

## PRODUCTION POTENTIAL OF SOME CORN GENOTYPES - RESOURCES FOR AGRICULTURAL PRACTICE AND BREEDING PROGRAMS

Alina Laura AGAPIE<sup>1</sup>, Florin SALA<sup>1,2</sup>

<sup>1</sup>Agricultural Research and Development Station Lovrin, Lovrin, 307250, Romania  
E-mails: alinamartinig@yahoo.com; florin\_sala@usvt.ro

<sup>2</sup>University of Life Sciences "King Mihai I" from Timisoara, Timișoara, 300645, Romania E-mail: florin\_sala@usvt.ro

**Corresponding author:** florin\_sala@usvt.ro

### Abstract

*The study evaluated 80 corn genotypes based on grain production under comparative crop conditions. The research took place within the ARSD Lovrin, Romania. The culture of the 80 corn genotypes was carried out in non-irrigated conditions. The hybrids were numbered in the form C01 to C80 (C – corn; 01 to 80 – genotype number). The height of the corn plants (PH) varied between  $PH = 2.05 - 2.71 \pm 0.02$  m. The height of corn ear insertion (EIH) varied between  $EIH = 0.74 - 1.25 \pm 0.01$  m. The weight of one thousand grains (TGW) varied between  $TGW = 230.10 - 345.20 \pm 2.95$  g. The hectoliter weight (HW) varied between  $HW = 75.20 - 84.45 \pm 0.21$  kg. Grain production (Y) varied between  $Y = 5,027.00 - 10,169.00 \pm 120.29$  kg ha<sup>-1</sup>. Under the aspect of the variability of the studied parameters values, based on the coefficient of variation (CV), a high value of variation was recorded in the case of production (CV=14.55874), followed by the variability within the EIH parameter (CV=11.14396), the TGW parameter (CV= 9.05588), PH (CV=5.67716) and HW (CV=2.39561). The multivariate analysis (PCA) led to the distribution diagram and principal component (PC1, PC2) explained the variance (PC1 = 44.857%; PC2 = 21.495%). The cluster analysis (CA) led to the obtaining of the dendrogram of the grouping of the maize genotypes in relation to the main parameters. The variation of production in relation to plants parameters (PH, EIH), and corn grains quality (TGW, HW) was described mathematically and in the form of graphic models, under statistical safety conditions.*

**Key words:** breeding programs, corn genotypes, grain production, multivariate analysis, productivity elements

### INTRODUCTION

Corn is one of the main crop plants and presents a rich diversity and genetic variability [5, 21, 23].

Corn collections were studied in different geographical basins, and were analyzed in terms of the diversity and conservation of genetic resources, breeding programs, but also the potential in relation to agricultural systems [2, 27].

Corn genetic resources have been cultivated and studied in relation to climatic conditions, soil conditions, different agricultural systems, culture technologies, stress factors, resistance to diseases and pests, etc. [4].

Different corn genotypes have been studied in terms of metabolic adaptations in relation to stress and nutrient imbalances, such as carbon, nitrogen and phosphorus [19].

The genotype to environment interaction was

studied in corn varieties, in order to identify valuable genetic resources for breeding programs [3, 11].

The adaptability, stability and variability of corn genotypes (hybrid forms) was analyzed and studied in order to evaluate the manner of expression of genetic resources in relation to ecological factors, to select valuable resources in relation to the objectives of breeding programs [14, 18, 22, 25, 30].

The productivity of different maize genotypes, associated with phenotypic elements, were studied in relation to various environmental conditions and technology for yield quantification [9, 15, 17, 20].

The protein content is a quality index with high importance in the production of corn grains, and it has been studied in relation to different genetic resources and culture conditions [8, 10, 16, 26].

The oil content is also a quality index of corn

grains, studied in relation to genetic resources and environmental and technological conditions [7, 31].

The aim of the study was the comparative analysis of 80 corn genotypes, and their characterization based on plant biometric parameters, production and quality indices of corn grains, classification of corn genotypes, and formulation of models of production variation in relation to plant biometric indices.

## MATERIALS AND METHODS

The experiments and the comparative study of corn hybrids were done within ARDS Lovrin. 80 genotypes of corn were cultivated, in non-irrigated cultivation system, chernozem soil,

weakly glazed. The soil tillages were in the classic system. Sowing was done at the beginning of April. Complex fertilizer (15:15:15) and ammonium nitrate (250, and 200 kg ha<sup>-1</sup> respectively) were applied. Cultivation was maintained by weeding. The climatic conditions for the year 2023 are presented in Table 1.

The comparative analysis of the maize genotypes was made on the basis of plant biometric parameters, production, grain quality indices. Plant height (PH, m) and ear insertion height (EIH, m) were determined. At physiological maturity, corn plants and ears samples were harvested for each separate hybrid.

Table 1. Climatic conditions, year 2023

Climatic elements		Monthly period, year 2023												
		I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	Avg / Sum
Rainfall (mm)	Monthly value	59	43.8	34.2	42	109.2	51.4	52.8	63.2	79	23.2	63.8	49.4	671
	Multiannual monthly average	32.7	29.6	32.3	42.7	57.3	68.1	55.8	32.3	42.4	40.5	48	39.7	521.4
	Deviation	26.3	14.2	1.9	-0.7	51.9	-16.7	-3	30.9	36.6	-17.3	15.8	9.7	149.6
Temperature (mm)	Monthly average	4.45	2.66	7.77	9.86	16.69	20.43	24.26	23.95	21.07	15.28	6.71	3.41	13.0
	Multiannual monthly average	-1.1	0.9	5.25	10.7	16.3	19.8	22.2	21.7	16.8	11.1	5.5	1.1	10.9
	Deviation	5.55	1.76	2.52	-0.84	0.39	0.63	2.06	2.25	4.27	4.18	1.21	2.31	2.2

Source: Original data, ARDS Lovrin Weather Station.

The production (Y, kg ha<sup>-1</sup>) was determined. The weight of one thousand grains (TGW, g) and the hectoliter weight (HW, kg) were determined.

