

## COMPARATIVE STUDY OF SEEDS AGRONOMIC ATTRIBUTES AND OF YIELD IN SOME SUNFLOWER GENOTYPES

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### Abstract

A collection of 45 sunflower genotypes (Express genotypes,  $N=21$ , T1 to T21; Clearfield genotypes,  $N = 24$ , T22 to T45) was studied based on the yield and agronomic traits of the seeds. The comparative crops were organized within ARDS Lovrin, in a non-irrigated system. In the case of the Express genotype group (EG), the mean yield value was  $YmEG = 2,245.56 \text{ kg ha}^{-1}$ , the mean value for the hectoliter weight was  $HWmEG = 40.64 \text{ kg hl}^{-1}$ , and the mean value for the weight of 1,000 seeds was  $TKWmEG = 63.71 \text{ g}$ . Trial T8 was highlighted, which presented positive, statistically guaranteed differences for each parameter,  $\Delta Y = 989.73 \text{ kg ha}^{-1}$ , (\*\*\*) ,  $\Delta HW = 1.56 \text{ kg hl}^{-1}$  (\*\*), respectively  $\Delta TKW = 7.89 \text{ g}$  (\*\*\*) . In the case of the Clearfield genotype group (CG), the mean yield value was  $YmCG = 2,087.41 \text{ kg ha}^{-1}$ , the mean value for the hectoliter weight was  $HWmCG = 40.10 \text{ kg hl}^{-1}$ , and the mean value for the weight of 1,000 seeds was  $TKWmEG = 56.85 \text{ g}$ . The T34 trial was highlighted, which presented positive differences, statistically assured ( $p < 0.001$ , \*\*\*), for each parameter ( $\Delta Y = 545.64 \text{ kg ha}^{-1}$ ;  $\Delta HW = 2.90 \text{ kg hl}^{-1}$ , and  $\Delta TKW = 8.75 \text{ g}$ , respectively). The Express genotype group (EG) presented higher mean values compared to the Clearfield genotype group (CG), under statistical safety conditions for TKW ( $p < 0.001$ ). Compared to the mean at the level of the experiment, genotypes with values above the mean were identified, under conditions of statistical safety. In the multivariate analysis, the main components (PC1, PC2) explained 81.966% of variance.

**Key words:** multivariate analysis, PCA, seed parameters, sunflower, yield

### INTRODUCTION

The sunflower (*Helianthus annuus* L.), is a crop plant originating from the United States, and was placed in the first five crop plants, within the 13 agricultural crops with major importance and weight for global food security [20].

Sunflower is important for the production of oil and derived products [9]. Within commercial crops, sunflower occupies an important place, with multiple agronomic, economic and ecological values [2, 18].

The sunflower shows preferences for warm climates, and the cultivated areas and the use of sunflowers have registered a significant expansion [18].

[17] communicated the influence of recent climate changes on the sunflower crop, along with other important agricultural crops, under the conditions in Romania. The sunflower is one of the main crop plants in Romania, with

an important share on the market of agricultural products in the country, but also on the European and international market [16, 22].

The agronomic traits for cultivated sunflower genotypes are based on the genetic diversity of germplasm collections worldwide (e.g. 2519 accessions within the USDA-ARS, with 53 species, of which 39 are perennial and 14, are annual) [20].

Multivariate analysis was used to classify and separate some groups, according to criteria of interest, in a study on 68 sunflower genotypes [23]. Based on the recorded similarity coefficient values, the authors of the study found a genetically restricted (narrow) base that was the basis of the studied genotypes, and at the same time they considered it necessary to expand the genetic base for future genotypes.

Ten genotypes of sunflower were studied in relation to pollination methods, for the

progress of productivity and yield parameters [1]. The authors of the study selected the genotypes with parameters that presented an essential contribution for increasing yields (e.g. morphological parameters in plants and parameters in seeds).

A collection of 32 sunflower genotypes was studied to evaluate attributes and traits associated with oil production [11]. The authors identified positive correlations of oil yield with different plant and seed attributes. Based on the results of the study, the authors classified the genotypes into eight distinct groups, and identified the differences between the groups, respectively the superior genotypes (with genetic advantages).

The genetic variability was studied in a collection of 33 sunflower genotypes, in order to characterize the respective accessions [10]. Based on the results of the applied tests, the authors found significant differences, which indicated the presence of sufficient variability between the analyzed genotypes. From the comparative analysis of PCV (coefficient of phenotypic variation) against GCV (coefficient of genotypic variation), the authors recorded the differentiated influence of the environment in character expression.

Improving the yield and some quality parameters of the seeds in commercial crops represent current and perspective objectives [2].

