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STUDY OF PHENOTYPIC VARIABILITY OF *Vicia faba* GERMPLASM BY USING OF VARIETAL DIVERSITY IN MONO-CROPPING AND INTERCROPPING SYSTEMS

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ABSTRACT

The objective of this study was to evaluate the phenotypic variability of *Vicia faba* germplasm by using varietal diversity in identifying genotypes with morpho-productive traits, disease and pest resistance, weed infestation, which can be used as a model in the development of genetic mixtures in integrated management practices for environmentally friendly, diseases, pests and weeds.

Productivity, disease and pest descriptors at 50 *Vicia faba* genotypes of different biological status (10 obsolete cultivars, 30 local populations, 10 inbreed lines), were determined, by testing in intercropping experiments with small grain cereals and mono-cropping, in two different climatic years under the northeastern part of Romania conditions.

The statistical estimators resulting from the unidirectional Anova analysis determined in mono-cropping and intercropping systems a hierarchy of heterogeneity of local populations for productivity traits and degree of attack of faba bean weevil *(Bruchus rufimanus)* and ascochyta blight (*Ascochyta fabae*) on seeds, for incidence of micromycete *Uromyces viciae fabae* and of aphids *Aphys fabae* in intercropping system.

There was a weak competition of *Vicia faba* species, regarding the presence of weeds compared to small grains cereals variants and potentially beneficial for nitrogen symbiotic fixation by increasing oat productivity, in two years of intercropping with faba bean.

By using Euclidean distance and Pearson correlation, in classification of genotypes and morpho-productive traits, diseases and pest in clusters from dendograms, similarities were highlighted between productivity and its components and between attacks to diseases and pests and dissimilarities between genotypes, members cluster three with phenotypic variability with maximum values of productivity traits and minimum attacks to disease and pest resistance compared to the other two clusters with possibilities for use in the development of genetic mixtures programs.

Keywords: phenotypic variability, agro-morphological traits, intercropping, mono-cropping.

INTRODUCTION

In the context of actual environmental concerns and of the impulse for sustainable agriculture, the control of diseases, pests and weeds in integrated systems is becoming increasingly important, restrictive chemical control options require the development of new cultural ways, in order to ensure stable and qualitative yields (Fadda et al., 2011).

Combinations of self-pollinating genotypes, being the way in which most plant species evolved before and after domestication (Murray and Milgroom, 2011), the concept of genetic mixture along with intercropping can be considered improved practices of integrated management environmentally friendly that through competitive natural principles allow a more efficient use of resources (Liebman and Dyck, 1983).

Renewed interest in intercropping and the development of varietal mixtures (obsolete cultivars, local populations, inbred lines) related to the need of reducing the fertilizer costs and soil erosion (Francis, 1986) and the production of high quality food sources for human consumption and animal feed they are features of major importance in organic farming systems with possibilities for expansion and in sustainable ones.

Conservation and utilization of crop genetic diversity can minimize damages caused by diseases and pests, contributing to

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the sustainability of crop production and the environment (Belqadi et al., 2011).

In some investigation on ICARDA germplasm, quantitative traits grain yield, seed weight per plant and pod weight per plant indicated the most coefficient of variation among a set of quantitative traits (Nariman et al., 2021). The important role of these characters in the genetic control of the studied genotypes can have positive results by introducing them in the process of *Vicia faba* breeding (Saghin et al., 2019)

The study of phenotypic variability on *Vicia faba* germplasm, by using varietal diversity in mono-croppig and intercropping with small grain cereals, represent an screening, in order to identify genotypes with morpho-productive traits, disease and pest resistance, weed infestation, which can be used as model in the development of genetic mixtures in integrated, environmentally friendly management practices, in order to combat diseases, pests and weeds, under the impact of climatic change.