As grain quality indices, the protein content of corn grains (Pro, %) and the oil content of corn grains (Oil, %) were determined.

The experimental results obtained in the comparative study of the 80 maize genotypes were processed and analyzed mathematically and statistically in an adequate way [6, 29].

## RESULTS AND DISCUSSIONS

The corn hybrids tested, under the conditions of a chernozem type soil, non-irrigated crop system, behaved differently, depending on the genetic potential of each one. Corn is a crop

intended for the production of grains, but also for fodder crops, or industrialization (protein, oil).

In relation to the interest for this crop plant, plant biometric parameters (PH, EIH), productivity, production and quality elements (Y, HW, TGW, Pro, Oil) were evaluated, Table 2.

The height of the plants (PH, m) varied between PH = 2.05 – 2.71±0.02 m, and the insertion height of the ears (EIH, m) varied between EIH = 0.74 – 1.25±0.01 m.

These parameters show an interesting relationship with the production of biomass, tall plants generating a higher biomass production, useful aspects for hybrids intended for fodder production.

Table 2. The values of the parameters studied in the tested corn genotypes

Cgn	PH	EIH	Y	HW	TGW	Pro	Oil	Cgn	PH	EIH	Y	HW	TGW	Pro	Oil
	(m)	(m)	(kg ha <sup>-1</sup> )	(kg)	(g)	(%)	(%)		(m)	(m)	(kg ha <sup>-1</sup> )	(kg)	(g)	(%)	(%)
C01	2.64	1.17	8,356	77.25	332.35	9.35	5.65	C41	2.71	1.25	6,842	81.75	294.65	9.60	6.10
C02	2.41	0.74	7,929	79.10	320.40	8.80	5.70	C42	2.71	1.15	7,748	81.90	258.20	9.55	5.80
C03	2.49	0.77	7,984	78.85	339.20	9.55	5.65	C43	2.57	1.03	8,767	79.55	285.45	8.75	5.40
C04	2.45	0.98	7,737	79.35	319.75	9.15	5.50	C44	2.49	1.19	7,388	79.40	307.60	9.35	5.90
C05	2.33	0.89	8,326	78.90	304.60	8.40	5.60	C45	2.30	0.97	5,783	75.20	254.40	9.05	5.80
C06	2.41	0.97	8,291	78.95	307.75	8.70	5.55	C46	2.23	0.78	6,207	80.55	230.10	9.50	5.80
C07	2.52	1.13	8,276	80.85	280.80	8.85	5.65	C47	2.41	1.02	7,929	76.05	293.70	8.90	5.90
C08	2.68	1.09	7,838	77.80	272.80	9.40	5.50	C48	2.41	0.91	8,502	81.65	312.40	8.60	5.90
C09	2.49	0.78	6,560	82.95	301.60	9.30	5.85	C49	2.48	0.83	7,301	75.90	301.95	8.65	5.80
C10	2.36	1.00	6,070	81.85	315.10	9.45	6.00	C50	2.44	0.99	8,823	76.40	325.70	8.85	5.65
C11	2.58	0.81	6,441	82.25	289.70	9.80	5.55	C51	2.41	0.90	7,002	81.10	278.40	9.85	5.95
C12	2.30	0.98	5,027	82.10	265.75	9.90	6.00	C52	2.52	0.98	8,837	82.20	314.85	9.45	6.10
C13	2.33	0.98	6,597	82.45	266.35	9.70	6.40	C53	2.68	0.98	8,908	77.50	319.40	9.40	5.65
C14	2.37	0.91	6,081	80.40	299.15	10.50	6.25	C54	2.62	0.90	7,410	82.00	256.25	10.55	6.20
C15	2.46	0.78	7,012	81.40	244.20	9.55	6.10	C55	2.43	1.03	6,725	80.75	295.05	9.50	5.70
C16	2.54	0.93	7,030	81.85	296.65	9.55	5.85	C56	2.22	0.96	6,737	82.45	291.80	9.50	5.75
C17	2.63	0.97	7,386	80.95	289.30	9.55	5.85	C57	2.24	0.84	6,649	81.95	272.10	9.45	6.00
C18	2.68	1.09	8,770	79.70	309.55	9.35	6.15	C58	2.33	0.95	8,498	80.80	286.05	9.15	5.50
C19	2.34	0.95	8,586	81.40	323.45	9.40	5.95	C59	2.45	1.07	6,709	80.10	241.75	9.10	5.60
C20	2.46	1.02	7,852	77.25	313.10	8.65	5.75	C60	2.36	0.96	10,169	77.05	308.35	8.10	5.45
C21	2.64	0.99	8,711	79.70	329.70	9.55	5.65	C61	2.43	1.00	7,682	80.40	274.85	11.00	6.10
C22	2.39	0.87	8,905	80.25	324.90	9.25	5.60	C62	2.56	1.04	8,448	79.35	330.05	10.00	5.55
C23	2.43	0.86	8,045	78.85	345.20	8.55	5.70	C63	2.59	1.12	6,725	82.25	282.15	9.80	5.65
C24	2.44	0.97	7,910	80.30	285.80	9.05	5.70	C64	2.50	1.23	7,411	77.60	273.15	9.20	5.65
C25	2.20	0.95	5,767	82.05	308.30	9.40	5.65	C65	2.21	0.90	7,201	81.75	285.20	9.90	5.95
C26	2.45	0.93	8,270	80.45	302.00	8.95	5.90	C66	2.49	1.01	7,559	78.40	236.20	9.25	5.65
C27	2.42	0.82	7,696	77.65	312.30	9.00	5.50	C67	2.57	0.97	9,826	80.55	291.30	10.00	5.50
C28	2.45	0.89	7,594	79.35	303.50	9.20	5.75	C68	2.41	1.12	9,043	79.15	283.10	9.45	5.75
C29	2.25	0.86	6,225	79.60	262.25	9.25	6.10	C69	2.51	1.11	8,053	80.20	315.75	10.25	5.85
C30	2.31	0.89	6,505	82.00	302.65	9.75	5.40	C70	2.05	0.92	5,694	81.20	258.80	9.45	5.85
C31	2.35	0.90	7,051	80.00	313.30	9.55	5.55	C71	2.68	1.00	7,581	79.65	295.05	9.10	5.65
C32	2.32	0.79	5,881	80.15	243.60	10.35	6.30	C72	2.48	0.85	7,873	81.50	283.65	10.35	5.85
C33	2.19	0.79	5,438	79.90	265.75	9.75	6.10	C73	2.31	0.98	5,152	80.20	277.15	10.00	6.20
C34	2.49	1.03	6,951	79.65	307.75	9.55	5.90	C74	2.49	0.90	6,532	82.50	249.50	10.40	6.25
C35	2.33	0.89	7,731	78.40	306.95	9.00	5.50	C75	2.34	0.89	6,879	82.55	245.65	9.95	6.70
C36	2.33	0.97	6,931	77.85	298.85	9.30	5.65	C76	2.42	0.98	6,373	81.60	256.30	10.80	6.25
C37	2.49	1.00	6,974	79.15	313.90	8.65	5.65	C77	2.36	0.85	6,090	84.45	283.50	10.95	6.10
C38	2.30	0.95	6,865	78.20	265.80	8.10	5.75	C78	2.36	1.01	8,306	78.55	295.45	9.45	5.70
C39	2.38	0.97	5,856	81.70	309.40	10.80	6.00	C79	2.23	0.95	6,445	83.25	276.95	9.20	6.05
C40	2.59	1.01	8,890	78.00	336.20	8.30	5.60	C80	2.23	0.95	7,069	83.55	265.70	9.85	6.00