From the perspective of the growth of the human population, and the growing requirements for food, increasing the yields of the main crop plants, including sunflowers, are priority objectives for plants breeding programs [3, 15].

The variation of sunflower production was studied in relation to climate and soil conditions, in mixed forest areas in Central Europe [24]. The authors of the study found the log-logistic model that appropriately described the variation in production, under the study conditions.

The high interest in the production of sunflowers associated with the expansion of the cultivated areas requires genotypes with improved traits, with tolerance to stress factors, at the same time with practical agricultural technologies appropriate to the

requirements of the genotypes and the environmental conditions [5].

Interactions of the genotype with the plant traits and interactions of the genotype with the environment in the expression of the plant traits were studied in ten sunflower genotypes [21]. The authors recorded the different variation of plant traits, as a result of the genotype x environment interaction. Based on the results, the authors identified genotypes suitable for several regions, as well as genotypes suitable for narrower regions, or only for certain regions.

Based on a study of 20 sunflower genotypes, considerable impact of irrigation treatments on the yield of some agronomic characteristics was recorded [9]. Based on the analyzed parameters, the authors of the study recorded a variable response of the studied genotypes to watering treatments and water stress conditions. The recorded results showed importance both for the agricultural practice and for the breeding program, in the selection of genotypes for the breeding programs.

Stagnant yields, with a certain inconsistency, have been identified as high constraints for agronomic efficiency in sunflower [4]. By cultivating a collection of sunflower genotypes in different ecological conditions, the authors were able to select genotypes of interest for agricultural practice, as well as for breeding programs.

The yield variation was studied in relation to different sunflower genotypes and crop locations [19]. The author of the study communicated different correlations between yield and plant parameters, respectively seed parameters.

Quality indices in sunflower production were analyzed and different positive or negative correlations, as well as different levels of variation, were communicated [14].

The variation of sunflower yield was studied in relation to different technological methods [7, 12, 13]. Based on the recorded results, the authors found the most suitable methods to ensure optimal yields in the study conditions.

In the context of climate change, high importance is given to the precise estimation of crop plant phenotypes, based on genotypes, and the "genotype × environment"

relationship and the way crop yields are formed in relation to biotic and abiotic conditions [8].

Based on the yield and some agronomic parameters of the seeds, the present study made a comparative analysis of 45 genotypes of sunflower, 21 genotypes in the Express group (EG), and 24 genotypes in the Clearfield group (CG).

## MATERIALS AND METHODS

The researches were organized within ARDS Lovrin, in order to evaluate the yield and some agronomic parameters of the seeds of 45 sunflower genotypes.

The Express group (EG; genotypes with the gene resistant to Express 75 WG; herbicide for post-emergence control of dicotyledonous weeds) included 21 genotypes (T1 to T21). The Clearfield group (CG; genotypes with better adaptation to environmental conditions and Pulsar herbicide) included 24 genotypes (T22 to 45).

The comparative sunflower crops were in a non-irrigated system, on a chernozem type soil. Sowing was done in the optimal time, the first decade of April. Fertilization was ensured with NPK complex, 1:1:1, in a dose of 300 kg ha<sup>-1</sup>.

The surface of the crop plot for each genotype was 714 m<sup>2</sup>. Harvesting was done mechanized, with a combine, between August 30 and September 1, 2023.

The yield (Y, kg ha<sup>-1</sup>) was quantified for each genotype. The hectoliter weight (HW, kg hl<sup>-1</sup>) and the weight of 1,000 seeds (TKW, g) were determined.

Based on the recorded data, the mean values were calculated for the two groups of genotypes and at the level of the experiment, for each parameter.

The comparative analysis between the groups of genotypes was done. Also, each genotype was analyzed against the mean value of the group it belonged to, as well as against the mean of the experiment, in the case of each parameter.

Appropriate mathematical and statistical tests were applied to assess the safety of the

differences.

The multivariate analysis was applied to obtain the distribution and correlation of the genotypes with the yield and agronomic parameters of the seeds.

Adequate statistical safety parameters were used to interpret the results. The mathematical analysis and experimental statistical processing was done with dedicated tools in EXCEL, and with dedicated applications [6].

## RESULTS AND DISCUSSIONS

Based on the comparative crops of the 45 sunflower genotypes, the yield values (Y, kg ha<sup>-1</sup>) and the seed parameters were obtained, in the form of hectoliter weight (HW, kg hl<sup>-1</sup>), and the weight of 1,000 seeds (TKW, g), (Table 1).

The result of each genotype was analyzed in relation to the mean value calculated for each genotype group.

