

Vegetative parameters in some grapevine cultivars - Comparative study

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Abstract

Fifteen grapevine genotypes, grown in five distinct locations, were comparatively analyzed based on vegetative parameters. The genotypes were grouped, five at a time, into three categories, red wine genotypes (RG), white wine genotypes (WG) and fresh consumption genotypes (FCG). The percentage of fertile shoots (FS, %) and the number of inflorescences per plant (IN, no) were determined. The Anova test confirmed the reliability of the experimental data ($p < 0.05$). For the FS parameter, the average value recorded was $\overline{FS} = 74.94 \pm 2.07\%$ (RG group), $\overline{FS} = 78.70 \pm 1.23\%$ (WG group) and $\overline{FS} = 76.60 \pm 2.43\%$ (FCG group). For the FS parameter (%) the RG5 genotype presented statistically significant differences ($p < 0.001$) compared to the calculated mean value. In the case of the other genotypes, differences were recorded, but without statistical significance. In the case of the IP parameter, the calculated mean values were $\overline{IP} = 20.38 \pm 1.33$ (RG group), $\overline{IP} = 19.46 \pm 1.62$ (WG group) and $\overline{IP} = 24.55 \pm 4.72$ (FCG group). For the IP parameter, the differences between the genotypes studied and the average calculated for each group did not present statistical significance ($p > 0.05$). The comparative analysis between the three genotype groups (RG, WG, FCG) showed differences without statistical significance ($p > 0.05$), both for the FS parameter and for the IP parameter. The presence of variance was proven by the principal components (PC1, PC2), and the genotypes were associated based on similarity and were ranked in relation to the values of the indices considered.

Keywords: cluster, comparative analysis, grapevine genotypes, morphological parameters, multivariate analysis

Introduction

The vine develops an extended aerial structure, fixed on certain support elements, depending on the cultivation system [16]. The biology of inflorescences in grapevines is of particular importance for yield, in relation to the number of clusters per plant and the number of berries in clusters and presents differentiated variability with these two elements within the formation cycles [4]. During the vine's dormant period, there is a common practice to determine the viability of the buds and predict the yield, and based on this, pruning work is established to balance growth and fruiting [11], [14], [5], [8].

Testing grapevine genotypes in various pedoclimatic conditions is of interest to observe the relationship of plants with the soil at the root system level, the balance of plants and the degree of adaptability of genotypes depending on the rootstock [3]. The architecture and development pattern of shoots and leaves in grapevines has been analyzed in relation to climatic factors, such as thermal regime [9]. Bud fertility and yield potential in grapevines were analyzed in relation to CO₂ concentration [17].

Spring weather conditions (late spring frosts) can significantly affect grapevine yields [7], [10]. Fertility of different types of buds in grapevines has been analyzed as alternatives to support and compensate for yield formation under the effects of spring frosts on grapevines [10]. The author reported the low fertility of certain types of buds and low possibility of yield compensation.

Grapevine bud fructification was analyzed in relation to grapevine management practices, such as

maintenance pruning, interventions on shoots, leaves and clusters [2]. Technological practices ensure plantation and plant management, for a balance between vegetative growth (e.g. shoots) and yield [16]. The degree of grapevine bunch compaction was analyzed in relation to vine management practices, respectively with shoot interventions [18].

This research comparatively analyzed fifteen grape genotypes for red wines, for white wines and for fresh consumption, based on vegetative parameters, namely the percentage of fertile shoots and the number of inflorescences per stem.

Material and Method

The study comparatively analyzed fifteen grapevine genotypes, cultivated in five locations, respectively in the areas of Sasciori, Loman, Ighiu, Sard and Alba Iulia, Alba County, Romania.