MATERIAL AND METHODS

The study for the assessment of phenotypic variability and the performance determination of *Vicia faba* genotypes, for different agronomic traits, disease and pest resistance was conducted in the experimental field of the Suceava Gene Bank in two consecutive years, 2019 and 2020 with different climatic conditions. Table 1 shows in the vegetation season, close values of the average temperatures and a water deficit of the average precipitation in 2020 (311.4 mm) compared to 2019 (400 mm).

Table 1. Climatic conditions (temperature and precipitations) during the vegetation period of the species

Month	III	IV	V	VI	VII	VIII	Average/ vegetation season
Average monthly temperature/°C							
Year 2019	6.1	9.3	14.3	20.8	19.2	20.4	15.01
Year 2020	4.8	8.2	13.6	19.0	19.5	19.1	14.65
Average monthly precipitation/mm							Total/ vegetation season
Year 2019	18.8	36.6	118.9	149.6	30.1	46.0	400
Year 2020	17.7	5.4	85.0	140.1	51.2	37.0	311.4

The biological material was represented by 50 faba bean genotypes from different biological status (30 local populations, 10 obsolete cultivars, 10 inbred lines) tested in two experimental variants: - intercropping with two genus (*Avena spp.* and *Hordeum vulgare*) and mono-cropping of *Vicia faba* (Table 2).

Table 2. The biologic material tested in mono-cropping and intercropping experimental systems

Experimental system	Intercropping with small grain cereals 2019 and 2020					Mono-cropping with *Vicia faba* 2020		
Tested cultivars	*Avena spp*	*Vicia faba subsp. faba var*			*Hordeum vulgare*	*Vicia faba subsp. faba var*		
		major	*minor*	*aequina*		*major*	*minor*	*aequina*
Local population	36	30	0	0	30	30	0	0
Obsolete cultivars	11	1	5	4	10	1	5	4
Inbreed lines	3	9	0	1	10	9	0	1

The experimental design for intercropping with small grain cereals was accomplished in 2 blocks with 50 variants, each variant having 6 rows. In mono-cropping the seeds of faba bean were sown in 2 blocks with 50 variants.

Different technologies have been used to protect against disease, pests and weeds. In the intercropping with small grain cereals, no chemical treatments and manual plowing were carried out.

The following works were carried out in mono-cropping:

- 1 chemical treatment with Benta 480 SL and 3 manual plows for weed destruction.
- 4 chemical treatments for diseases such as: ascochyta blight (*Ascochyta fabae),* chocolate spot (*Botrytis fabae*), faba bean rust (*Uromyces viciae fabae*) in phenophases (3 leaves, before and after flowering, the pods appearance) with specific phytosanitary products (Bravo 500 SC, Topsin 70 PU, Curzate Manox).
- 4 chemical treatments for pests: aphids (*Aphys fabae*), faba bean weevil (*Bruchus rufimanus*) in the phenophases (3 leaves, before and after flowering, the pods appearance) with specific phytosanitary products (Mospilan 20 SG, Karate Zeon, Decis Expert).

To evaluate the phenotypic variability, the following morpho-physiological descriptors were performed:

1. Intercropping system: number of pods/ genotype, number of seeds/genotype, yield/ genotype, one thousand seeds weight, degree of attack of foliar diseases: chocolat spot (*Botrytis fabae* %), ascochyta blight (*Ascochyta fabae* %), faba bean rust (*Uromyces viciae fabae* %), degree of attack of aphids (*Aphys fabae* %) on plants, degree of attack of ascochyta blight (*Ascochyta fabae* %) on seeds, degree of attack of faba bean weevil (*Bruchus rufimanus %*) on seeds.
2. Mono-cropping system: number of pods/genotype, number of seeds/genotype, yield/genotype, one thousand seeds weight, degree of attack of ascochyta blight (*Ascochyta fabae %)* on seeds, degree of attack of faba bean weevil (*Bruchus rufimanus %*) on seeds.

Weed species and their distribution in variants were determined to highlight the behavior of *Vicia faba* regarding competition with them.

