

**MULTIPLE REGRESSION ANALYSIS OF PROLIFICACY AND
EFFECTS ON YIELD IN A SYNTHETIC POPULATION OF MAIZE (*ZE
MAYS L.*)**

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Borovoje V. Trifunović, Goran Stanković, and Vladimir Trifunović (2000): *Multiple regression analysis of prolificacy and effects on yield in a synthetic population of maize (Zea mays L.)*. – Genetika, Vol. 32, No. 3, 355-362.

In order to evaluate a synthetic population, as a source breeding material, and the applied method of selection, it is necessary to consider not only standard methods of visual estimation and testing of combining abilities, but also inter-relation of grain yield and its components. Multiple regression analysis was applied in this study in order to determine both the effects of certain traits on grain yield in the prolific synthetic population ZP SynP1(M)C_n and changes of correlation coefficients after three cycles of phenotypic recurrent selection (FRS) with control of both parents. Coefficients of determination reached high values at the genetic level, indicating that all essential components of grain yield (number of silks per plant, number of seed set ears, number of kernels per plant and 1000-kernel weight) were included in the investigation. It is obvious that the effects of recurrent selection (FRS) for greater number of ears were positively correlated to other components and that the number of ears per plant, with its direct impact on grain yield, was one of the fundamental factors.

Key words: multiple regression analysis, prolificacy, synthetic population, maize

INTRODUCTION

Prolificacy is a yield component and selection for ear number can contribute to a greater production of grain per plant and/or area unit, i.e. this trait shows a correlation with yield. Phenotypic recurrent (mass) selection was broadly used both as an efficient method for highly hereditary traits, such as ear number, and indirectly for yield increase. This motivated breeders to develop populations, inbreds and hybrids with a strictly expressed tendency to prolificacy. The improvement of populations should lead to an increase of the initial frequency of favourable alleles, by the choice and recombination of selected individuals over generations.

Quantitative genetics has an important role in obtaining theoretical information necessary for the choice and/or development of methods used in solving practical problems during breeding of organisms. Knowledge of relative levels of variability and interrelation between yield and other biologically related traits contributes to a better understanding of their genetic control. Interrelations lead to the correlative expression of the traits. Hence, estimates of path and regression coefficients can serve in the breeding process for indirect improvement of these traits and therefore for a possible change of selection effects. Correlation and regression analyses provide selection of the best combinations of traits that can be used in the breeding process.

Different theoretical aspects of these studies and possibilities of their application (GALTON, 1889; PEARSON, 1900; FISHER, 1918; WRIGHT, 1921; 1923; SNEDECOR, 1956; ROBERTSON, 1959; LI, 1956; 1975; EDWARDS, 1979; IVANOVIĆ i ROSIĆ, 1986), as well as, practical research (LONQUIST, 1967; HALLAUER, 1967, 1974; GARDNER, 1969, MOLL *et al.*, 1978; 1981; TRIFUNOVIĆ and RISTANOVIĆ, 1978; SEGOVIA and PATERNIANI, 1983; TRIFUNOVIĆ, 1995) on prolific populations indicate that the number of ears per plant is an efficient criterion that provides development of favourable germplasm and utilisation of such genotypes in maize hybrid production.

MATERIAL AND METHODS

The population ZP SynP1(M)C_n is one of the first prolific synthetic maize populations of unrelated genetic origin in relation to widely used introduced and local basic populations. The aim of deriving this synthetic was to provide the initial material for selection of new, non-standardised models of maize hybrids that would, according to the presumption of the promoters of this programme (TRIFUNOVIĆ and RISTANOVIĆ, 1978), provide permanent progress in maize production by higher yield stability under different growing conditions.

With the desire to maintain this divergent maize germplasm, the method of phenotypic recurrent selection (FRS) with control of both parents (bi-parental mass selection) was employed. The success of FRS on prolificacy and the selection value of ZP SynP1 were ascertained (TRIFUNOVIĆ, 1995).

The breeding material was planted according to the Nested design (incomplete block design, COCHRAN and COX, 1957) with replications within the set

in two locations (Zemun Polje and Bečej). Three independent trials with S_1 families were set up for each cycle of SynP1 (C_0 and C_3) and Syn BS11 C_0 .