The grapevine genotypes were grouped into three groups, red wine grape genotypes (RG), white wine grape genotypes (WG) and fresh consumption genotypes (FCG). The RG group included the following genotypes: 'Ploapa' (RG1), 'Vechi de Ighiu' (RG2), 'Izabela de Ighiu' (RG3), 'Rosu rezistent' (RG4), and 'Cabernet Sauvignon' (RG5). The WG group included the following genotypes: 'Sard I' (WG1), 'Ruginiu de Alba' (WG2), 'Busuioaca de Ighiu' (WG3), 'Aromat alb' (WG4), and 'Feteasca Regala' (WG5). The FCG group included the following genotypes: 'Mare timpuriu' (FCG1), 'Precupeasca' (FCG2), 'Butuc alb' (FCG3), 'Fraga' (FCG4), and 'Chasselas doré' (FCG5). The parameters analyzed were the percentage of fertile shoots (FS, %) and the number of inflorescences per plant (IP, no).

The comparative analysis of each genotype was made in relation to the average value of the parameters (FS, IP) in the classification group. A comparative analysis was also made between the groups, for each parameter considered in the characterization of the 15 genotypes.

The Anova test and comparative analysis (t Test, Wilcoxon test, Mann-Whitney) were used to determine and evaluate the differences between genotypes and groups of grapevine genotypes considered in the study. Established statistical parameters were used to certify the results. The mathematical and statistical calculation module in EXCEL was used, as well as the PAST software [6].

Results and Discussion

For each grapevine genotype, fertile shoots (FS, %) and the number of inflorescences per plant (IP) parameters were determined, and the calculated average values are presented in Table 1. High values for the FS parameter were recorded in FCG1 (FS = 82.4±2.43%) and low values were recorded in the RG5 genotype (FS = 67.4±2.07%). In the case of the IP parameter, high values were recorded in the FCG2 genotype (IP = 34.71±4.72), and low values were recorded in the FCG1 genotype (12.12±4.72). Statistical reliability was recorded in the overall data analysis (Table 2).

Table 1. Parameter values for the analyzed grape genotypes

Red genotypes			White genotypes			Fresh consumption genotypes		
Genotype	FS	IP	Genotype	FS	IP	Genotype	FS	IP
	(%)	(no)		(%)	(no)		(%)	(no)
RG1	78.3	22.8	WG1	76.7	15.6	FCG1	82.4	12.12
RG2	75.2	19.4	WG2	80.8	15.8	FCG2	71.9	34.71
RG3	74.7	16.5	Wg3	75.5	20.5	FCG3	81.8	32.03
RG4	79.1	23.9	WG4	78.4	23.71	FCG4	70.7	29.64
RG5	67.4	19.3	WG5	82.1	21.7	FCG5	76.2	14.23
SE	±2.07	±1.33	SE	±1.23	±1.62	SE	±2.43	±4.72

Table 2. Anova Test results

Source of Variation	SS	df	MS	F	P-value	F crit
Between Groups	23031.32	5	4606.264	144.023	4.39E-17	2.620654
Within Groups	767.5882	24	31.98284			
Total	23798.91	29				

The differences between each genotype and the average values of the group it belongs to were calculated. For the FS parameter the results are presented in Table 3, and for the IP parameter they are

presented in Table 4.

Table 3. Comparative analysis results for FS parameter

Genotype	Given mean (%)	Sample mean (%)	95% conf. interval:	Difference and Sig	95% conf. interval	t	p (same mean)
RG1	78.30	74.94	(69.197 80.683)	3.36 ^{ns}	(-2.383 9.103)	-1.624	0.180
RG2	75.20			0.26 ^{ns}	(-5.483 6.003)	-0.126	0.906
RG3	74.70			-0.24 ^{ns}	(-5.503 5.983)	0.116	0.913
RG4	79.10			4.16 ^{ns}	(-1.583 9.903)	-2.011	0.115
RG5	67.40			-7.54 ^{ooo}	(1.797 13.283)	3.645	0.022
WG1	76.70	78.70	(75.283 82.117)	-2.00 ^{ns}	(-1.4174 5.4174)	1.625	0.180
WG2	80.80			2.10 ^{ns}	(-1.3174 5.5174)	-1.706	0.163
WG3	75.50			-3.20 ^{ns}	(-0.2174 6.6174)	2.600	0.060
WG4	78.40			-0.30 ^{ns}	(-3.1174 3.7174)	0.244	0.819
WG5	82.10			3.40 ^{ns}	(-0.017397 6.8174)	-2.762	0.051
FCG1	82.40	76.60	(69.863 83.337)	5.80 ^{ns}	(-0.93653 12.537)	-2.391	0.075
FCG2	71.90			-4.70 ^{ns}	(-2.0365 11.437)	1.937	0.125
FCG3	81.80			5.20 ^{ns}	(-1.5365 11.937)	-2.143	0.099
FCG4	70.70			-5.90 ^{ns}	(-0.83653 12.637)	2.432	0.072
FCG5	76.20			0.40 ^{ns}	(-6.3365 7.1365)	0.165	0.877