Statistical analyses

All analyses were conducted using SPSS 26. The following estimators were calculated for all the descriptors mentioned: average (x), variation amplitude (min-max), standard deviation (ƃ), F-Anova test (p/0.05), Tukey test (p/0.05) presented in tables and dendrograms by statistical analysis techniques such as: one-way ANOVA and Hierarchical Cluster Analysis.

RESULTS AND DISCUSSION

A considerable variation was found in faba bean germplasm tested for productivity traits. The average results of the analysis revealed the high number of pods which were recorded for obsolete cultivars in 2019, in intercropping system (89.3) and local populations (91.5); high yield was achieved in mono-cropping system in 2020 by inbreed lines (163.7 g/m) (Table 3). Due to water stress from June (140.1 mm; Table 1) which affected the binding of the pods, aspect also specified by Mwanamwenge et al. (1999), low average values regarding the number of pods/ genotype were noticed in 2020, in obsolete cultivars (25.2; 73.8), local populations (20.6; 70.7) in intercropping and mono-cropping system and inbreed lines (36.4) in intercropping.

Also it may be noticed that in 2020, in mono cropping system the inbreed lines show the variation amplitude of 80 and 384 number of seeds/genotype. Anova F factor, emphasize significantly high values (Table 3) statistically differentiating local populations from obsolete cultivars and inbreed lines by a high heterogeneity of productivity traits (number of pods/genotype, F (2, 87) - 53.754, p-0.000; number of seeds/genotype, F (2, 87) - 48.292, p-0.000; yield/genotype, F (2, 87) -

47.724, p-0.000) in intercropping and mono cropping systems. Tukey test values show statistically significant differences between the two types of experiments, at local populations for the number of pods/genotype (p-0.011*) between 2019 intercropping and 2020 mono-cropping, and for number of seeds/ genotype and productivity/genotype (p-0.000*) between intercropping and mono-cropping systems, from year 2020.

Table 3. Values of productivity descriptors for *Vicia faba* in intercropping and mono-cropping systems

Genotype	Obsolete cultivars			Local populations			Inbreed lines		
Experimental design	Intercropping		Mono-cropping	Intercropping		Mono-cropping	Intercropping		Mono-cropping
Tested years	2019	2020	2020	2019	2020	2020	2019	2020	2020
Number of samples	10	10	10	30	30	30	10	10	10
Descriptors	Number of pods / genotype								
Average	89.3	25.2	73.8	91.5	20.6	70.7	67.4	36.4	95.4
Minimum values	33	3	11	45	2	8	10	6	59
Maximum values	242	102	148	159	56	124	119	90	162
Standard deviation	64.39	29.36	38.71	33.6	16.3	28.8	37.56	24.84	36.08
F - Anova/*p (0.05)*	F (2; 27) - 5.156; p-0.013			F (2; 87) - 53.754; p-0.000			F (2; 27) - 7.845; p-0.002		
Tukey - Test *p (0.05)*	0.013*	0.013*	0.740/ 0.068	0.000*	0.000*	0.011*/ 0.000*	0.113	0.113	0.164/ 0.001*
Descriptors	Seeds number / genotype								
Average	205.8	56.4	174.1	158.5	38.5	150.8	138.3	74.8	190.8
Minimum values	77	8	8	56	3	50	19	10	80
Maximum values	320	254	539	325	110	304	236	191	384
Standard deviation	64.39	29.36	38.71	65.5	30.4	56.4	80.99	51.68	100.29
F - Anova/*p (0.05)*	F (2; 27) - 5.679; p-0.009			F (2; 87) - 48.292; p-0.000			F (2; 27) - 5.247; p-0.012		
Tukey - Test *p (0.05)*	0.010*	0.010*	0.778/ 0.046*	0.000*	0.000*	0.840/ 0.000*	0.198	0.198	0.324/ 0.009*
Descriptors	Yield / genotype (g/m)								
Average	124.7	39.3	131.97	142.0	35.9	152.6	124.1	68.2	163.7
Minimum values	35.6	6	9.6	43.2	2.04	31.2	21	7.4	66.1
Maximum values	324.2	178	246.6	365.2	107.6	341.4	231	170.7	296.8
Standard deviation	83.55	51.32	66.9	55.5	27.19	63.4	74.69	54.96	75.94
F - Anova/*p (0.05)*	F (2; 27) - 5.656; p-0.009			F (2; 87) - 47.724; p-0.000			F (2; 27) - 4.810; p-0.016		
Tukey - Test *p (0.05)*	0.025*	0.025*	0.970/ 0.015*	0.000*	0.000*	0.702/ 0.000*	0.187	0.187	0.418/ 0.012*
Descriptors	One thousand seeds weight / genotype (g)								
Average	612.3	683.5	775.6	905.8	947.1	977.4	905.7	843.9	839.5
Minimum values	462.58	344	662.3	561.6	472.1	624.8	719.1	517	706
Maximum values	808.2	1069	969.2	1229.4	1453.3	1375.1	1110.5	1292.5	985.5
Standard deviation	102.5	240.6	105.7	165.3	227.1	156.9	127.8	194.3	103.9
F - Anova/*p (0.05)*	F (2; 27) - 2.526; p-0.099			F (2; 87) - 1.120; p-0.331			F (2; 27) - 0.634; p-0.538		
Tukey - Test *p (0.05)*	0.598	0.598	0.082/ 0.427	0.668	0.668	0.300/ 0.803	0.620	0.620	0.579/ 0.998

