YIELD COMPARATIVE ANALYSIS OF SOME WINTER RAPESEED GENOTYPES

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Abstract

The study analyzed the behavior of some rapeseed genotypes, in comparative crops within ARDS Lovrin, Timis County, Romania. Nineteen genotypes were cultivated, in chernozem soil conditions, non-irrigated crop system, agricultural year 2022-2023. The yield (Y) varied between 1,288.24 kg ha⁻¹ (Absolute genotype, RCH19 trial code) and 3,703.70 kg ha⁻¹ (Excited genotype, RCH2 trial code). The hectoliter weight (HW) varied between 51.60 kg hl⁻¹ (Immortal genotype, RCH5 trial code), and 75.00 kg hl⁻¹ (Excited genotype, RCH2 trial code). The weight of one thousand seeds (WTS) varied between 3.70 g (Ultimo genotype, RCH17 trial code), and 6.00 g (Umberto genotype, RCH11 trial code). Compared to the mean of the experiment (M_Exp = 2,347.65 kg ha⁻¹), the following genotypes stood out: Excited (RCH2) with $\Delta Y = 1,356.05$ kg ha⁻¹, Expectation (RCH3) and P314 (RCH9) with $\Delta Y = 1,195.02$ kg ha⁻¹, respectively Momento (RCH14) with $\Delta Y = 1,033.99$ kg ha⁻¹. In the case of the hectoliter weight (HW), compared to the mean of the e2.51 kg hl⁻¹). In relation to parameters Y, HW and WTS, PC1 explained 53.155% of variance, and PC2 explained 26.458% of variance.

Key words: comparative crops, multivariate analysis, ranking scaling, rapeseed, yield gap

INTRODUCTION

Rapeseed (*Brassica napus* L.) is an important crop mainly for oil production, but it has multiple ecosystems, economic, and agronomic valences [11, 15, 16].

Rapeseed is also important for the production of vegetable proteins, as a honey plant, a protective crop for the soil (cover crop), as a green manure, forage crop (biomass production), ornamental attraction in agro tourism (rural tourism), as a resource for natural pollinators, the biomass resource for fuels (biodiesel, pellets), the ingot-cellulosic resource for composite materials, etc. [5, 15, 19].

The nutritional importance of rape was studied in terms of nutritional principles (e.g. fibers, minerals, vitamins, amino acids, etc.) compared to samples of beans [17]. Based on the recorded results, the authors of the study highlighted the nutritional balance of rapeseed sprouts, compared to the other bean samples. The authors concluded the importance of rape seeds, their quality in food, and the obtaining of functional foods, and they considered rape as a "functional vegetable".

Rapeseed is the third crop worldwide, in terms of importance and size of cultivated areas for oil production, and in some countries it is the main plant for oil, e.g. China [17].

Rapeseed is an important crop for Romania, and from this perspective, the concentration of rapeseed crops areas and the dynamics of areas cultivated with oleaginous and protein plants in Romania were analyzed, based on some representative indicators (distribution areas, surfaces, yields, etc.) and were formulated models that expressed trends in the evolution of the respective crops [13, 14].

As a result of the importance of rapeseed, progress has been made to improve cultivated genotypes, seed production, and studies are underway to adapt crop technologies and reduce harvest losses [15].

The production potential and yield of rapeseed crops is considerably affected by climate changes [16]. Also, the depreciation of rapeseed crops and harvests due to diseases and pests, associated with the expansion of cultivated areas, was recorded [16]. In the context of these conditions, it is considered necessary to develop more adapted genotypes, but at the same time it is considered important to preserve gene banks for rape, with natural germplasm (wild relatives of rape) and to preserve the rapeseed genetic biodiversity reserve [16].

Drought, associated with climate change, has become an abiotic stress factor, which seriously affects crops and the yield of rapeseed crops [1].

Various rapeseed genotypes were studied under conditions of water stress, in order to evaluate how seed germination is affected [1]. Based on some biometric parameters of the seedlings, the authors evaluated the behavior of the genotypes in the experimental conditions, and identified genotypes with tolerance to water stress, which represent the germplasm in the improvement of varieties with increased tolerance.

The influence of some agricultural practices, such as the distance between the rows and the density of rapeseed plants, were studied as an effect on the elements of productivity and vield [7]. The authors communicated favorable effects on the productivity elements (e.g. the degree of branching of the plants, the number of pods (elongated siliquae), the number of seeds in the pod, the weight of 1000 seeds, and associated with them, the yield per plant, respectively per surface unit. Also, the authors recorded a better yield with mechanical harvesting, associated with structural changes at the plant level.