Table 4. Comparative analysis results for IP parameter

Genotype	Given mean (no)	Sample mean (no)	95% conf. interval	Difference and Sig	95% conf. interval	t	p (same mean)
RG1	22.80	20.38	(16.685 24.075)	2.42 ^{ns}	(-1.2753 6.1153)	-1.818	0.143
RG2	19.40			-0.98 ^{ns}	(-2.7153 4.6753)	0.736	0.502
RG3	16.50			-3.88 ^{ns}	(0.18472 7.5753)	2.915	0.043
RG4	23.90			3.52 ^{ns}	(-0.17528 7.2153)	-2.645	0.057
RG5	19.30			-1.08 ^{ns}	(-2.6153 4.7753)	0.811	0.463
WG1	15.60	19.46	(14.965 23.959)	-3.86 ^{ns}	(-0.63451 8.3585)	2.385	0.076
WG2	15.80			-3.66 ^{ns}	(-0.83451 8.1585)	2.261	0.087
WG3	20.50			1.04 ^{ns}	(-3.4585 5.5345)	-0.641	0.556
WG4	23.71			4.25 ^{ns}	(-0.24851 8.7445)	-2.623	0.059
WG5	21.70			2.24 ^{ns}	(-2.2585 6.7345)	-1.382	0.239
FCG1	12.12	24.55	(11.433 37.659)	-12.43 ^{ns}	(-0.68651 25.539)	2.631	0.058
FCG2	34.71			10.16 ^{ns}	(-2.9485 23.277)	-2.152	0.098
FCG3	32.03			7.48 ^{ns}	(-5.6285 20.597)	-1.585	0.188
FCG4	24.64			0.09 ^{ns}	(-13.019 13.207)	-0.020	0.985
FCG5	14.23			-10.32 ^{ns}	(-2.7965 23.429)	2.184	0.094

In the case of the FS parameter, the calculated mean values were $\overline{FS} = 74.94 \pm 2.07\%$ (RG group), $\overline{FS} = 78.70 \pm 1.23\%$ (WG group), and $\overline{FS} = 76.60 \pm 2.43\%$ (FCG group). According to the results recorded (Table 3), for the FS parameter (%) the RG5 genotype presented statistically significant differences ($p < 0.001$) compared to the calculated mean value. In the case of the other genotypes, differences were recorded, but without statistical significance. In the case of the IP parameter, the calculated mean values were $\overline{IP} = 20.38 \pm 1.33$ (RG group), $\overline{IP} = 19.46 \pm 1.62$ (WG group), and $\overline{IP} = 24.55 \pm 4.72$ (FCG group). For the IP parameter (Table 4), the differences between the studied genotypes and the average calculated for each group did not present statistical significance ($p > 0.05$).

The comparative analysis between the three genotype groups (RG, WG, FCG) showed differences

without statistical significance ($p > 0.05$), both for the FS parameter and for the IP parameter. For the FS parameter, the analysis of the RG group with the WG group led to a value of 3.75% difference between means ($p > 0.05$), and $U = 5$ ($p > 0.05$). In the case of this parameter (FS), the analysis of the RG group with FCG led to a value of 1.66% difference between means ($p > 0.05$), respectively $U = 10$ ($p > 0.05$). In the case of the FS parameter, the analysis of the WG group with FCG led to a value of 2.10% difference between means ($p > 0.05$), respectively $U = 10$ ($p > 0.05$). Therefore, in the case of the FS parameter, the three groups presented differences between the mean values ranging between 1.66% and 3.75%, but without statistical certainty.