In the case of the group of Express genotype (EG), the mean yield value was  $Y_{mEG} = 2,245.56$  kg ha<sup>-1</sup>, the mean value for the hectoliter weight was  $HW_{mEG} = 40.64$  kg hl<sup>-1</sup>, and the mean value for the weight of 1,000 seeds was  $TKW_{mEG} = 63.71$  g. The calculated differences for each sunflower genotype from the Express group (EG), in relation to the mean value for each parameter, are presented in Table 2.

In the case of the group of Express genotypes (EG), the T8 trial was highlighted, which presented positive differences, statistically assured, for each parameter ( $\Delta Y = 989.73$  kg ha<sup>-1</sup>, \*\*\*),  $\Delta HW = 1.56$  kg hl<sup>-1</sup> (\*\*), and  $\Delta TKW = 7.89$  g (\*\*\*) respectively.

In the case of yield, five genotypes were recorded with a positive increase in yield ( $\Delta Y$ ) between  $\Delta Y = 387.49$  kg ha<sup>-1</sup> (T9), and ( $\Delta Y = 989.73$  kg ha<sup>-1</sup> (T8), under statistical safety conditions ( $p < 0.001$ , \*\*\*).

In the case of the HW parameter, four genotypes with positive growth ( $\Delta HW$ ) were recorded, between  $\Delta HW = 1.56$  kg hl<sup>-1</sup> (T8;  $p < 0.01$ , \*\*), and  $\Delta HW = 7.76$  kg hl<sup>-1</sup> (T2,  $p < 0.001$ , \*\*\*).

Table 1. Values of the yield and some seeds parameters of tested sunflower genotypes

Genotypes group	Company	Trial	Genotype	Y	HW	TKW
				(kg ha <sup>-1</sup> )	(kg hl <sup>-1</sup> )	(g)
Express genotypes group (EG)	ALTA SEEDS	T1	Hysun 310	1,848.73	41.20	57.60
		T2	Hysun 189	2,030.81	48.40	50.00
	BASF	T3	Acordis	2,100.84	41.00	53.20
	BAYER	T4	Averon	2,114.84	38.70	61.60
		T5	Hudson	2,044.81	41.20	55.60
	CORTEVA	T6	HE 118	2,352.94	41.20	77.60
		T7	LE 162	2,422.96	42.70	73.60
		T8	LE163	3,235.29	42.20	71.60
		T9	P64LE99	2,633.05	39.40	71.20
	EXPERT AGRO	T10	LE25	2,647.05	38.70	70.60
		T11	Demetera	1,904.76	37.60	53.60
		T12	Soleea	2,058.82	39.20	55.20
	KWS	T13	Geea	2,226.89	39.20	55.20
		T14	Artenes	2,184.87	42.50	66.00
	MAISADOUR	T15	Suvex	3,011.20	41.20	65.60
		T16	MAS83	2,086.83	44.00	62.40
		T17	MAS85SC	2,352.94	38.90	65.40
		T18	MDS5123LS	1,876.75	39.90	64.40
	NS SEME	T19	DT3402TT	2,759.10	39.90	77.60
		T20	NS NSH8002	1,540.61	37.10	66.00
		T21	NS NSH8005	1,722.68	39.20	64.00
Clearfield genotypes group (CG)	ALTA SEEDS	T22	Hysun180it	1,960.78	39.40	60.80
		T23	Hysun232ITHO	2,380.95	38.90	52.80
		T24	Hysun238IT	1,064.42	34.80	48.80
	BASF	T25	Coloris	2,338.93	38.10	45.60
		T26	Insun 200	2,408.96	40.70	54.40
		T27	Dracaris	2,198.87	40.20	60.80
		T28	Insun222	1,750.70	41.70	54.40
		T29	Acordis	2,422.96	40.40	59.60
	CORTEVA	T30	LP170	2,212.88	40.40	76.40
		T31	LP180	2,492.99	38.90	66.00
	KWS	T32	S2201	2,072.82	39.40	61.60
	LIDEA	T33	Oasis CLP	2,591.03	41.00	57.20
		T34	Belfis	2,633.05	43.00	65.60
	MAISADOUR	T35	CL Blade	2,044.81	41.00	58.00
		T36	MAS920	2,002.80	38.10	65.60
	NUSEED	T37	N5LE442	1,540.61	38.10	65.20
		T38	N4L215E	1,456.58	39.40	46.00
		T39	NH4161	1,288.51	40.20	55.60
		T40	N4H471	1,414.56	41.20	54.40
		T41	NHK12M010	2,464.98	40.40	44.40
		T42	X9767	2,240.89	41.00	46.80
SAATEN UNION	T43	Marquesa	2,170.86	42.20	64.00	
	T44	Surimi	2,549.01	40.40	50.40	
	T45	Integral	2,394.95	43.50	50.00	

Source: Original data.