Source: Original data from the experiment; Cgn – corn genotype number.

At the same time, larger genotypes also have a larger number of internodes and leaves, so conditions for a more intensive conversion of

solar energy through photosynthesis, and a higher grain production. Grain production (Y, kg ha<sup>-1</sup>) varied between

$Y = 5,027.00 - 10,169.00 \pm 120.29 \text{ kg ha}^{-1}$ . The hectoliter weight (HW) varied between  $HW = 75.20 - 84.45 \pm 0.21 \text{ kg hl}^{-1}$ . The weight of 1000 grains (TGW) varied between  $TGW = 230.10 - 345.20 \pm 2.95 \text{ g}$ . The protein content (Pro) varied between  $Pro = 8.10 - 11.00 \pm 0.007\%$ . The oil content (Oil) varied between  $Oil = 5.40 - 6.70 \pm 0.03\%$ .

The ANOVA Test confirmed the presence of variance and statistical reliability for the experimental data recorded, regarding the corn hybrids tested (Table 3).

Table 3. ANOVA test values

Source of Variation	SS	df	MS	F	P-value	F crit
Between Groups	3.68E+09	6	6.14E+08	3711.3	0	3.8060
Within Groups	91507636	553	165474.9			
Total	3.78E+09	559				

Source: Original data generated by calculation.

The level of correlation between production, quality indices and biometric parameters of the plants was analyzed. Positive correlation was recorded between production (Y) and plant height (PH),  $r = 0.475^{***}$ , between Y and TGW,  $r = 0.502^{***}$ .

Negative correlation was recorded between production (Y) and protein content (Pro),  $r = -0.415^{***}$ , respectively between production (Y) and oil content (Oil),  $r = -0.468^{***}$ .

Positive correlation was recorded between the protein content (Pro) and the oil content (Oil),  $r = 0.538^{***}$ , between the protein content (Pro) and the hectoliter weight (HW),  $r = 0.558^{***}$ , respectively between the content of oil (Oil) and hectoliter weight (HW),  $r = 0.46^{***}$ .

The values of the correlation coefficient, resulting from the analysis, are presented in Figure 1.

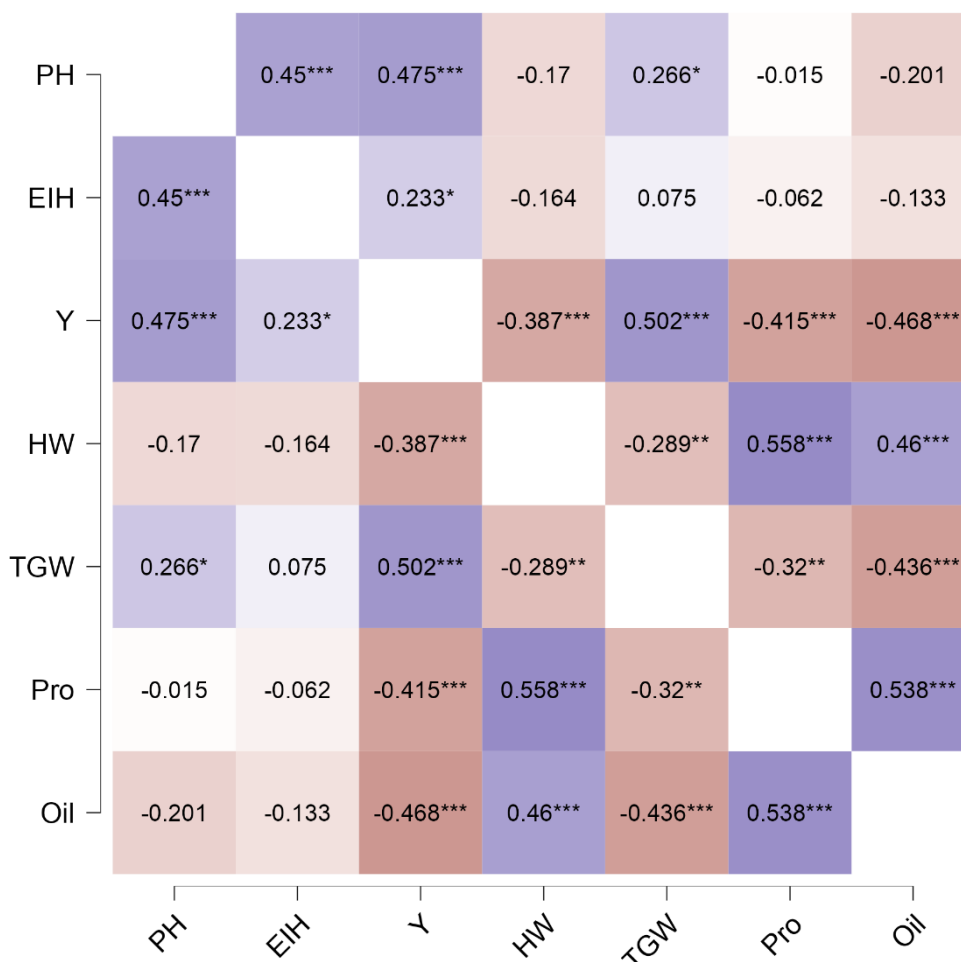


Fig. 1. Graphical representation of the correlation level in the analysis of the corn genotypes studied  
 Source: Original figure.