For the IP parameter, the comparative analysis of the RG series with the WG series led to a difference of 0.918 between the means of the two groups ($p > 0.05$), respectively at the value $U = 10$, with $p > 0.05$. In the case of the comparative analysis of the RG groups with FCG, the difference between the means of the value series ($p > 0.05$), respectively $U = 10$ ($p > 0.05$). In the case of the comparative analysis of the WG group with FCG, the value resulted in 5.084, as the difference between the means of the data series ($p > 0.05$), respectively $U = 10$ ($p > 0.05$). In the case of the IP parameter, differences were recorded between the three groups, with values ranging between 0.918 and 5.084, but without statistical certainty.

The multivariate analysis led to the PCA diagram in figure 1. The grapevine genotypes were positioned differently, in relation to the level of correlation with the FS and IP parameters.

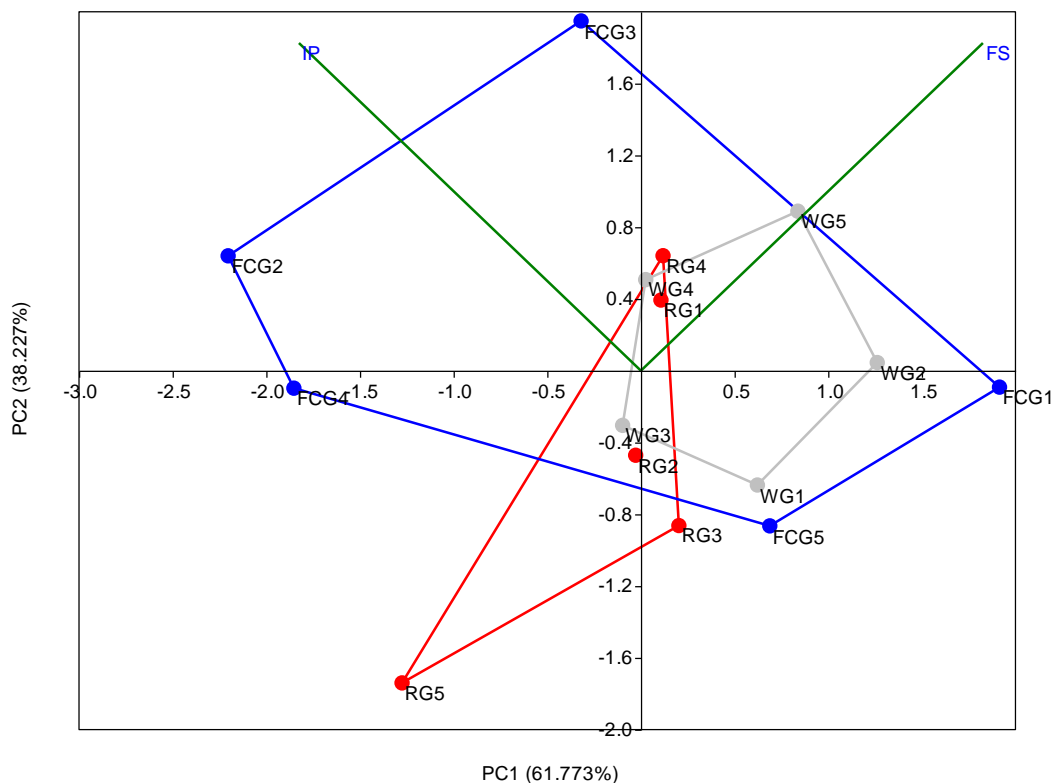


Figure 1. PCA distribution diagram of the analyzed grapevine genotypes, in relation to FS and IP

It was observed that some genotypes were oriented towards FS (e.g. RG1, RG4, WG5), and other genotypes towards IP (e.g. FCG2, FCG3). It was observed that the genotypes in the WG group fell within the scope of the genotypes in the FCG group (blue line). In the case of genotypes in the RG group, three genotypes (RG1, RG2 and RG4) were included in the FCG genotype field, RG3 was positioned outside the FCG field, but close to it, while the RG5 genotype was positioned independently. The position in the PCA diagram is confirmed by the negative, statistically significant difference of this genotype compared to the others in the group (Table 3).