Table 2. Differences and significance for parameters determined in sunflower genotypes, Express group (EG)

Trial	ΔY			ΔHW			ΔTKW		
	Differences	Significance	p value	Differences	Significance	p value	Differences	Significance	p value
T1	-396.83	ooo	0.0003	0.56	ns	0.3138	-6.11	oo	0.0026
T2	-214.75	o	0.0303	7.76	***	5.99E-12	-13.71	ooo	1.97E-07
T3	-144.72	ns	0.1319	0.36	ns	0.5133	-10.51	ooo	8.51E-06
T4	-130.72	ns	0.1713	-1.94	oo	0.0019	-2.11	ns	0.2473
T5	-200.75	o	0.0414	0.56	ns	0.3138	-8.11	ooo	0.0002
T6	107.38	ns	0.2575	0.56	ns	0.3138	13.89	***	1.63E-07
T7	177.40	ns	0.0685	2.06	**	0.0011	9.89	***	1.87E-05
T8	989.73	***	9.34E-10	1.56	**	0.0094	7.89	***	0.0002
T9	387.49	***	0.0004	-1.24	o	0.0339	7.49	***	0.0004
T10	401.49	***	0.0003	-1.94	oo	0.0019	6.89	***	0.0009
T11	-340.80	oo	0.0014	-3.04	ooo	1.81E-05	-10.11	ooo	1.40E-05
T12	-186.74	ns	0.0562	-1.44	o	0.0156	-8.51	ooo	0.0001
T13	-18.67	ns	0.8414	-1.44	o	0.0156	-8.51	ooo	0.0001
T14	-60.69	ns	0.5175	1.86	**	0.0027	2.29	ns	0.2123
T15	765.64	***	6.43E-08	0.56	ns	0.3138	1.89	ns	0.3005
T16	-158.73	ns	0.1003	3.36	***	4.87E-06	-1.31	ns	0.4674
T17	107.38	ns	0.2575	-1.74	oo	0.0045	1.69	ns	0.3533
T18	-368.81	ooo	0.0007	-0.74	ns	0.1898	0.69	ns	0.7032
T19	513.54	***	1.86E-05	-0.74	ns	0.1898	13.89	***	1.63E-07
T20	-704.95	ooo	2.30E-07	-3.54	ooo	2.42E-06	2.29	ns	0.2123
T21	-522.88	ooo	1.48E-05	-1.44	o	0.0156	0.29	ns	0.8737

Note: o – the symbol of negative differences; \* the symbol of positive differences; ns - non-significant differences  
 Source: Original data..

In terms of the TKW parameter, six genotypes were recorded that showed a positive increase (ΔTKW), between ΔTKW = 6.89 g (T10, p<0.001, \*\*\*), and ΔTKW = 13.89 g (T6, and T19, p<0.001, \*\*\*).

In the case of the group of Clearfield genotype (CG), the mean yield value was YmCG = 2,087.41 kg ha<sup>-1</sup>, the mean value for the hectoliter weight was HWmCG = 40.10 kg hl<sup>-1</sup>, and the mean value for the weight of 1,000 seeds was TKWmEG = 56.85 g. The calculated differences for each sunflower genotype from the Clearfield group (CG), in relation to the mean value for each parameter, are presented in Table 3. In the case of the Clearfield genotype group (CG), the T34 trial was highlighted, which presented positive, statistically assured differences (p<0.001, \*\*\*), for each parameter (ΔY = 545.64 kg ha<sup>-1</sup>; ΔHW = 2.90 kg hl<sup>-1</sup>, and ΔTKW = 8.75 g respectively), (Table 3).

In the case of yield, 10 genotypes with positive increase in yield (ΔY) between ΔY =

251.52 kg ha<sup>-1</sup> (T25, p<0.05, \*), and ΔY = 545.64 kg ha<sup>-1</sup> (T34, p<0.001, \*\*\*). In the case of the HW parameter, eight genotypes with positive growth (ΔHW) were recorded, between ΔHW = 0.90 kg hl<sup>-1</sup> (T33, T35, T42; p<0.05, \*), and ΔHW = 3.40 kg hl<sup>-1</sup> (T45, p<0.001, \*\*\*). In the case of the TKW parameter, nine genotypes were recorded that showed a positive increase (ΔTKW), between ΔTKW = 3.95 g (T22, T27; p<0.05, \*), and ΔTKW = 19.55 g (T30; p<0.001, \*\*\*). The results indicated performing genotypes in each group, for the study conditions.