Besides grain yield (y) the following plant and ear traits were observed:

- number of silks per plant
- number of seed set ears per plant (number of ears)
- number of kernels per plant
- 1000-kernel weight.

Coefficients of genetic and phenotypic correlations, estimated on the basis of common variation and products of common variation of traits. Interdependence of the studied traits was determined by a standardised regression coefficient (path coefficient), which was evaluated by the method of inversion symmetrical correlation matrices (EDWARDS, 1979). The coefficient of multiple determination ($R^2_{y_i}$) was calculated in the following fashion:

$$R^2_{y_{1...k}} = p_{y_1} \times r_{y_1} + p_{y_2} \times r_{y_2} + \dots + p_{y_k} \times r_{y_k};$$

Statistical significance of the difference (\bar{d}) between the corresponding $R^2_{y_i}$ ($R^2_{y_{xi...xk}}$) was determined on the basis of p_{y_i} significance for the trait that was omitted in regression (i.e. in the coefficient of multiple determination) of the lower order that forms regression of a higher order:

$$\begin{array}{ccccc} R^2_{y_i} & R^2_{y_{ij}} & \bar{d} & p_{y_j} & \text{of} & R^2_{y_{ij}} \\ R^2_{y_{ij}} & R^2_{y_{ijk}} & \bar{d} & p_{y_k} & \text{of} & R^2_{y_{ijk}} \\ \text{etc.} & & & & & \end{array}$$

The minimum factor, as a criterion of the “best” regression equation was determined from the following relation (WONNACOTT and WONNACOTT, 1981):

$$\text{M.F.} = \frac{1 - R^2}{(n - k - 1)^2}$$

The aim of the present study was to observe effects of mass bi-parental selection for the number of ears per plant and a correlated response for grain yield in a narrow genetic base maize synthetic population ZP SynP1(M) C_n .

The evaluation of genetic and phenotypic correlations, a portion of their direct and indirect effects (path coefficient analysis), as well as the best regression equation were obtained using S_1 families of the observed synthetic populations.

The use of prolificacy, as a selection criterion, was expected to emphasise the potential of ZP SynP1(M) C_n as the initial material and its value at the current level of selection.

RESULTS AND DISCUSSION

The results of correlation and path analyses (TRIFUNOVIĆ, 1995) obtained in the initial cycles of phenotypic recurrent selection in SypP1(M) C_n indicate a sufficiently strong correlation between yield and prolificacy. Selection for this trait

did not disturb the balance in other traits that significantly affect yield expression. Therefore the number of ears can be used as a criterion in selection for prolificacy and increased yield, but attention should be paid to the compromise, considering indirect effects in the correlative relation of the traits. The presence of a multiple pleiotropic gene effect, as well as linked genes that are principal reasons of trait interdependence cannot be rejected (FALCONER, 1989). Changes in magnitudes of the evaluated parameters indicate that recombination in the selection process led to modifications of effects and linkage of common genes, but these modifications were positive. Their extents in S_1 families were sufficient to show that the applied procedure of recurrent selection within $SynP1(M)C_n$ was mainly controlled by additive genes and that the improvement of this synthesised maize germplasm was justified. In order to have more complete information on the significance of both individual and common effects of particular traits on grain yield, the method of multiple regression analysis was applied.

The evaluations of multiple regression coefficients ($R^2_{y_i...k}$) reached high and/or very reliable values at the genetic level (of 0.915** and 0.999**) (Table 1) indicating that the present study encompassed the essential components of grain yield. Coefficients of non-determination (residual) would show low values. Hence effects of traits not included into this study would not crucially affect the obtained results. It is obvious that recurrent selection for a greater number of ears had a positive correlative response in other components too, and that recurrent selection for prolificacy, by its direct effects on yield, was one of its essential factors. The levels of significance of all genetic and phenotypic parameters of observed traits and yield corresponded with each other. Hence, it was observed that the strength of multiple regression coefficients in the studied progenies, depended, to a certain extent, on the source of genetic material ($SynP1 : BS11$) and fluctuated over the selection process ($SynP1C_0 : SynP1C_3$).