Cluster analysis generated the grouping of grapevine genotypes based on similarity (Table 5), in relation to the values of the FS and IP parameters (Coph.corr. = 0.835), figure 2.

Table 5. SDI values for grapevine genotypes

	RG1	RG2	RG3	RG4	RG5	WG1	WG2	Wg3	WG4	WG5	FCG1	FCG2	FCG3	FCG4	FCG5
RG1		4.601	7.256	1.360	11.448	7.376	7.433	3.624	0.915	3.956	11.440	13.521	9.871	10.225	8.824
RG2	4.601		2.943	5.955	7.801	4.085	6.657	1.140	5.368	7.273	10.239	15.662	14.251	11.185	5.266
RG3	7.256	2.943		8.609	7.819	2.193	6.140	4.079	8.104	9.044	8.859	18.424	17.076	13.735	2.721
RG4	1.360	5.955	8.609		12.572	8.640	8.277	4.952	0.725	3.720	12.233	12.988	8.567	10.174	10.095
RG5	11.448	7.801	7.819	12.572		10.009	13.850	8.188	11.851	14.895	16.630	16.054	19.220	10.854	10.156
WG1	7.376	4.085	2.193	8.640	10.009		4.105	5.045	8.286	8.147	6.678	19.704	17.203	15.268	1.458
WG2	7.433	6.657	6.140	8.277	13.850	4.105		7.084	8.266	6.042	4.013	20.900	16.261	17.133	4.861
Wg3	3.624	1.140	4.079	4.952	8.188	5.045	7.084		4.326	6.708	10.855	14.659	13.139	10.324	6.309
WG4	0.915	5.368	8.104	0.725	11.851	8.286	8.266	4.326		4.211	12.261	12.777	8.988	9.719	9.732
WG5	3.956	7.273	9.044	3.720	14.895	8.147	6.042	6.708	4.211		9.585	16.532	10.334	13.893	9.519
FCG1	11.440	10.239	8.859	12.233	16.630	6.678	4.013	10.855	12.261	9.585		24.911	19.919	21.068	6.549
FCG2	13.521	15.662	18.424	12.988	16.054	19.704	20.900	14.659	12.777	16.532	24.911		10.256	5.210	20.927
FCG3	9.871	14.251	17.076	8.567	19.220	17.203	16.261	13.139	8.988	10.334	19.919	10.256		11.354	18.660
FCG4	10.225	11.185	13.735	10.174	10.854	15.268	17.133	10.324	9.719	13.893	21.068	5.210	11.354		16.362
FCG5	8.824	5.266	2.721	10.095	10.156	1.458	4.861	6.309	9.732	9.519	6.549	20.927	18.660	16.362	