The comparative analysis was made between the two groups of sunflower genotypes, the Express group (EG; N = 21) and the Clearfield group (CG, N = 24). In the case of the yield, the mean value (Ym) for the genotypes from the Express group (EG) was YmEG = 2,245.56 kg ha<sup>-1</sup>, and in the case of the genotypes from the Clearfield group (CG), the mean value of the yield was YmCG = 2,087.41 kg ha<sup>-1</sup>.

Table 3. Differences and significance for parameters analyzed in sunflower genotypes, Clearfield group (CG)

Trial	Y			HW			TKW		
	Differences	Significance	p value	Differences	Significance	p value	Differences	Significance	p value
T22	-126.63	ns	0.1770	-0.70	ns	0.0715	3.95	*	0.0248
T23	293.54	**	0.0037	-1.20	oo	0.0036	-4.05	o	0.0217
T24	-1,022.99	ooo	7.90E-11	-5.30	ooo	6.14E-13	-8.05	ooo	6.04E-05
T25	251.52	*	0.0110	-2.00	ooo	1.75E-05	-11.25	ooo	5.61E-07
T26	321.55	**	0.0018	0.60	ns	0.1190	-2.45	ns	0.1498
T27	111.46	ns	0.2327	0.10	ns	0.7896	3.95	*	0.0248
T28	-336.71	oo	0.0012	1.60	***	0.0003	-2.45	ns	0.1498
T29	335.55	**	0.0012	0.30	ns	0.4264	2.75	ns	0.1080
T30	125.47	ns	0.1809	0.30	ns	0.4264	19.55	***	2.65E-11
T31	405.58	***	0.0002	-1.20	oo	0.0036	9.15	***	1.16E-05
T32	-14.59	ns	0.8739	-0.70	ns	0.0715	4.75	**	0.0083
T33	503.62	***	1.24E-05	0.90	*	0.0233	0.35	ns	0.8333
T34	545.64	***	4.05E-06	2.90	***	6.22E-08	8.75	***	2.11E-05
T35	-42.60	ns	0.6438	0.90	*	0.0233	1.15	ns	0.4913
T36	-84.61	ns	0.3617	-2.00	ooo	1.75E-05	8.75	***	2.11E-05
T37	-546.80	ooo	3.92E-06	-2.00	ooo	1.75E-05	8.35	***	3.84E-05
T38	-630.83	ooo	4.51E-07	-0.70	ns	0.0715	-10.85	ooo	9.85E-07
T39	-798.90	ooo	8.27E-09	0.10	ns	0.7896	-1.25	ns	0.4548
T40	-672.85	ooo	1.59E-07	1.10	**	0.0069	-2.45	ns	0.1498
T41	377.57	***	0.0004	0.30	ns	0.4264	-12.45	ooo	1.09E-07
T42	153.48	ns	0.1049	0.90	*	0.0233	-10.05	ooo	3.10E-06
T43	83.45	ns	0.3683	2.10	***	9.03E-06	7.15	***	0.0002
T44	461.60	***	3.86E-05	0.30	ns	0.4264	-6.45	ooo	0.0007
T45	307.54	**	0.0026	3.40	***	3.76E-09	-6.85	ooo	0.0004

Note: o – the symbol of negative differences; \* the symbol of positive differences; ns - non-significant differences  
 Source: Original data.

According to Two-sample tests, the difference between the mean values (158.15 kg ha<sup>-1</sup>) did not show statistical certainty (t test, t=1.2174, p = 0.230; Mann-Whitney test, U=229, p = 0.608). In the case of hectoliter weight, the mean value (HWm) was very close, HWmEG = 40.64 kg hl<sup>-1</sup>, respectively HWmCG = 40.10 kg hl<sup>-1</sup>.

According to the applied statistical analysis test, the difference did not show statistical certainty (t test, t=0.8350, p = 0.408; Mann-Whitney test, U=236.5, p = 0.732).

In the case of the weight of 1,000 seeds (TKW), the mean value (TKWm) was TKWmEG = 63.71 g (Express group), respectively TKWmCG = 56.85 g (Clearfield group). According to the applied statistical analysis test, the differences showed statistical certainty (t test, t=2.8397, p = 0.0068; Mann-Whitney test, U=137, p = 0.0091).

A comparative analysis was made of each

group of genotypes, as well as for each genotype, in relation to the mean calculated at the level of the experiment for each parameter (Table 4, Figure 1).

From the analysis of the values obtained, and the graphic representation (Figure 1), it was found that the genotypes from the Express group (EG) presented an average value above the average of the experiment, for each parameter. Also, the individual values of the studied parameters (Y, HW, TKW), recorded by each genotype, are compared to the mean value at the experiment level (Table 4). In the case of yield, compared to the mean per experiment (YmExp = 2,161.21 kg ha<sup>-1</sup>), 18 genotypes showed a positive increase in production ( $\Delta Y$ ), with values between  $\Delta Y = 193.73$  kg ha<sup>-1</sup> (T6, T17) and  $\Delta Y = 1,074.08$  kg ha<sup>-1</sup> (T8).