Productivity indicators in rapeseed crop were studied in relation to improved rapeseed cultivation techniques [2]. In order to optimize the crop of rapeseed, different interactions of the technological elements, plant density, fertilization, in relation to the nutritional requirements of rapeseed and pedoclimatic conditions were studied [4, 6].

Different techniques were promoted for the study of rapeseed crops, monitoring during the vegetation period and yield estimation [10].

Aspects of the rape crop yield, such as the

yield potential, yield constraints and the respective yield gap, were analyzed in different pedoclimatic conditions, in relation to different genotypes and technologies [18]. Through the complex analysis of 118 studies, the authors identified different effects of agronomic practices on rape yield, and reported yields in the range of 37-56% compared to the yield potential in the study area. The authors identified different categories of factors that limited the yield, such as environmental factors, agronomic management, and socioeconomic factors.

Rapeseed crop yield is of high importance in production, agricultural for optimizing technologies and ensuring oil production, important in the agro-food market [8]. For this purpose, the monitoring of rapeseed crops and yield estimation is of high importance [8]. The authors used imaging analysis, based on aerial images (UAV) and satellite images (GF-1, Sentinel 2) for the study of rapeseed crop, and the estimation of the yield. Based on the working methods, the considered parameters and the recorded data, the authors obtained vield estimation models under statistical safety conditions ($\mathbb{R}^2 > 0.78$).

Both genetic information and different neural networks were also used to estimate the yield of rape seeds [12]. The authors obtained training models based on information of a physiological and morphological nature, and molecular markers. Based on a considerable number of parameters trained in the study, and an appropriate analysis, the authors detected certain parameters that facilitated models with a high degree of certainty in estimation, for obtaining valuable genotypes.

The development of the rapeseed agricultural industry was designed, and is considered sustainable, by optimizing plant architecture, by improving yields and, respectively, seed quality [9]. The authors analyzed 24 rapeseed genotypes, evaluate morphological to parameters, productivity elements, and yield and seed quality indices. Based on the recorded results, the authors quantified the contribution of the considered parameters to achieving the yields. They also identified genotypes suitable for mechanized harvesting, with high yield potential, and seed quality

indices.

The present study quantified the yield and certain elements of seed quality in 19 rapeseed genotypes, organized in comparative crops within ARDS Lovrin, Timis County, the representative area within the Western Plain of Romania.

MATERIALS AND METHODS

The study took place within ARDS Lovrin, under conditions specific to the Western Plain of Romania. Rapeseed crops were organized on a chernozem type soil, in a non-irrigated system. Rapeseed genotypes were sown in autumn, in the optimal season.

During the study period, the climatic conditions were characterized by the thermal and precipitation regime presented in Figure 1.



Fig. 1. Climatic conditions during the study period, ARDS Lovrin records Source: Original figure.

Nineteen rapeseed genotypes from different companies were cultivated. In the study, certain groupings of genotypes were made in relation to companies, and certain experimental codings: RCH - commercial rape hybrids; RG1 – Bayer genotypes group; RG2 – Corteva genotypes group; RG3 – group of KWS genotypes; RG4 – group of Lidea genotypes; RG5 – group of Limagrain genotypes.

The group of RG1 genotypes included the following genotypes: Exbury – RCH1, Excited – RCH2, Expectation – RCH3, Exsun – RCH4, Immortal – RCH5, Inprint – RCH6.

Group RG2 included genotypes: P298 – RCH7, P303 – RCH8, P314 – RCH9, P315 – RCH10.

Group RG3 included the genotypes: Umberto – RCH11, Hilico – RCH12, Granos – RCH13. Group RG4 included genotypes: Momento – RCH14, Palermo – RCH15, Vito – RCH16, Ultimo – RCH17. The RG5 group included the genotypes: Arhitecto – RCH18, Absolut – RCH19.

The area occupied by each rapeseed genotype was $1,242 \text{ m}^2$. Adequate technology, specific to rapeseed crop, was provided in uniform conditions on the experimental plots.

In relation to the purpose of the study, the yield for each genotype was determined, at mechanically harvesting moment. Samples were taken from seed production to determine moisture (MST, %), Hectoliter weight (HW, kg hl⁻¹), and Weight of thousand seeds (WTS, g).