Table 1. Genetic and phenotypic multiple regression coefficients for prolificacy in S_1 families of the synthetic populations observed

$R^2_{y_i}$	ZPSynP1 C_0	ZPSynP1 C_3	BS11 C_0
$R^2_{y,123}$ (g)	0.6072**	0.5139**	0.7566**
$R^2_{y,123}$ (ph)	0.4956**	0.4426**	0.6805**
$R^2_{y,124}$ (g)	0.6281**	0.4491**	0.5751**
$R^2_{y,124}$ (ph)	0.4706**	0.4106**	0.5216**
$R^2_{y,134}$ (g)	0.9999**	0.9113**	0.9042**
$R^2_{y,134}$ (ph)	0.7096**	0.7544**	0.8039**
$R^2_{y,234}$ (g)	0.9999**	0.9037**	0.9273**
$R^2_{y,234}$ (ph)	0.8215**	0.8357**	0.8617**
$R^2_{y,1234}$ (g)	0.9999**	0.9151**	0.9455**
$R^2_{y,1234}$ (ph)	0.8239**	0.8385**	0.8685**

** - $p < 0.01$

Genetic determinations differed insignificantly from phenotypic ones and therefore it seems that they would not be a significant cause of differences under

impacts of environmental conditions or non-additive effects. The magnitude of genetic coefficients of regression of the studied traits reflected the level of the corresponding genes that determine them. Such a correlation could be expected since these traits are yield components.

Observing multiple regression coefficients of prolificacy over the number of silks per plant (1), number of seed set ears per plant (2) and number of kernels per plant (Table 2), it is noticeable that their values were higher at the genetic ($R^2_{y_{123}} = 0.6072^{**}$ for C_0 and 0.5139^{**} for C_3) than at the phenotypic level.

Table 2. Multiple regression coefficients of prolificacy of ZPSynP1(M) C_n (S1)

$R^2_{y_i}$	ZPSynP1 C_0	ZPSynP1 C_3
$R^2_{y_{12}}$ (g)	0.2222**	0.2389**
$R^2_{y_{12}}$ (PH)	0.2067**	0.3275**
$R^2_{y_{13}}$ (g)	0.5764**	0.4803**
$R^2_{y_{13}}$ (PH)	0.4437**	0.4230**
$R^2_{y_{23}}$ (g)	0.5973**	0.4079**
$R^2_{y_{23}}$ (PH)	0.4851**	0.4184**
$R^2_{y_{123}}$ (g)	0.6072**	0.5139**
$R^2_{y_{123}}$ (PH)	0.4956**	0.4426**

** - $p < 0.01$

Genetic and phenotypic coefficients of determination for grain yield and their observed components were insignificantly lowered after three cycles of recurrent bi-parental selection (except for the determination from C_3 : $R^2_{y_{12}} = 0.2389^{**}$), presenting an indirect effect (population per se) of selection.

Table 3. Analysis of the significance of differences (d) between genetic multiple regression coefficients of prolificacy for ZPSynP1(M) C_n (S1)

Lower order			Higher order			d
$R^2_{y_1}$	C_0	0.2209**	$R^2_{y_{12}}$	C_0	0.2222**	NS
$R^2_{y_1}$	C_3	0.1963**	$R^2_{y_{12}}$	C_3	0.2389**	NS
$R^2_{y_1}$	C_0	0.2209**	$R^2_{y_{13}}$	C_0	0.5764**	NS
$R^2_{y_1}$	C_3	0.1963**	$R^2_{y_{13}}$	C_3	0.4803**	NS
$R^2_{y_2}$	C_0	0.1640**	$R^2_{y_{23}}$	C_0	0.2222**	**
$R^2_{y_2}$	C_3	0.1421**	$R^2_{y_{23}}$	C_3	0.2389**	**
$R^2_{y_3}$	C_0	0.2391**	$R^2_{y_{23}}$	C_0	0.5973**	**
$R^2_{y_3}$	C_3	0.1545**	$R^2_{y_{23}}$	C_3	0.4079**	NS
$R^2_{y_{12}}$	C_0	0.2222**	$R^2_{y_{123}}$	C_0	0.6072**	**
$R^2_{y_{12}}$	C_3	0.2389**	$R^2_{y_{123}}$	C_3	0.5139**	NS

** - $p < 0.01$; NS – not significant

In the course of RFS with parental control (C_0 : C_3), coefficients of determinations, within the system of these three factors, contained the same independent variables affecting the yield. By comparison of different levels of regression in

analysing the significance of differences it can be concluded that prolificacy was a sufficient criterion for the selection of plants that affected the yield increase of ZPSynP1(M)C₃ (Table 3).