Regarding the resistance to *Botrytis fabae*, high values of variation amplitude (0-10) and standard deviation (3.33) were recorded for the inbreed lines sown in mono-cropping system, in year 2020. Referring to the resistance to *Uromyces viciae fabae*, the local populations sown in intercropping system, in 2020, high values of variation amplitude (0-10) and standard deviation (2.77) were recorded (Table 4). Concerning the resistance to *Ascochyta fabae*, the obsolete cultivars sown in intercropping system in 2020, high values of variation amplitude (0-10) and standard deviation (3.09) were recorded (Table 4). The inbreed lines sown in mono-cropping system 2020, recorded high values of the variation amplitude (0-40) and of the standard deviation (12.05), regarding the resistance to *Aphys fabae* (Table 4). It was also observed that in both years of experiments, in intercropping system, the F factor Anova had high values, statistically differentiating local populations from obsolete cultivars and inbread lines in terms of susceptibility to *Uromyces viciae fabae* [F (1, 18) - 15.012, p-0.000] and *Aphys fabae* [F (1, 18) - 11.667, p-0.001] (Table 4).

Table 4. Biotic stress susceptibility (pest and diseases) of faba bean plants, in intercropping systems

Genotype	Obsolete cultivars		Local populations		Inbreed lines	
Experimental design	Intercropping					
Tested years	2019	2020	2019	2020	2019	2020
Number of samples	10	10	30	30	10	10
Disease (Fungi)	*Botrytis fabae (%)*					
Average	1.62	1.10	1.96	1.31	0.47	1.60
Minimum values Maximum values	0.00-3.40	0.00-5.00	0.00-4.08	0.00-10.00	0.00-2.35	0.00-10.00
Standard deviation	1.38	2.07	1.48	2.23	0.86	3.33
F - Anova/*p (0.05*)	F (1; 18) - 0.443; p-0.514		F (1; 18) - 1.816; p-0.183		F (1; 18) - 1.056; p-0.318	
Disease (Fungi)	*Uromyces viciae fabae (%)*					
Average	0.00	1.70	0.00	1.93	0.00	0.90
Minimum values	0.00	0.00-5.00	0.00	0.00-10.00	0.00	0.00-3.00
Standard deviation	0.00	1.88	0.00	2.77	0.00	1.44
F - Anova/*p (0.05*)	F (1; 18) - 8,103; p-0.011		F (1; 18) - 15.012; p-0.000		F (1; 18) - 3.857; p-0.065	
Disease (Fungi)	*Ascochyta fabae (%)*					
Average	1.02	2.60	1.62	1.79	1.37	2.30
Minimum values Maximum values	0.00-2.35	0.00-10.00	0.00-4.59	0.00-5.00	0.00-5.30	0.00-15.0
Standard deviation	1.05	3.09	1.33	1.73	1.37	2.30
F - Anova/*p (0.05*)	F (1; 18) - 2.321; p-0.145		F (1; 18) - 0.189; p-0.666		F (1; 18) - 0.347; p-0.563	
Pests	*Aphys fabae (%)*					
Average	0.00	4.10	0.87	7.17	1.08	6.80
Minimum values	0.00	0.00-15.0	0.00-20.00	0.00-40.00	0.00-4.08	0.00-40.00
Standard deviation	0.00	5.52	3.66	9.53	1.76	12.05