The mean value of the experiment (M_Exp) was calculated for yield (Y, kg ha⁻¹) and hectoliter weight (HW, kg hl⁻¹), and the mean value for each group of rapeseed genotypes (M_RG1 to M_RG5).

The analysis and processing of the experimental data was done by appropriate methods [3].

RESULTS AND DISCUSSIONS

The harvesting of the 19 rapeseed genotypes was done mechanically, at the time of physiological maturity, on July 10, 2023, on each experimental variant (area of 1,242 m²). Based on the primary data recorded, the yield (Y, kg ha⁻¹) was calculated, and the values are presented in Table 1. Seeds samples were taken from each genotype, and determinations were made for moisture (MST, %), hectoliter weight (HW, kg hl⁻¹), and Weight of thousand seeds (WTS, g). The values are presented in Table 1. The ANOVA Test confirmed the reliability of the experimental data (Alpha = 0.001) (Table 2).

In the experimental conditions, rapeseed genotypes behaved differently, in relation to the biological potential, and the "genotype x environment" interaction.

Genotype	Company	Genotype	Trial code	Yield (Y)	Moisture (MST)	Hectoliter weight (HW)	Weight of thousand seeds (WTS)	
		group		(kg ha ⁻¹)	(%)	(kg hl ⁻¹)	(g)	
Exbury			RCH1	1,932.36	8.30	56.10	4.20	
Excited			RCH2	3,703.70	5.00	75.00	3.80	
Expectation	DAVED	DC1	RCH3	3,542.67	5.90	66.10	4.00	
Exsun	BAYER	KGI	RCH4	1,610.30	5.70	67.20	4.40	
Immortal			RCH5	1,932.36	8.10	51.60	4.60	
Inprint	-		RCH6	1,449.27	5.20	67.50	4.40	
P298			RCH7	1,610.30	5.80	65.10	4.60	
P303	CODTEVA	RG2	RCH8	2,254.42	6.70	53.10	4.20	
P314	CORTEVA		RCH9	3,542.67	5.30	62.10	4.20	
P315			RCH10	3,220.61	4.10	66.60	4.20	
Umberto			RCH11	1,932.36	8.20	59.10	6.00	
Hilico	KWS	RG3	RCH12	1,932.36	7.80	61.80	5.10	
Granos			RCH13	1,932.36 8.00		60.00	4.80	
Momento			RCH14	3,381.64	5.60	57.90	4.40	
Palermo		RG4	RCH15	2,737.52	6.30	58.00	4.40	
Vito	LIDEA		RCH16	2,737.52	4.30	70.50	4.20	
Ultimo			RCH17	1,771.33	5.10	65.70	3.70	
Arhitecto		DCS	RCH18	2,093.39	6.30	58.80	4.40	
Absolut	LIMAGKAIN	KGO	RCH19	1,288.24	4.60	65.40	4.00	
SE				±180.28	±0.31	±1.37	±0.12	

Table 1. Values of yield and some quality indices for rapeseed

Source: Original data.

Table 2. ANOVA Test

Source of Variation	SS	df	MS	F	P-value	F crit
Between Groups	76,959,715	3	25,653,238.26	166.1672	2.78845E-32	6.0377
Within Groups	11,115,512	72	154,382.1045			
Total	88,075,226	75				
Total	88,075,226	/5				

Source: Original data, resulted by calculation.

The yield analysis of the genotypes was made compared to the mean of the experiment (M_Exp), in the amount of M_Exp = 2,347.65 kg ha⁻¹. In relation to the mean value, the yield of each genotype was comparatively analysed, and Figure 2 was generated.

Compared to the mean value (M_Exp), seven genotypes had higher values, with increased yield $\Delta Y = 1,356.05$ kg ha⁻¹ in the case of RCH2 (Excited), $\Delta Y = 1,195.02$ kg ha⁻¹ in the case of RCH3 (Expectation) and in the case of RCH9 (P314), $\Delta Y = 872.96$ kg ha⁻¹ in the case of RCH10 (P315), $\Delta Y = 1,033.99$ kg ha⁻¹ in the case of RCH14 (Momento), $\Delta Y = 389.87$ kg ha⁻¹ in the case of RCH15 (Palermo) and RCH16 (Vito). The first three positions, in descending order, were occupied by RCH2 (Excited), RCH3 (Expectation) on par with RCH9 (P314), and RCH14 (Momento).