Table 4. The results of the analysis of sunflower genotypes compared to the mean value of the experiment

Trial	ΔY			ΔHW			ΔTKW		
	Difference	Significance	p value	Difference	Significance	p value	Difference	Significance	p value
T1	-312.48	ooo	1.89E-05	0.85	*	0.0111	-2.45	ns	0.0656
T2	-130.40	ns	0.0516	8.05	***	9.99E-28	-10.05	ooo	9.6E-10
T3	-60.37	ns	0.3592	0.65	*	0.0489	-6.85	ooo	3.86E-06
T4	-46.37	ns	0.4804	-1.65	ooo	5.79E-06	1.55	ns	0.2402
T5	-116.40	ns	0.0809	0.85	*	0.0111	-4.45	oo	0.0013
T6	191.73	**	0.0052	0.85	*	0.0111	17.55	***	2.95E-17
T7	261.75	***	0.0002	2.35	***	3.74E-09	13.55	***	1.81E-13
T8	1,074.08	***	1.91E-20	1.85	***	7.31E-07	11.55	***	2.22E-11
T9	471.84	***	5.08E-09	-0.95	oo	0.0048	11.15	***	6.02E-11
T10	485.84	***	2.47E-09	-1.65	ooo	5.79E-06	10.55	***	2.73E-10
T11	-256.45	ooo	0.0003	-2.75	ooo	5.88E-11	-6.45	ooo	1.07E-05
T12	-102.39	ns	0.1233	-1.15	ooo	0.0008	-4.85	ooo	0.0005
T13	65.68	ns	0.3190	-1.15	ooo	0.0008	-4.85	ooo	0.0005
T14	23.66	ns	0.7183	2.15	***	3.07E-08	5.95	***	3.84E-05
T15	849.99	***	1.01E-16	0.85	*	0.0111	5.55	***	0.0001
T16	-74.38	ns	0.2598	3.65	***	1.04E-14	2.35	ns	0.0777
T17	191.73	**	0.0052	-1.45	ooo	4.48E-05	5.35	***	0.0002
T18	-284.46	ooo	7.58E-05	-0.45	ns	0.1661	4.35	**	0.0017
T19	597.89	***	8.86E-12	-0.45	ns	0.1661	17.55	***	2.95E-17
T20	-620.60	ooo	2.94E-12	-3.25	ooo	4.24E-13	5.95	***	3.84E-05
T21	-438.53	ooo	2.85E-08	-1.15	ooo	0.0008	3.95	**	0.0040
T22	-200.43	oo	0.0036	-0.95	oo	0.0048	0.75	ns	0.5684
T23	219.74	**	0.0016	-1.45	ooo	4.48E-05	-7.25	ooo	1.38E-06
T24	-1,096.79	ooo	8.6E-21	-5.55	ooo	2.82E-21	-11.25	ooo	4.61E-11
T25	177.72	**	0.0091	-2.25	ooo	1.04E-08	-14.45	ooo	2.25E-14
T26	247.75	***	0.0004	0.35	ns	0.2821	-5.65	ooo	7.92E-05
T27	37.66	ns	0.5663	-0.15	ns	0.6395	0.75	ns	0.5684
T28	-410.51	ooo	1.22E-07	1.35	***	0.0001	-5.65	ooo	7.92E-05
T29	261.75	***	0.0002	0.05	ns	0.8794	-0.45	ns	0.7288
T30	51.67	ns	0.4321	0.05	ns	0.8794	16.35	***	3.56E-16
T31	331.78	***	7.12E-06	-1.45	ooo	4.48E-05	5.95	***	3.84E-05
T32	-88.39	ns	0.1819	-0.95	oo	0.0048	1.55	ns	0.2402
T33	429.82	***	4.48E-08	0.65	*	0.0489	-2.85	o	0.0334
T34	471.84	***	5.08E-09	2.65	***	1.67E-10	5.55	***	0.0001
T35	-116.40	ns	0.0809	0.65	*	0.0489	-2.05	ns	0.1211
T36	-158.41	o	0.0192	-2.25	ooo	1.04E-08	5.55	***	0.0001
T37	-620.60	ooo	2.94E-12	-2.25	ooo	1.04E-08	5.15	***	0.0003
T38	-704.63	ooo	5.67E-14	-0.95	oo	0.0048	-14.05	ooo	5.6E-14
T39	-872.70	ooo	3.99E-17	-0.15	ns	0.6395	-4.45	oo	0.0013
T40	-746.65	ooo	8.52E-15	0.85	*	0.0111	-5.65	ooo	7.92E-05
T41	303.77	***	2.92E-05	0.05	ns	0.8794	-15.65	ooo	1.57E-15
T42	79.68	ns	0.2279	0.65	*	0.0489	-13.25	ooo	3.6E-13
T43	9.65	ns	0.8830	1.85	***	7.31E-07	3.95	**	0.0040
T44	387.80	***	3.98E-07	0.05	ns	0.8794	-9.65	ooo	2.69E-09
T45	233.74	***	0.0008	3.15	***	1.13E-12	-10.05	ooo	9.6E-10