Moreover, by comparing the coefficients of determination ($R^2_{y-1} : R^2_{y-12}$; $R^2_{y-1} : R^2_{y-13}$; $R^2_{y-2} : R^2_{y-23}$; $R^2_{y-12} : R^2_{y-123}$) of C₃ it can be concluded that there are no significant differences among them at the genetic level, but that the number of silks per plant in the combination with one trait out of two (2 and 3) was and will be the essential guideline for accumulation of favourable alleles for yield of the newly developed synthetic population.

Table 4. The "best" regression equation at the genetic and phenotypic level of prolificacy of ZPSynP1(M)C₃ (S1), with the level of the minimum factor

R^2_y	C ₃ (g)	M.F. (10 ⁻⁵)	R^2_y	C ₃ (ph)	M.F. (10 ⁻⁵)
R^2_{y-1234}	0.9151**	0.94	R^2_{y-234}	0.8357**	1.78
R^2_{y-134}	0.9113**	0.96	R^2_{y-1234}	0.8385**	1.79
R^2_{y-234}	0.9037**	1.04	R^2_{y-134}	0.7544**	2.66
R^2_{y-123}	0.5139**	5.27	R^2_{y-34}	0.4433**	5.92
R^2_{y-13}	0.4803**	5.52	R^2_{y-123}	0.4426**	6.05
R^2_{y-34}	0.4693**	5.64	R^2_{y-13}	0.4230**	6.13
R^2_{y-14}	0.4477**	5.87	R^2_{y-23}	0.4184**	6.18
R^2_{y-124}	0.4491**	5.99	R^2_{y-24}	0.4047**	6.33
R^2_{y-24}	0.4261**	6.10	R^2_{y-124}	0.4106**	6.40
R^2_{y-23}	0.4079**	6.29	R^2_{y-14}	0.3809**	6.58
R^2_{y-12}	0.2389**	8.09	R^2_{y-12}	0.3275**	7.15

** - $p < 0.01$

The estimation of the best regression equation, with the level of the minimum factor (Table 4) for R^2_{y-123} and R^2_{y-13} of C₃ over both the rank and the approximate value, confirms that allele frequency for yield was "linked" with alleles for prolificacy (by common genes).

Table 5. The "best" regression equation of the genetic level of prolificacy of ZPSynP1(M)C₃ (S1)

Lower order		Higher order		d	M.F. (10 ⁻⁵)
R^2_{y-12}	0.2389**	R^2_{y-124}	0.4491**	*	5.98
R^2_{y-13}	0.4803**	R^2_{y-134}	0.9113**	**	0.96
R^2_{y-23}	0.4079**	R^2_{y-234}	0.9037**	**	1.04
R^2_{y-123}	0.5139**	R^2_{y-1234}	0.9151**	**	0.94

* - $p < 0.05$; ** - $p < 0.01$

Indirect effects in correlation among traits occurred during the selection process. Hence, 1000-kernel weight per plant (4), with two or three variables, significantly affected yield at all levels of comparison. Based on observing the significance of the difference (\bar{d}) and the estimate of the minimum factor, the best

regression equation, for further selection process or formation of the selection index, would be established from the relation R^2_{y-134} (Table 5).

CONCLUSION

Multiple regression analysis shows that the changes in yield depend, to a great extent, on observed yield components, and that the effect of the number of ears on grain yield was significant. The number of ears can be used as a criterion in selection for prolificacy and greater yield, but attention should be paid to the need for compromise, regardless of the fact that accumulation of favourable alleles for these two traits occurred in this case. According to our obtained results (TRIFUNOVIĆ and RISTANOVIĆ, 1978, TRIFUNOVIĆ, 1995) ZPSynP1 can be an efficient genotype with high yield, based on the correlative relation among traits, that should be improved per se with simultaneous use of this source for the development of maize inbreds and hybrids with high and stable grain yield under different agroecological conditions.

Received October 20th, 2000
Accepted November 7th, 2000

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