The yield analysis of the genotypes compared to the mean values within each group (M_RG) was done.

Within the genotypes from the RG1 group, the mean was M_RG1 = 2,361.78 kg ha⁻¹. Within the RG1 group, the RCH2 genotype had a yield increase $\Delta Y = 1,342.92$ kg ha⁻¹, and the RCH3 genotype showed a yield increase $\Delta Y = 1,180.89$ kg ha⁻¹ (Figure 3).

Within the genotypes from the RG2 group, the calculated mean value was $M_RG2 = 2,657.00 \text{ kg ha}^{-1}$ (Figure 3).



Fig. 2. Graphic representation of the yield of rapeseed genotypes, compared to the mean value of the experiment Source: Original figure.



Fig. 3. Graphic representation of the yield, mean value of the genotypes group, and of each rapeseed genotype Source: Original figure.

Within the RG2 group, the genotype RCH9 showed a yield increase $\Delta Y = 885.67$ kg ha⁻¹, and the genotype RCH10, with a yield increase $\Delta Y = 563.61$ kg ha⁻¹ (Figure 3). Within the genotypes from the RG3 group, the calculated mean value was M_RG3 = 1,932.36 kg ha⁻¹. Within the RG3 group, the cultivated genotypes registered the same yield level, under the study conditions (Figure 3). Within the genotypes from the RG4 group, the calculated mean value was M_RG4 = 2,657.00 kg ha⁻¹. Within the RG4 group, the RCH14 genotype showed a yield increase ΔY = 724.64 kg ha⁻¹, and the RCH15 and RCH16 genotypes showed a yield increase $\Delta Y = 80.52 \text{ kg ha}^{-1}$ (Figure 3). Within the genotypes from the RG5 group, the calculated mean value was M_RG5 = 1,690.82 kg ha^{-1}. Within the RG5 group, the RCH18 genotype showed a yield increase $\Delta Y = 402.57 \text{ kg ha}^{-1}$ (Figure 3). The comparative presentation of the averages on the five groups of hybrids, and the value of each hybrid compared to the average of the group, is presented in Figure 3. The mean value for each group of genotypes (M_RG1 to M_RG5) presented differences in relation to the mean value of the experiment (M_Exp) (Figure 4).

The groups of genotypes RG2 and RG4 presented differences for the mean value of the group, M_RG2, M_RG4, at the level of

 $\Delta Y = 309.35$ kg ha⁻¹ compared to the mean value of the experiment (M_Exp).



Fig. 4. Mean value of the genotypes groups, compared to the mean of the experiment Source: Original figure.

In the case of the hectoliter weight index (HW), the mean at the level of the experiment showed the value of HW = 62.51 kg hl^{-1} . The mean value calculated for each genotypes group was HW = 63.92 kg hl^{-1} (RG1), HW = 61.73 kg hl^{-1} (RG2), HW = 60.30 kg hl^{-1} (RG3), HW = 63.03 kg hl^{-1} (RG4), and HW =

62.10 kg hl⁻¹ (RG5). The distribution of HW values for the rapeseed genotypes studied in relation to the mean value of the experiment (M_Exp), and the mean value for each group of genotypes (M_RG) is shown graphically in Figure 5.



Fig. 5. Graphic distribution of the values of the HW parameter for rapeseed genotypes, in relation to the mean value of the experiment (red line), and the mean value for each group of genotypes (black line) Source: Original figure.

At the experiment level, the genotype RCH2 with the best value was identified for the HW

index (HW = 75.00 kg hl⁻¹), followed by the RCH16 genotype (HW = 70.50 kg hl⁻¹).

Genotypes with very good HW values were also identified, for each group of genotypes, in relation to the average value at group level. Multiparameter analysis was applied to obtain the distribution of genotypes in relation to yield (Y), Hectoliter weight (HW, kg hl⁻¹), and Weight of thousand seeds (WTS, g). The PCA diagram in figure 6 resulted, in which PC1 explained 53.155% of variance, and PC2 explained 26.458% of variance.

The RCH2 genotype presented a balanced position between Y and HW. It is the genotype that recorded maximum values for Y and for HW, in the comparative rapeseed crops (Table 1). The RCH3 genotype was positioned towards the Y parameter, and the RCH9 genotype was positioned close to the Y parameter. In relation to the other two components (HW, WTS), genotypes were identified with positioning associated with these indices, as biplot.