Source: Original data.

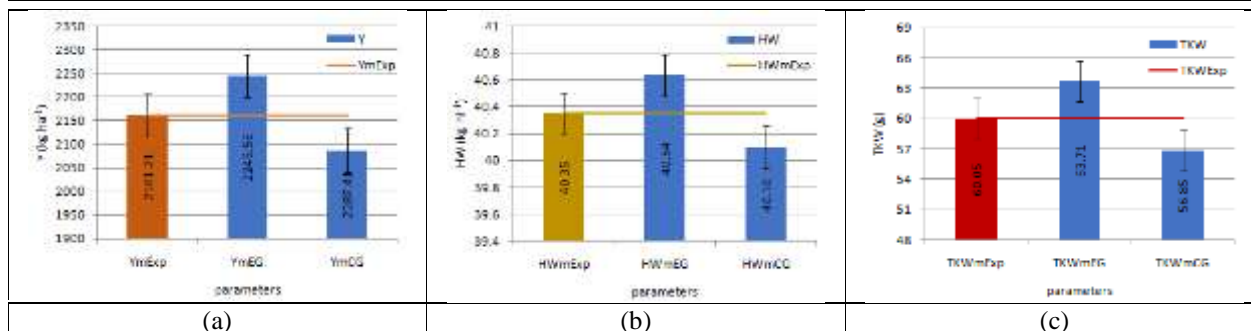


Fig. 1. Graphic representation of the mean values by genotype groups, in relation to the mean of the experiment; (a) yield values; (b) HW values; (c) TKW values  
 Source: Original data.

Among these genotypes, 8 genotypes were from the Express genotype group (EG) and 10 genotypes were from the Clearfield genotype group (CG). In the case of hectoliter weight (HW), compared to the mean per experiment ( $HWmExp = 40.35 \text{ kg hl}^{-1}$ ), a number of 18 genotypes showed positive increase ( $\Delta HW$ ), with values between  $\Delta HW = 8.05 \text{ kg hl}^{-1}$  (T3, T33, T35) and  $\Delta HW = 0.65 \text{ kg hl}^{-1}$  (T2). Of these, 10 genotypes were from the Express group (EG), and 8 genotypes were from the Clearfield group (CG). In the case of the TKW parameter, compared to the mean value

at the experiment level ( $TKWmExp = 60.05 \text{ g}$ ), a number of 18 genotypes showed a positive increase, with values between  $\Delta TKW = 3.95 \text{ g}$  (T21, T43) and  $\Delta TKW = 17.55 \text{ g}$  (T6, T19). Of these, 12 genotypes were from the Express group (EG) and 6 genotypes were from the Clearfield group (CG).

Multivariate analysis (PCA) was applied to obtain the distribution of sunflower genotypes in relation to the considered parameters (Y, HW, TKW). The result was the diagram in figure 2, in which the main components explained 81.966% of variance.