According to PCA, the diagram in Figure 2 resulted, in which the corn hybrids studied were distributed according to the values of the

analyzed parameters. PC1 explained 44.857% of variance, and PC2 explained 21.485% of variance.

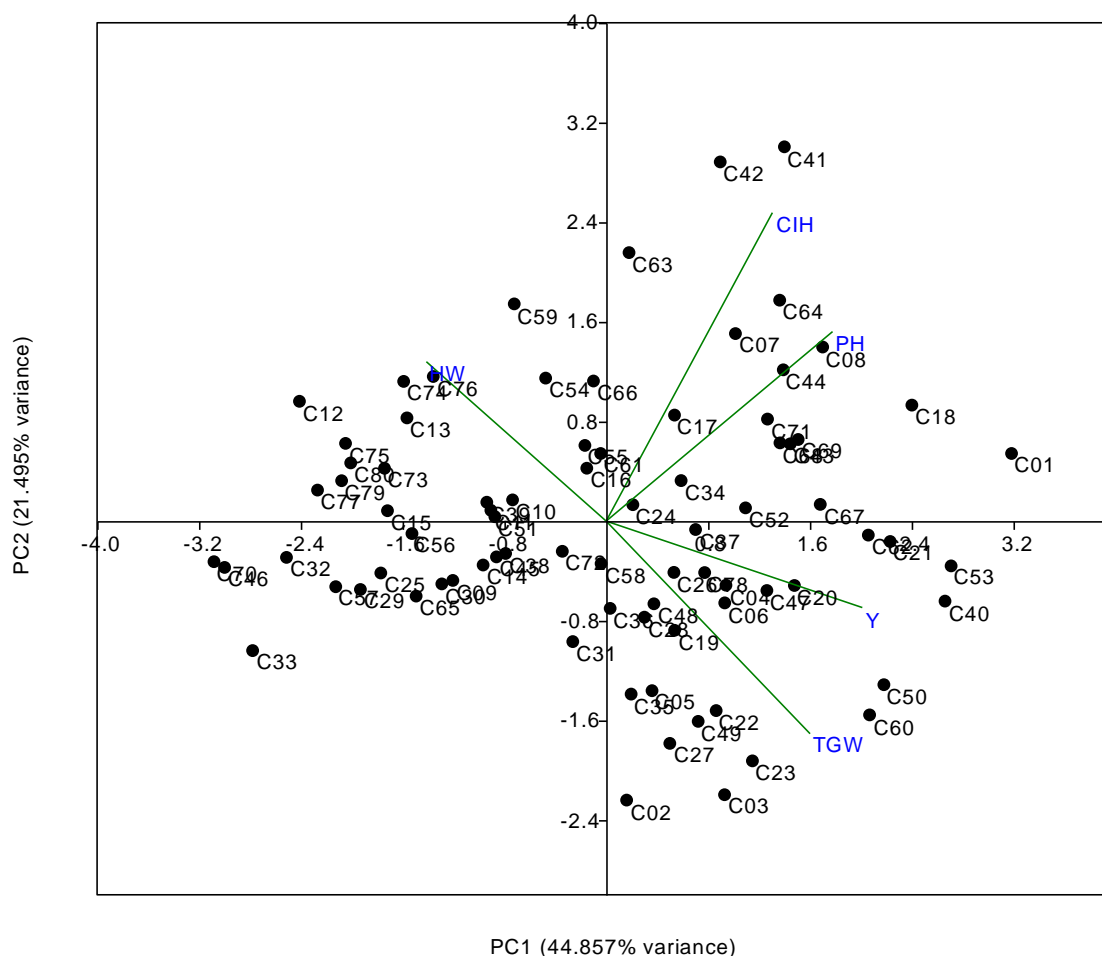


Fig. 2. PCA diagram of the distribution of corn genotypes  
 Source: Original figure.

The cluster analysis, in relation to the main production parameters (Y, TGW, HW) led to the dendrogram in Figure 3 (Coph corr. = 0.741). The grouping of maize genotypes into two distinct clusters was found. A cluster included genotypes C60 and C67 (marked in red) with the best production potential. The other hybrids were grouped in a cluster with several sub-clusters, based on similarity in relation to production potential. In relation to the protein content (Pro), the Cluster Analysis led to the dendrogram in Figure 4 (Coph.corr = 0.796). The corn genotypes were grouped in two distinct clusters, with several sub-clusters each. The corn genotypes C61 and C77 presented the highest protein content and other genotypes were also included in the respective sub-

cluster, based on similarity. In relation to the oil content (Oil), the Cluster Analysis led to the dendrogram in Figure 5 (Coph.corr = 0.765). The C75 corn genotypes, positioned separately in the dendrogram, presented the highest oil content. Within each sub-cluster in which there are the genotypes with the best results for the analyzed parameters, there are also other valuable genotypes for the respective character, which can constitute genetic sources for the corn improvement process. Also, the respective genotypes can be finalized through the improvement process as hybrids for agricultural production, with the destination for the crop for productive purposes.