The Cluster Analysis was made in relation to Y and HW parameters, considered as important parameters for the commercial characterization of rapeseed production. The result was the dedrogram in Figure 7, in which rapeseed genotypes were grouped based on similarity in relation to the values of the two parameters (Y, HW), under conditions of Coph.corr. = 0.865.



Fig. 6. PCA distribution diagram of rapeseed genotypes in relation to Y, HW and WTS parameters Source: Original figure.

Two distinct clusters (C1, and C2) resulted, each with several sub-clusters. Cluster C1 included genotypes with high yield values (RCH2, RCH3, RCH9, RCH10, RCH14, RCH15, and RCH16), above the mean of the experiment (M_Exp = 2,347.65 kg ha⁻¹).

Within this cluster, a high level of similarity was recorded between RCH3 and RCH9 (SDI = 4.0) (Table 3).



Fig. 7. Dendrogram grouping rapeseed genotypes based on Euclidean distances, in relation to Y, HW parameters Source: Original dendrogram.

Cluster C2 included the other genotypes, with yield values below the mean value of the experiment. At the level of cluster C2, a high level of similarity was recorded between RCH11 and RCH13 (SDI = 0.9), which was also the highest level of similarity among the

tested rapeseed genotypes (Table 3).

The Ranking scaling analysis led to the diagram in figure 8, in which the rapeseed genotypes were ranked according to the values of the Y and HW parameters.

Table 3. SDI values for describi	ng the similarity of rapeseed genotypes
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	RCH1	RCH2	RCH3	RCH4	RCH5	RCH6	RCH7	RCH8	RCH9	RCH10	RCH11	RCH12	RCH13	RCH14	RCH15	RCH16	RCH17	RCH18	RCH19
RCH1		1,771.4	1,610.3	322.3	4.5	483.2	322.2	322.1	1,610.3	1,288.3	3.0	5.7	3.9	1,449.3	805.2	805.3	161.3	161.1	644.2
RCH2	1,771.4		161.3	2,093.4	1,771.5	2,254.4	2,093.4	1,449.4	161.6	483.2	1,771.4	1,771.4	1,771.4	322.5	966.3	966.2	1,932.4	1,610.4	2,415.5
RCH3	1,610.3	161.3		1,932.4	1,610.4	2,093.4	1,932.4	1,288.3	4.0	322.1	1,610.3	1,610.3	1,610.3	161.2	805.2	805.2	1,771.3	1,449.3	2,254.4
RCH4	322.3	2,093.4	1,932.4		322.4	161.0	2.1	644.3	1,932.4	1,610.3	322.2	322.1	322.1	1,771.4	1,127.3	1,127.2	161.0	483.2	322.1
RCH5	4.5	1,771.5	1,610.4	322.4		483.4	322.3	322.1	1,610.3	1,288.3	7.5	10.2	8.4	1,449.3	805.2	805.4	161.7	161.2	644.3
RCH6	483.2	2,254.4	2,093.4	161.0	483.4		161.1	805.3	2,093.4	1,771.3	483.2	483.1	483.2	1,932.4	1,288.3	1,288.3	322.1	644.2	161.0
RCH7	322.2	2,093.4	1,932.4	2.1	322.3	161.1		644.2	1,932.4	1,610.3	322.1	322.1	322.1	1,771.4	1,127.2	1,127.2	161.0	483.1	322.1
RCH8	322.1	1,449.4	1,288.3	644.3	322.1	805.3	644.2		1,288.3	966.3	322.1	322.2	322.1	1,127.2	483.1	483.4	483.3	161.1	966.3
RCH9	1,610.3	161.6	4.0	1,932.4	1,610.3	2,093.4	1,932.4	1,288.3		322.1	1,610.3	1,610.3	1,610.3	161.1	805.2	805.2	1,771.3	1,449.3	2,254.4
RCH10	1,288.3	483.2	322.1	1,610.3	1,288.3	1,771.3	1,610.3	966.3	322.1		1,288.3	1,288.3	1,288.3	161.3	483.2	483.1	1,449.3	1,127.2	1,932.4
RCH11	3.0	1,771.4	1,610.3	322.2	7.5	483.2	322.1	322.1	1,610.3	1,288.3		2.7	0.9	1,449.3	805.2	805.2	161.2	161.0	644.2
RCH12	5.7	1,771.4	1,610.3	322.1	10.2	483.1	322.1	322.2	1,610.3	1,288.3	2.7		1.8	1,449.3	805.2	805.2	161.1	161.1	644.1
RCH13	3.9	1,771.4	1,610.3	322.1	8.4	483.2	322.1	322.1	1,610.3	1,288.3	0.9	1.8		1,449.3	805.2	805.2	161.1	161.0	644.1
RCH14	1,449.3	322.5	161.2	1,771.4	1,449.3	1,932.4	1,771.4	1,127.2	161.1	161.3	1,449.3	1,449.3	1,449.3		644.1	644.2	1,610.3	1,288.3	2,093.4
RCH15	805.2	966.3	805.2	1,127.3	805.2	1,288.3	1,127.2	483.1	805.2	483.2	805.2	805.2	805.2	644.1		12.5	966.2	644.1	1,449.3
RCH16	805.3	966.2	805.2	1,127.2	805.4	1,288.3	1,127.2	483.4	805.2	483.1	805.2	805.2	805.2	644.2	12.5		966.2	644.2	1,449.3
RCH17	161.3	1,932.4	1,771.3	161.0	161.7	322.1	161.0	483.3	1,771.3	1,449.3	161.2	161.1	161.1	1,610.3	966.2	966.2		322.1	483.1
RCH18	161.1	1,610.4	1,449.3	483.2	161.2	644.2	483.1	161.1	1,449.3	1,127.2	161.0	161.1	161.0	1,288.3	644.1	644.2	322.1		805.2
RCH19	644.2	2,415.5	2,254.4	322.1	644.3	161.0	322.1	966.3	2,254.4	1,932.4	644.2	644.1	644.1	2,093.4	1,449.3	1,449.3	483.1	805.2	