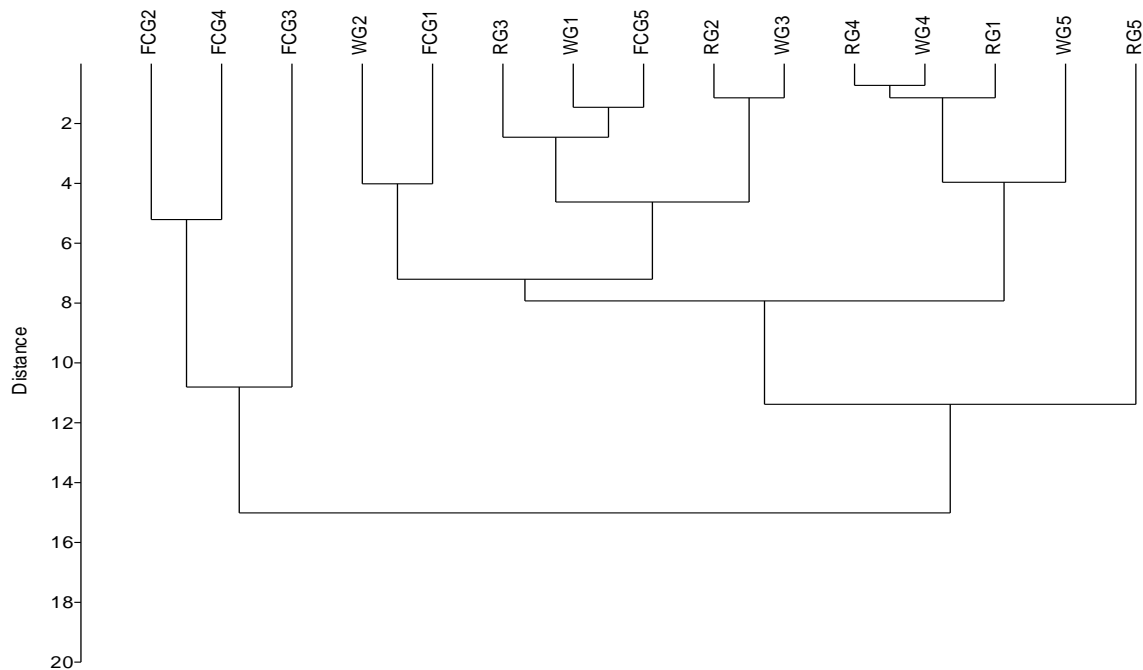


Figure 2. Cluster diagram grouping grapevine genotypes, according to FS and IP values

The RG5 genotype was positioned independently, according to the values recorded, both in the comparative analysis (Table 3) and in the multivariate analysis (Figure 1). The other genotypes were positioned associated in sub-clusters. A high level of similarity was recorded between the RG4 and WG4 genotypes (SDI = 0.725).

Based on the values of the two indices (FS, IP), a hierarchy of the studied grapevine genotypes was made, figure 3, with the confidence interval, figure 4.