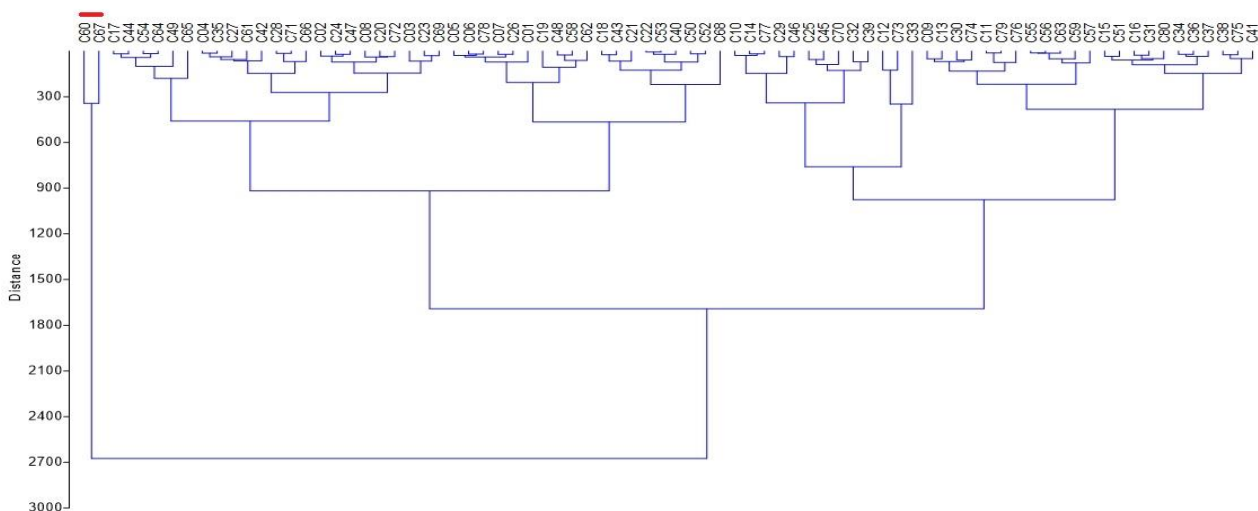


Fig. 3. Dendrogram for classification of corn genotypes based on Euclidean distances, in relation to Y, TGW, HW  
 Source: Original figure.

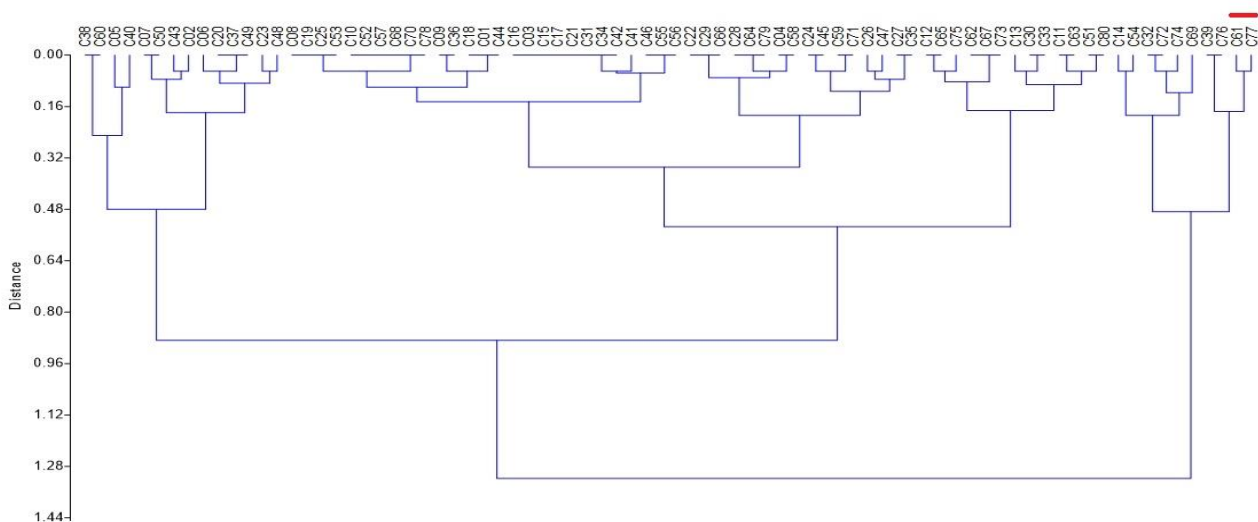


Fig. 4. Dendrogram for the classification of corn genotypes based on Euclidean distances, in relation to Pro  
 Source: Original figure.

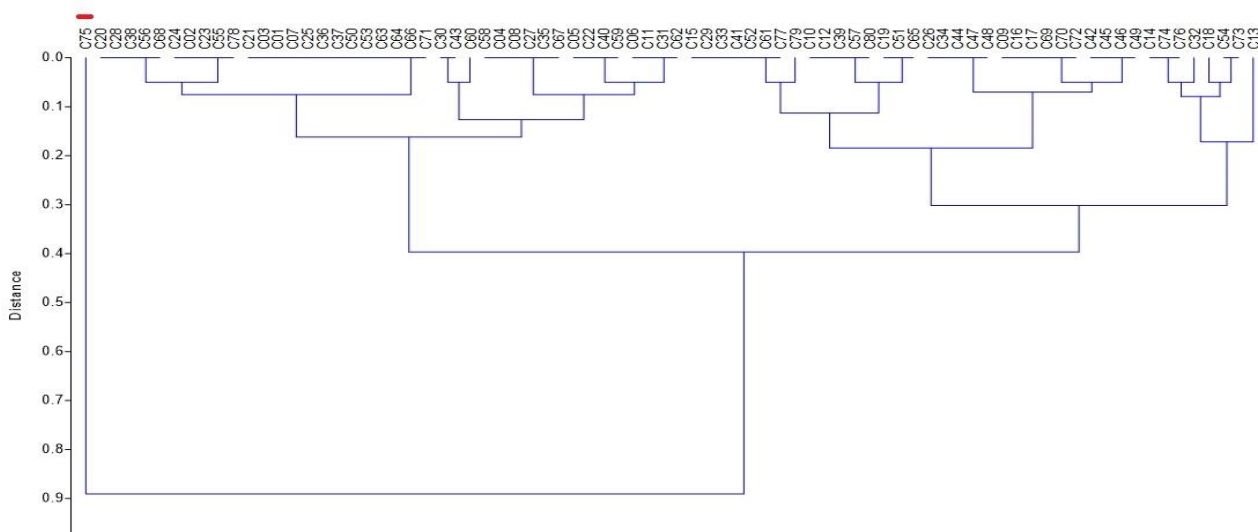


Fig. 5. Dendrogram for the classification of corn genotypes based on Euclidean distances, in relation to Oil  
 Source: Original figure.