F - Anova/*p (0.05*)	F (1; 18) - 5.503; p-0.031		F (1; 18) - 11.667; p- 0.001		F (1; 18) - 2.199; p-0.155	

Regarding the attack of *Ascochyta fabae* on seeds, it is observed that in the intercropping system, in 2020, in the case of obsolete cultivars, the variation amplitude is 14.9-46.8 and standard deviation, 9.22. Instead on the lines the amplitude of variation is 7.05-50.0, and the standard deviation 12.10 (Table 5).The presence of *Bruchus rufimanus* on seeds, in intercropping system, in 2020, was highlighted by high values of variation amplitude (0-45.9) and standard deviation (8.88) at local populations (Table 5).

Regarding the variability of susceptibility to ascochyta blight on seeds, the significantly high values for Anova factors [F (2, 87) - 25.259, p-0.000] statistically differentiated the local populations from obsolete cultivars and inbreed lines. Referring to the presence of pests on seeds, there were differences between the local populations [F (2, 87) - 9.208, p-0.000], obsolete cultivars and inbreed lines. Regarding the attack of *Ascochyta fabae* and *Bruchus rufimanus* in both cropping system in two consecutive years, the values of the Tukey post hoc test show a statistically significant difference on local populations (p-0.000*).

Table 5. Biotic stress susceptibility (pest and diseases) of faba bean seeds, in mono-cropping and intercropping systems

Genotype	Obsolete cultivars			Local populations			Inbreed lines		
Experimental design	Intercropping		Mono-cropping	Intercropping		Mono-cropping	Intercropping		Mono-cropping
Tested years	2019	2020	2020	2019	2020	2020	2019	2020	2020
Number of samples	10	10	10	30	30	30	10	10	10
Diseases (Fungi)	*Ascochyta fabae (%)*								
Average	9.46	25.48	17.47	8.74	14.84	5.78	8.26	22.94	16.12
Minimum values	3.70	14.9	8.80	2.90	0.00	4.34	0.00	7.05	5.58
Maximum values	19.50	46.80	31.40	16.90	45.90	29.50	18.40	50.00	27.60
Standard deviation	4.66	9.22	7.32	3.50	8.88	5.78	5.20	12.10	6.98
F - Anova/*p (0.05)*	F (2; 27) - 11.975; p-0.000			F (2; 87) - 25.259; p-0.000			F (2; 27) - 7.287; p-0.003		
Tukey - Test *p (0.05)*	0.000*	0.000*	0.054/ 0.053	0.000*	0.000*	0.001*/ 0.004*	0.002*	0.002*	0.121/ 0.198
Pests	*Bruchus rufimanus (%)*								
Average	6.85	15.65	15.1	8.74	14.8	15.1	6.28	13.79	13.16
Minimum values	2.50	6.90	8.43	2.90	0.00	4.34	2.10	0.00	7.60
Maximum values	19.00	28.10	29.40	16.90	45.90	29.50	10.80	29.70	19.20
Standard deviation	4.70	7.05	6.41	3.50	8.88	5.78	2.99	8.17	4.05
F - Anova/*p (0.05)*	F (2; 27) - 6.467; p-0.005			F (2; 87) - 9.208; p-0.000			F (2; 27) - 5.643; p-0.009		
Tukey - Test *p (0.05)*	0.009*	0.009*	0.015*/ 0.980	0.001*	0.001*	0.001*/ 0.981	0.014*	0.014*	0.026/ 0.965*