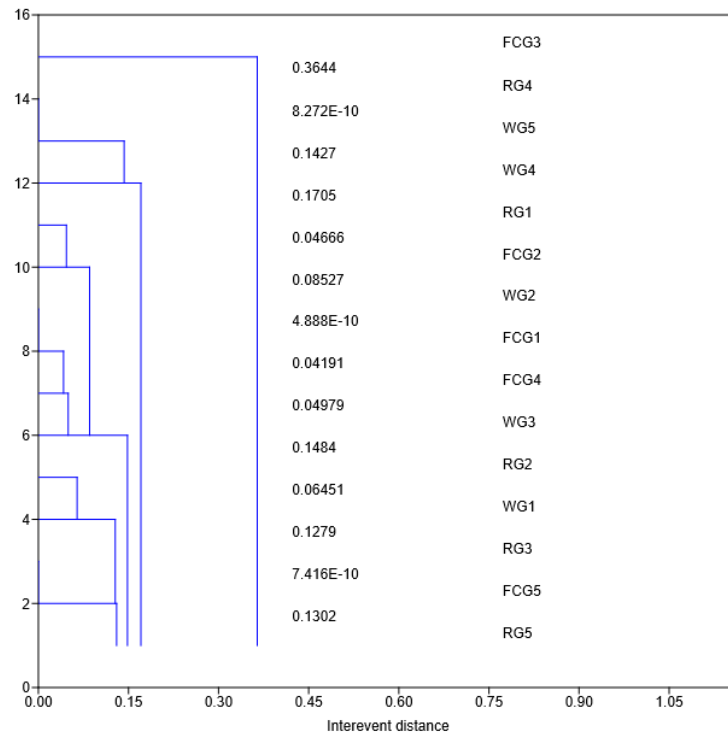


Figure 3. Rank of grapevine genotypes based on FS and IP

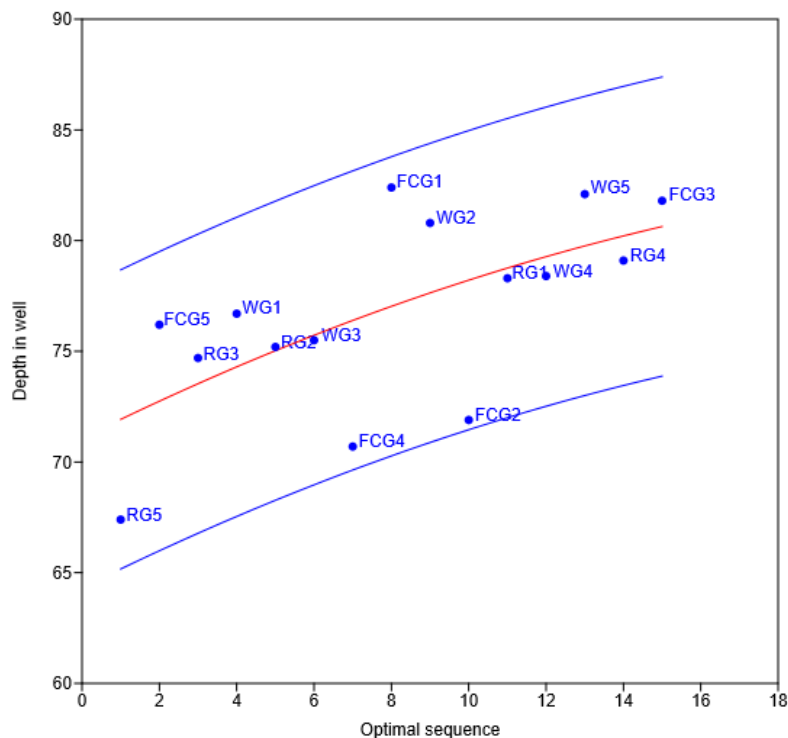


Figure 4. Framing grapevine genotypes in the confidence interval, associated with ranking

Variations in inflorescence formation and bud fertility in grapevines were recorded in relation to water stress and nitrogen nutrition during the two specific grapevine cycles [4].

The vigor of the vines, the Burgund variety, and the content of mineral elements were influenced by mineral and organic fertilization [15]. The content and mobility of mineral elements in parts of the vine plants

were analyzed with importance for the fertilization system [1].

Variation in grapevine bud fertility was studied in relation to physiological indices, associated with the soil tillage system [13].

Variations in the degree of bud fecundity in grapevines have been recorded in relation to the influence of light, shoot growth, and the level of supply of buds with metabolic products, e.g. carbohydrates [2].

Comparative studies in grapevines have shown variation in bud viability in relation to the content of total soluble sugars in canes, bud position on canes (string), genotypic variety and cultivation locations [12].

In the context of the present study, differences were recorded between FS and IP parameters in the analyzed grapevine genotypes, but within limits of variation without statistical certainty, except for the FS parameter in the 'Cabernet Sauvignon' genotype (RG5 experimental code), with negative differences from the mean at the $p < 0.05$ level.

Conclusions

The groups of red grape (RG), white grape (WG) and fresh grape (FCG) genotypes considered in the study presented differences between them for the analyzed FS and IP parameters, but without statistical significance ($p > 0.05$).

Comparative analysis of the genotypes included in each group (five genotypes in each group), with the average value of the FS and IP parameters, showed that only in the case of the RG5 genotype was there a statistically significant difference ($p < 0.05$) compared to the average of the respective group. In the case of the other genotypes, there were differences compared to the averages calculated at group level (RG, WG, FCG) but without statistical significance.

The results recorded showed that under the study conditions (climate, soil, technology), the studied genotypes presented similar results for the considered parameters (FS, IP). The results may be useful for improving crop technologies, in relation to other elements of productivity and yield.

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