The variation of grain production ( $Y$ ,  $\text{kg ha}^{-1}$ ) was analyzed in relation to plant biometric parameters, respectively plant height (PH) and ear insertion height (EIH). The result was equation (1), which described the  $Y$  variation in relation to PH and EIH parameters under conditions of Multiple  $R = 0.536$ ,  $F = 5.9752$ ,  $p < 0.001$ . The graphic representation of the  $Y$  variation in relation to PH (x-axis) and EIH (y-axis) is presented in Figure 6, respectively Figure 7.

$$Y = ax^2 + by^2 + cx + dy + exy + f \quad (1)$$

where:  $Y$  – grains production ( $\text{kg ha}^{-1}$ );  $x$  – plant height (PH, m);  $y$  – ear insertion height (EIH, m);  
 $a, b, c, d, e, f$  – coefficients of the equation (1);  
 $a = -7,824.1109672$ ;  
 $b = -13,108.3911987$ ;  
 $c = 38,232.1022416$ ;  
 $d = 16,608.8083044$ ;  
 $e = 3,779.6484971$ ;  
 $f = -51,712.372054$ .

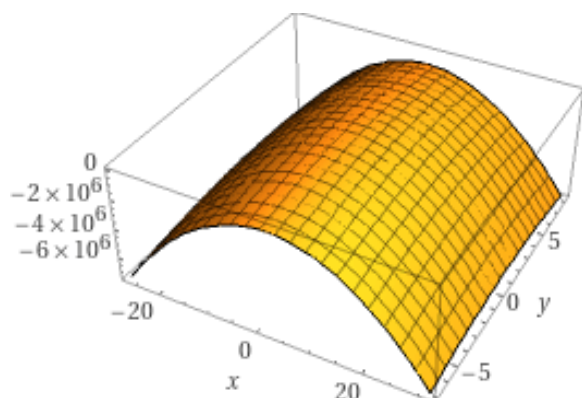


Fig. 6. 3D model of  $Y$  variation in relation to PH (x-axis) and EIH (y-axis)  
 Source: Original figure.

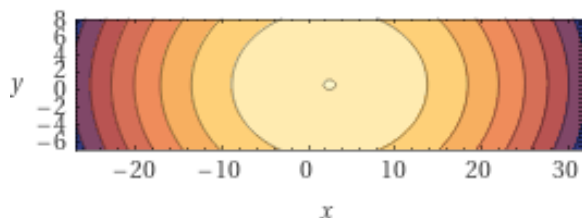


Fig. 7. Model in isoquants format of  $Y$  variation in relation to PH (x-axis) and EIH (y-axis)  
 Source: Original figure.

The variation of grain production ( $Y$ ,  $\text{kg ha}^{-1}$ ) in relation to HW and TGW was described by equation (2), under conditions of Multiple  $R = 0.597$ ,  $F = 8.2076$ ,  $p < 0.001$ . The graphic representation of the  $Y$  variation in relation to

HW (x-axis) and TGW (y-axis) is presented in Figure 8, respectively Figure 9.

$$Y = ax^2 + by^2 + cx + dy + exy + f \quad (2)$$

where:  $Y$  – grains production ( $\text{kg ha}^{-1}$ );  $x$  – hectoliter weight (HW, kg);  $y$  – mass of 1,000 grains (TGW, g);  
 $a, b, c, d, e, f$  – coefficients of the equation (2);  
 $a = -36.5281783$ ;  
 $b = -0.0549752$ ;  
 $c = 6,734.74360966$ ;  
 $d = 340.9586975$ ;  
 $e = -3.6687497$ ;  
 $f = -306,626.4315039$ .

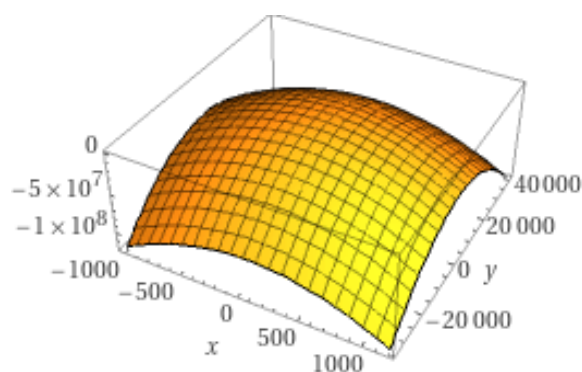


Fig. 8. 3D model of  $Y$  variation in relation to HW (x-axis) and TGW (y-axis)  
 Source: Original figure.

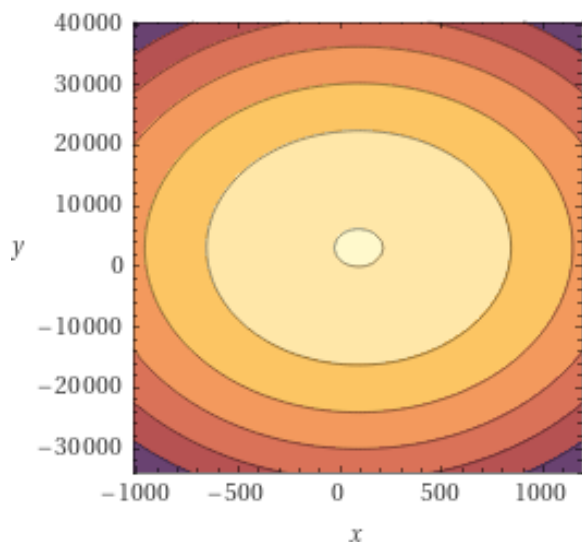


Fig. 9. Model in isoquants format of  $Y$  variation in relation to HW (x-axis) and TGW (y-axis)  
 Source: Original figure.