Figure 1 shows the phenotypic variability of the three biological categories analyzed in mono-cropping system, in 2020, and intercropping system, in two consecutive years (2019, 2020) on productivity traits, pest and diseases attack on plant and seeds, observing a hierarchy of heterogeneity in local populations followed by obsolete cultivars and inbreed lines.

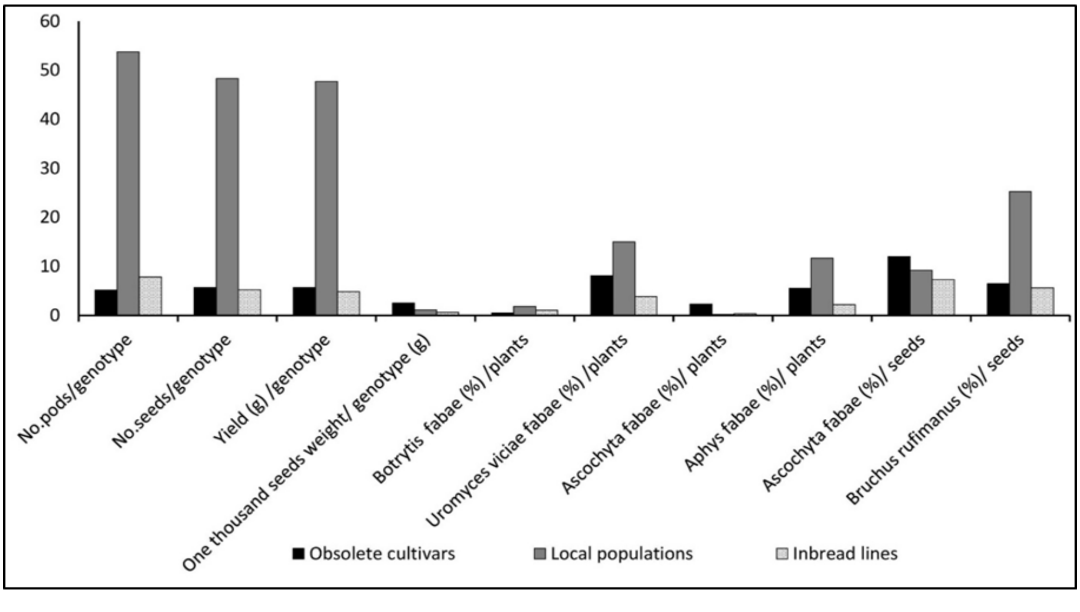

Figure 1. Phenotypic variability in the tested faba bean genotypes in mono-cropping and intercropping experiment systems

The behavior of the faba bean genotypes in association with small grain cereals in the intercropping systems in two consecutive years (2019, 2020) was characterized by:

- poor plants competition in the variants *Avena spp.-Vicia faba* with weed species determined in much higher numbers compared to the cereals variants *Avena spp.-*

Avena spp., *Avena spp.-Hordeum spp.* (Table 6);

- increasing the oats yields, by fixing symbiotic nitrogen (yield/genotype - 90.48 g in 2019 and 44.65 g in 2020) (Table 6).