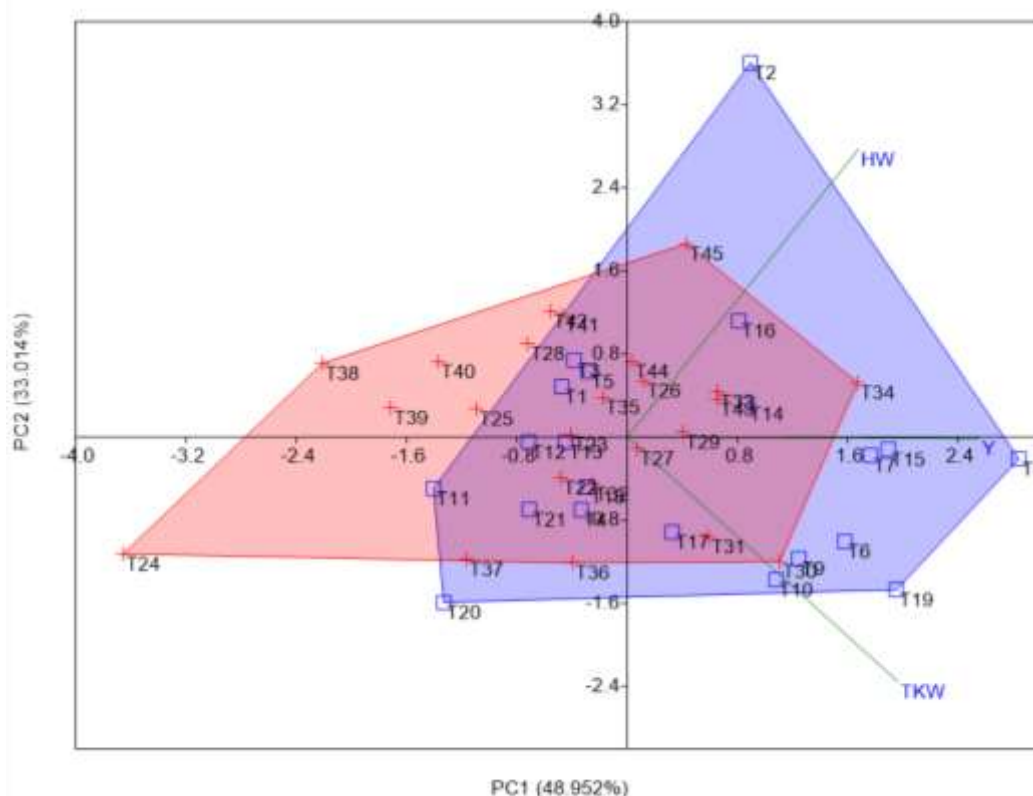


Fig. 2. PCA diagram (blue field – Express genotypes; red field – Clearfield genotypes)  
 Source: Original figure.



The Express genotype group is represented in blue, and the Clearfield genotype group is represented in red. From the analysis of the two fields (blue - EG, red - CG), an overlapping area was found, which includes genotypes with similar behaviour under the study conditions, as well as independent areas, which includes genotypes with different behaviour. It was also found from the PCA diagram (Figure 2), the orientation/correlation of some genotypes towards the Y parameter (e.g. T8, T15, T17), the correlation of some genotypes with the HW parameter (e.g. T16), and the correlation of some genotypes with the TKW parameter (e.g. T10, T30).

Sunflower seed parameters vary in relation to genotype and environmental and technological conditions, and quality improvement represents an objective of interest for commercial crops [2]. Seed quality is important in ensuring seed yield as well as oil production [1, 11]. Seed mass was considered important for genotypes with improved yield [1]. Correlations were communicated between plant parameters (e.g. height, calathidium diameter), seed parameters (e.g. TKW, HW) and seed yield per surface unit [19].

The description of "genotype  $\times$  environment" interaction relationships in the formation of yields, associated with climate changes, is considered important in the selection of genotypes with high adaptability for agricultural practice [8].

The results communicated by the present study are integrated into the area of interest for the present and the perspective regarding the efficiency and sustainability of the sunflower crop, with direct applicability for the study area and extension of the approach for other areas, or crop of interest.

## CONCLUSIONS

The sunflower genotypes analyzed under similar crop conditions generated differentiated values for agronomic parameters of seed quality (HW, TKW), and yield (Y).

The genotypes from the Express group (EG) presented higher mean values for yield and

HW parameters, respectively TKW, compared to the genotypes from the Clearfield group (CG).

Within the group of Express genotypes, the T8 trial was highlighted, which showed positive differences, statistically ensured, for each parameter ( $\Delta Y = 989.73 \text{ kg ha}^{-1}$ , \*\*\*),  $\Delta HW = 1.56 \text{ kg hl}^{-1}$  (\*\*), respectively  $\Delta TKW = 7.89 \text{ g}$  (\*\*\*)).

In the case of the Clearfield (CG) genotype group, the T34 trial was highlighted, which presented positive, statistically assured differences ( $p < 0.001$ , \*\*\*), for each parameter ( $\Delta Y = 545.64 \text{ kg ha}^{-1}$ ;  $\Delta HW = 2.90 \text{ kg hl}^{-1}$ , and respectively  $\Delta TKW = 8.75 \text{ g}$ ).

Compared to the mean values per experiment ( $Y_{mExp} = 2,161.21 \text{ kg ha}^{-1}$ ;  $HW_{mExp} = 40.35 \text{ kg hl}^{-1}$ ;  $TKW_{mExp} = 60.05 \text{ g}$ ) genotypes were identified that presented values above the mean, within each group of genotypes (EG, CG).

Multivariate analysis (PCA) facilitated the distribution, correlation and association of genotypes in relation to the values generated for the parameters considered in the analysis..

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