The variability of the parameters analyzed in the corn hybrids studied was described based on the coefficient of variation values. In the study conditions, the coefficient of variation presented CV values = 14.55874 in the case of production ( $Y$ );  $CV = 11.14396$  in the case of

EIH parameter;  $CV = 9.05588$  in the case of TGW parameter;  $CV = 5.67716$  in the case of PH parameter;  $CV = 2.39561$  in the case of HW parameter.

The coefficient of variation has shown interest in several studies regarding the classification of some culture areas in relation to different climates [28], the description of some crops through imaging analysis [1, 13]. Tokatlidis et al. (2023) [24] used the coefficient of variation (CV) and the homeostasis index (HI) to identify valuable lines for descent. Magar et al. (2021) [12] used the coefficient of variation to evaluate the phenotypic and genotypic variation in ten maize genotypes, as selection indices for the purpose of improving maize productivity.

The cluster analysis (CA) in relation to production elements (Y) and quality (Pro, Oil) led to specific dendrograms in which the maize genotypes were grouped based on similarity in relation to the considered parameters. This made it possible to highlight the valuable genotypes (genotypes C60 and C67 in the case of Y, TGW, HW parameters; genotypes C61, C67 in the case of protein content, Pro; genotype C75 in the case of oil content, Oil) and the clusters that include the most good genotypes. The information is useful for the selection of genotypes in future breeding programs, but also for agricultural practice.

Langyan et al. (2022) [8] reported the variation in the nutritional content of protein, and fat, along with other nutritional principles, in sources of corn germplasm, and identified valuable genotypes for breeding programs.

Similar studies were carried out by Lu et al. (2022) [10] and Varalakshmi et al. (2023) [26], within genetic studies with molecular markers. The variation of protein content in relation to stress factors was reported by Ramazan et al. (2023) [16], and numerous other studies have analyzed protein content in relation to environmental and technological factors as an interaction with cultivated maize genotypes.

From the analysis of the values of the coefficients of equation (1) and from the graphic analysis of the variation of Y production in relation to PH and EIH, figures

4 and 5, it was found the much stronger influence of the height of the plants (PH, x-axis), compared to the influence of the height of corn ear insertion height (EIH, y-axis).

## CONCLUSIONS

The study carried out on the 80 maize genotypes, under the same culture conditions, facilitated the expression of the genetic potential of each hybrid, highlighted by plant biometric parameters (PH, EIH), by production (Y), grain quality indices (TGW, HW) and nutritional quality indices (Pro, Oil). The cluster analysis facilitated the classification of the best genotypes for production (C60, C67), for protein content (C61, C77) and for oil content (C75). These results facilitate the selection of valuable genotypes for corn breeding programs, in relation to the destination of the hybrids - production, or nutritive principles.

The PCA diagram highlighted the distribution of the genotypes in relation to determined parameters, data that completes the findings of the multivariate analyzes about the collection of analyzed genotypes.

The level of correlations identified between the analyzed parameters facilitates a knowledge of the mode of interdependence (positive or negative) useful in the improvement process, as well as for agricultural practice.

The models resulting from the regression analysis, described with high precision the variation of the production in relation to the biometric parameters of the plants, useful aspects both for the improvement process and for agricultural practice.

## ACKNOWLEDGMENTS

The authors thank the ARDS Lovrin for facilitating this study.

## REFERENCES

[1]Agapie, A.L., Sala, F., 2023, Comparative analysis of some maize genotypes production potential and quality indices. Scientific Papers. Series "Management, Economic Engineering in Agriculture and rural development", 23(4):23-30.