Similar studies specify this aspect, for increasing the nutritional potential of the soil being recommended grain legumes or combinations between grain legumes and oats, barley or wheat (Bogdan et al., 2015).

Table 6. The behavior of *Vicia faba*, related to weed presence, in intercropping systems in two consecutive experiment years (2019, 2020)

Experimental years	Intercropping 2019			Intercropping 2020		
Variants	*Avena spp.* *Avena spp.*	***Avena spp.*** ***Vicia faba***	*Avena spp.* *Hordeum spp.*	*Avena spp.* *Avena spp.*	***Avena spp.*** ***Vicia faba***	*Avena spp.* *Hordeum*
Number total of weed species	14	**16**	14	10	**13**	11
Average yield (g)/genotype/ *Avena spp*.	89.53	**90.48**	86.78	34.7	**44.65**	34.04

The descriptors of productivity, resistance to diseases and pests determined to obsolete cultivars, local populations and inbreed lines of *Vicia faba* in intercropping experiments in two consecutive years (2019, 2020) and mono-cropping experiment in 2020, were statistically classified into 3 clusters (Table 7) by the method of average linkage between groups, highlighting the similarities between members by different values of the correlation coefficients. So, it observe in dendogram (Figure 2) their similarities, by strongly significant correlations between the number of pods/genotype and the number of seeds/genotype (r=0.945***), respectively the number of pods/genotype and the production/genotype (r=0.914***) in mono cropping system in 2020, and intercropping system in two consecutive years (2019, 2020). Also there is a significant correlation between the attack degree of *Aphis fabae*/plants and *Ascochyta fabae*/plants (r=0.454**) in intercropping system for both years, low significant correlations between the attack degree of *Bruchus rufimanus* on seeds and *Ascochyta fabae*/seeds (r=0.276) in mono-cropping experiment (2020).

Table 7. Classification of agro-morphological traits of productivity, resistance to diseases and pests in clusters, by the method of average linkage between groups and Pearson correlation distance

No. of clusters	Cluster membership	No. membership in dendogram	Cluster combined from agglomeration schedule to method average linkage between groups		Pearson correlation coefficients
			Cluster 1	Cluster 2	
1	No. pods/genotype	1	1	2	**.945**
1	No. seeds/genotype	2	1	3	**.914**
1	Yield (g)/genotype	3	6	8	**.454**
2	*Uromyces viciae fabae (%)/plants*	7	9	10	**.276**
3	*Botrytis fabae (%)/plants*	5	7	9	.106
3	*Aphis fabae (%)/plants*	6	5	6	.091
3	*Ascochyta fabae (%)*/plants	8	4	7	.066
2	*Bruchus rufimanus* (%)/seeds	9	4	5	.026
2	*Ascochyta fabae* (%)/seeds	10	1	4	-.228
2	One thousand seeds weight/ genotype (g)	4	-	-	-

