorospeloe-66	5					0.12	0.13
Turghai	6						0.16
Tall Dawn	7						
$l_{ij}$ variance		0.01					

This procedure of genetic analysis permits the particularization of both additivity and dominance effects at the level of each genotype. Taking into account the additivity effects of genes involved into number of nodes per stem manifestation (Table 4, component  $g_i$ ), the most valuable sources are the following genotypes: Pop. Socodor-1 and Pop. Lovrin Rosu, which transmit relatively uniform this trait to offsprings. Positive deviations of supplementary dominance due to genotype have been registered by the population Socodor-1 and Iantarnoe-414 cultivar (Table 4, component  $l_i$ ). The hybrid combinations with positive specific reaction superior for this trait (that present deviations of dominance due to crossing  $i \times j$ , table 5) were: Pop. Lovrin Rosu x Pop. Socodor-1, Minerva x Tall Down, Pop. Lovrin Rosu x Turghai.

Based on variance and covariance of hybrid rows with a common parent, the components of

netic parameters D, H1, H2, F,  $h^2$  and E as well as the ratio with genetic significance between them were obtained (Table 6). The values of all tested parameters proved that, from the genetic control viewpoint, the trait was not too much influenced by the environmental conditions. The significant values of D parameter (that estimates the additivity effects) and very significant ones of H1, H2 and  $h^2$  parameters (that estimate the dominance effects) confirm the fact that both types of gene effect play an important role in this trait, the dominance effects having a prevalent contribution. The negative value of F parameter shows that the recessive gene frequency is in excess vs. dominant gene one.

The ratios  $(H1/D)^{1/2}$  and  $Vr/Wr$  with sub-unitary values, but close to 1, underline the fact that there is a complete dominance and that, as part of total variance, the gene dominance effects

involved in the control of this trait have a prevalent weight.

The ratio  $[(4DH1)^{1/2} + F/(4DH1)^{1/2} - F]$ , being sub-unitary, emphasizes the fact that the dominant and recessive genes are lop-sided distributed among parents and the ratio  $H2/4H1$  confirms the fact that the dominant and recessive alleles have not an equal frequency among parents, having a smaller value than the theoretical one, of 0.25. The value of the relationship  $1/2F/[D(H1-H2)^{1/2}]$  shows that the gene dominance and additivity effects for this trait are very variable from one locus to another. The ratio  $h^2/H1$  indicates the existence of a group of 4.4 genes, with an enough high dominance degree, that influences very significantly this trait. The heredity coefficients certify the trait transmission to offspring.

In table 7, by comparing the values of variance and covariance sum ( $W_r + V_r$ ) of hybrid row with a common parent with the values of theoretical ones with maximum of dominant ( $W_r + V_r$ ) or recessive ( $W_r'' + V_r''$ ) genes, one can conclude that the Pop. Socodor-1 has the highest number of dominant genes while the Iantarnoe-414, the highest number of recessive ones.

The negative but significant correlation between the variance and covariance sum of hybrid row with a common parent ( $W_r + V_r$ ) and the average parental values ( $Y_r$ ) certifies that the dominant genes involved in the number of nodes per stem have a positive effect.

The dominance order is: Pop. Socodor-1, Tall Down, Pop. Lovrin Rosu, Turghai, Minerva, Skorospeloe-66 and Iantarnoe-414.

## CONCLUSIONS

Table 6. The values of genetic variance components for protein yield (t/ha)

Genetic parameters and their derivates	Number of nodes per stem
D	0.702 ± 0.012
H1	0.561 ± 0.028
H2	0.438 ± 0.025
F	-0.459 ± 0.028
$h^2$	1.915 ± 0.017
E	0.011 ± 0.001
$(H1/D)^{1/2}$	0.893
$V_r/W_r$	0.935
$(H2/4H1)$	0.195
$(4DH1)^{1/2} + F/(4DH1)^{1/2} - F$	0.464
$1/2F/[D(H1-H2)^{1/2}]$	-0.783
$h^2/H1$	4.368
Heredity coefficient in narrow sense	0.842
Heredity coefficient in large sense	0.986

Table 7. Selection limits

Genotypes	Number of nodes per stem			
	$Y_r$	$W_r + V_r$	$W_r' + V_r'$	$W_r'' + V_r''$
Pop. Lovrin Rosu	5.77	0.97		
Pop. Socodor-1	7.41	0.01	0.01	
Minerva	5.40	1.09		
Iantarnoe-414	4.73	1.39		1.66
Skorospeloe-66	5.25	1.14		
Turghai	5.33	1.05		
Tall Dawn	5.57	0.69		
Correlation between $Y_r$ and $W_r + V_r$ ; Dominance order	-0.96 2, 7, 1, 6, 3, 5, 4			

Based on the performed genetic study, one can estimate the value of the number of nodes per stem for the breeding process of those seven millet cultivars.

The additivity ( $g_i$ ) and dominance ( $I$ ,  $I_i$  and  $I_{ij}$ ) effects of genes involved in the control of this trait are very significant. In the genetic control of this trait, both effect types play an important role, the dominance effects being prevalent. In the case of complete dominance effects, the positive and negative alleles are unequally distributed among parents.

The presence of a residual dominance due to some hybrids with specific reaction has been noticed.

The dominant and recessive genes are lopsided distributed among parents, the recessive gene frequency being in excess. For the tested genotypes, the existence of about 4.4 dominant genes in the genetic control of the number of nodes per stem has been emphasized.

The heredity coefficients, in narrow and large sense, demonstrate that this trait has a high transmission to offspring.

The theoretical parents with a maximum number of dominant ( $Wr' + Vr'$ ) and recessive ( $Wr'' + Vr''$ ) genes give the possibility to estimate, with a good probability, the selection limits in the case of the studied genitors.

The negative and distinctly significant correlation between  $Wr + Vr$  certifies the manifestation

of bidirectional heredity, with the participation of both dominant and recessive genes.

The best genitors for the obtainment of new genotypes, superior for grain yielding ability, are Pop. Socodor-1 and Tall Down.

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