- [2]Andjelkovic, V., Nikolic, A., Kovacevic, D., Mladenovic-Drinic, S., Kravic, N., Babic, V., Srebric, M., Jankulovska, M., Ivanovska, S., Bosev, D., 2018, Conserving maize in gene banks: Changes in genetic diversity revealed by morphological and SSR markers, *Chilean Journal of Agricultural Research*, 78(1):30-38.
- [3]do Couto, D.P., Oliveira, W.B.d.S., de Oliveira, J.S., Guillhen, J.H.S., Bernardes, C.d.O., Posse, S.C.P., Ferreira, M.F.d.S., Ferreira, A., 2023, Analysis of the effect of the interaction of genotype and environment on the yield stability of maize varieties; Genetic resources for breeding, *Agronomy*, 13:1970.
- [4]Dossa, E.N., Shimelis, H., Mrema, E., Shayanowako, A.I.T., Laing, M., 2023, Genetic resources and breeding of maize for Striga resistance: a review, *Frontiers in Plant Science*, 14:1163785.
- [5]Galić, V., Anđelković, V., Kravić, N., Grčić, N., Ledенčan, T., Jambrović, A., Zdunić, Z., Nicolas, S., Charcosset, A., Šatović, Z., Šimić, D., 2023, Genetic diversity and selection signatures in a gene bank panel of maize inbred lines from Southeast Europe compared with two West European panels, *BMC Plant Biology*, 23:315.
- [6]Hammer, Ø., Harper, D.A.T., Ryan, P.D., 2001, PAST: Paleontological Statistics software package for education and data analysis, *Palaeontologia Electronica*, 4(1):1-9.
- [7]Hou, Q., Zhang, T., Sun, K., Yan, T., Wang, L., Lu, L., Zhao, W., Qi, Y., Long, Y., Wei, X., Wan, X., 2022, Mining of potential gene resources for breeding nutritionally improved maize, *Plants (Basel)*, 11(5):627.
- [8]Langyan, S., Bhardwaj, R., Kumari, J., Jacob, S.R., Bisht, I.S., Pandravada, S.R., Singh, A., Singh, P.B., Dar, Z.A., Kumar, A., Rana, J.C., 2022, Nutritional diversity in native germplasm of maize collected from three different fragile ecosystems of India, *Frontiers in Nutrition*, 9:812599.
- [9]Ljubičić, N., Popović, V., Kostić, M., Pajić, M., Buđen, M., Gligorević, K., Dražić, M., Bižić, M., Crnojević, V., 2023, Multivariate interaction analysis of *Zea mays* L. genotypes growth productivity in different environmental conditions, *Plants*, 12:2165.
- [10]Lu, X., Zhou, Z., Wang, Y., Wang, R., Hao, Z., Li, M., Zhang, D., Yong, H., Han, J., Wang, Z., Weng, J., Zhou, Y., Li, X., 2022, Genetic basis of maize kernel protein content revealed by high-density bin mapping using recombinant inbred lines, *Frontiers in Plant Science*, 13:1045854.
- [11]Mafouasson, H., Gracen, V., Yeboah, M.A., Ntsomboh-Ntsefong, G., Tandzi, L.N., Mutengwa, C.S., 2018, Genotype-by-environment interaction and yield stability of maize single cross hybrids developed from tropical inbred lines, *Agronomy*, 8:62.
- [12]Magar, B.T., Acharya, S., Gyawali, B., Timilsena, K., Upadhyaya, J., Shrestha, J., 2021, Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits, *Heliyon*, 7(9):e07939.
- [13]Marcial-Pablo, M.d.J., Ontiveros-Capurata, R.E., Jiménez-Jiménez, S.I., Ojeda-Bustamante, W., 2021, Maize crop coefficient estimation based on spectral vegetation indices and vegetation cover fraction derived from UAV-based multispectral images, *Agronomy*, 11:668.
- [14]Oliveira, T.R.A., Carvalho, H.W.L., Nascimento, M., Costa, E.F.N., Oliveira, G.H.F., Gravina, G.A., Amaral Junior, A.T., Carvalho Filho, J.L.S., 2020, Adaptability and stability evaluation of maize hybrids using Bayesian segmented regression models, *PLoS ONE*, 15:e0236571.
- [15]Pires, M.V., de Castro, E.M., de Freitas, B.S.M., Lira, J.M.S., Magalhães, P.C., Pereira, M.P., 2020, Yield-related phenotypic traits of drought resistant maize genotypes, *Environmental and Experimental Botany*, 171:103962.
- [16]Ramazan, S., Jan, N., John, R., 2023, Comparative protein analysis of two maize genotypes with contrasting tolerance to low temperature, *BMC Plant Biology*, 23:183.
- [17]Rusinamhodzi, L., Makumbi, D., Njeru, J.M., Kanampiu, F., 2020, Performance of elite maize genotypes under selected sustainable intensification options in Kenya, *Field Crop Research*, 249:107738.
- [18]Santos, D.C., Pereira, C.H., Nunes, J.A.R., Lepre, A.L., 2019, Adaptability and stability of maize hybrids in unreplicated multi-environment trials, *Revista Ciencia Agronomica*, 50:83-89.
- [19]Schlüter, U., Colmsee, C., Scholz, U., Bräutigam, A., Weber, A.P.M., Zellerhoff, N., Bucher, M., Fahnenstich, H., Sonnewald, U., 2013, Adaptation of maize source leaf metabolism to stress related disturbances in carbon, nitrogen and phosphorus balance, *BMC Genomics*, 14:442.
- [20]Shrestha, S., Niraula, D., Regmi, S., Basnet, S., Chhetri, S.T., Kandel, B.P., 2023, Performance evaluation and genetic parameters estimation of multi-companies maize hybrids in Lamahi Dang, Nepal, *Heliyon*, 9(3):e14552.
- [21]Soliman, E.R.S., El-Shazly, H.H., Börner, A., Badr, A., 2021, Genetic diversity of a global collection of maize genetic resources in relation to their subspecies assignments, geographic origin, and drought tolerance, *Breeding Science*, 71(3):313-325.
- [22]Souza, M.H., Pereira Júnior, J.D., Steckling, S.M., Mencalha, J., Dias, F.S., Rocha, J.R.A.S.C., Carneiro, P.C.S., Carneiro, J.E.S., 2020, Adaptability and stability analyses of plants using random regression models, *PLoS ONE*, 15:e0233200.
- [23]Teixeira, F.F., Guimarães, C.T., 2021, Chapter 5 - Maize Genetic Resources and Pre-Breeding, *Wild Germplasm for Genetic Improvement in Crop Plants*, pp. 81-99.
- [24]Tokatlidis, I.S., Vrochidis, I., Sistanis, I., Pankou, C.I., Sinapidou, E., Papathanasiou, F., Vlachostergios, D.N., 2023, Testing the validity of CV for single-plant yield in the absence of competition as a homeostasis index, *Agronomy* 13:176.
- [25]Vana, C.D., Varga, A., Călugăr, R.E., Ceclan, L.A., Tritean, N., Tărău, A., 2023, Study of phenotypic and genetic variability in maize crossings between inbred lines (Cycle I) and elite lines (Cycle II), *AgroLife*

Scientific Journal, 12(2):214-222.

[26]Varalakshmi, S., Sahoo, S., Singh, N.K., Pareek, N., Garkoti, P., Senthilkumar, V., Kashyap, S., Jaiswal, J.P., Jacob, S.R., Nankar, A.N., 2023, Marker–trait association for protein content among maize wild accessions and coix using SSR markers, *Agronomy*, 13:2138.

[27]Vilaró, M., Vidal, R., Abadie, T., 2020, Diversity of maize landraces in germplasm collections from South America, *Agrociencia (Uruguay)*, 24(1):e108.

[28]Whelen, T., Siqueira, P., 2018, Coefficient of variation for use in crop area classification across multiple climates, *International Journal of Applied Earth Observation and Geoinformation*, 67:114-122.

[29]Wolfram, Research, Inc., *Mathematica*, Version 12.1, Champaign, IL (2020).

[30]Yamamoto, L.E., Gonçalves, M.C., Davide, L.M.C., Santos, A., Candido, L.S., 2021, Adaptability and stability of maize genotypes in growing regions of central Brazil, *Ceres*, 68:201-211.

[31]Zhang, X., Wang, M., Guan, H., Wen, H., Zhang, C., Dai, C., Wang, J., Pan, B., Li, J., Liao, H., 2023, Genetic dissection of QTLs for oil content in four maize DH populations, *Frontiers in Plant Science*, 14:1174985.