Source: Original data.



Fig. 8. Scaling dendrogram for the ranking of rapeseed genotypes

Source: Original diagram.

Rapeseed yield is an essential element for the sustainability of this crop at the level of agricultural holdings and farmers. A series of bibliographic sources, based on solid studies [1, 12, 16] evaluated the yield in relation to different influencing factors, and formulated practical recommendations, correlated with the study conditions. Seed quality parameters and indices are also important in relation to the destination of rapeseed production and the capitalization of seed production on the market.

The need to promote new genotypes and to test genotypes has been supported in various studies [12, 18], in relation to climate changes, to pedoclimatic conditions specific to agricultural areas, to the adaptation of crop technologies, and optimizing yields.

The analysis of the results by appropriate methods is also important to objectively

detect the genotypes in relation to the yield or quality parameters [8, 12].

In the context of the present study, the genotype Excited (RCH2) presented high values for yield (Y) and hectoliter weight (HW). important parameters for the valorisation of seed production. According to PCA, Figure 6, the Excited genotype was balanced against the two parameters (Y, HW). According to the Cluster Analysis, the association of the genotypes was found for the considered parameters, values recorded in the study conditions. This ranking of genotypes facilitates the selective choice of certain genotypes, depending on the similarity of response in relation to the best results recorded in the case of each group of genotypes.

CONCLUSIONS

Under the study conditions, the 19 rapeseed genotypes provided different responses in terms of yield and seed quality indices.

Compared to the mean value of the experiment (M_Exp = 2,347.65 kg ha⁻¹), seven genotypes showed higher yield values. Several genotypes were highlighted: Excited (RCH2) with $\Delta Y = 1,356.05$ kg ha⁻¹, Expectation (RCH3) and P314 (RCH9) with $\Delta Y = 1,195.02$ kg ha⁻¹, and Momento (RCH14), with $\Delta Y = 1,033.99$ kg ha⁻¹, respectively.

In the case of hectoliter weight, compared to the mean of the experiment HW = 62.51 kg hl⁻¹, the genotype Excited (RCH2) with HW = 75.00 kg hl⁻¹, and the genotype Vito (RCH16) with HW = 70.50 kg hl⁻¹ stood out.

In relation to yield (Y) and seed quality parameters (HW, WTS), the multivariate analysis facilitated the distribution of the genotypes according to the association with considered parameters, and the first two components (PC1, PC2) explained 79.61% of variance. Cluster Analysis facilitated the grouping of genotypes based on similarity, and ranking scaling led to the ranking of rapeseed genotypes in relation to Y and HW parameters.

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