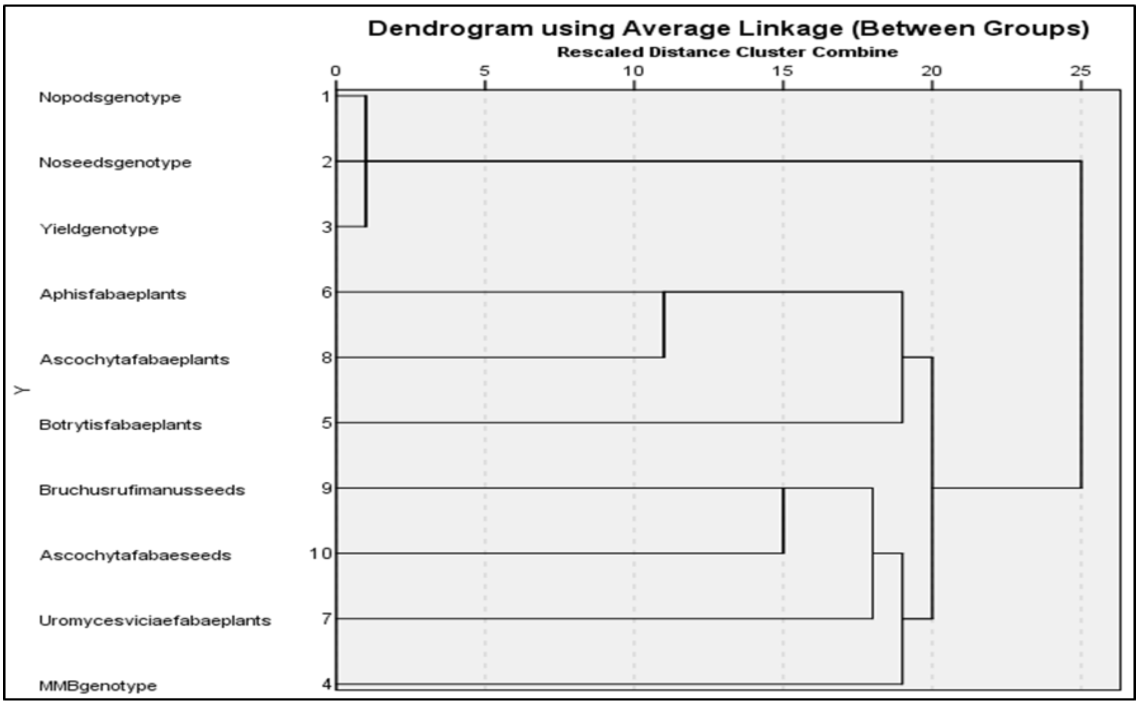

Figure 2. Hierarchical clustering of 50 faba bean genotypes based on Pearson correlation distance using data from three experiments and ten agro-morphological traits

Vicia faba genotypes tested in intercropping experiments in two consecutive years (2019 and 2020) and mono-cropping experiment in 2020, were analyzed hierarchically by the Ward variance method based on the dissimilarity of the performance of agronomic productivity traits and the attack degree of some diseases and pests, grouping in three clusters with different number of members (82 in cluster 1, 57 in cluster 2, 11 in cluster 3) (Table 8). Results of this study were in agreement with the findings of Demirkol and Yilmaz (2019).

Table 8. Cluster membership on *Vicia faba* accessions tested in three experiments

No. of cluster	No. of members	Types of members		
		Obsolete cultivars	Local populations	Inbreed lines
Clustering I	82	SVGB-16, SVGB-19, SVGB-75, SVGB-102	SVGB-52, SVGB-141, SVGB-150, SVGB-153, SVGB-155, SVGB-204, SVGB-278, SVGB-285, SVGB-303, SVGB-10230, SVGB-10441, SVGB-14792, SVGB-14796, SVGB-14804, SVGB-14805, SVGB-14834, SVGB-11111	SVGB-15575 SVGB-15581 SVGB-15588 SVGB-16039 SVGB-16042
Clustering II	57	SVGB-58	SVGB-148, SVGB-215, SVGB-272, SVGB-293, SVGB-298, SVGB-11109, SVGB-14789, SVGB-14802, SVGB-14803, SVGB-14827	SVGB-15572 SVGB-15573 SVGB-16041
Clustering III	11	SVGB-15592, SVGB-15596, SVGB-15608, SVGB-39, SVGB-50	SVGB-15596, SVGB-142, SVGB-294, SVGB-10543	SVGB-15587 SVGB-15580

Data on the variation amplitude (min-max) and average values of all clusters showed that the maximum values of the following descriptors: number of pods/genotype (144.73), number of seeds/genotype (326.27), yield (g)/genotype (239.49), the degree attack of seed infestation with *Bruchus rufimanus* (8.25) and *Ascochyta fabae* (10.24) were observed at members of cluster III, followed by members of cluster II (Table 9).

Table 9. Range values of various traits in different clusters

Clusters	Cluster I		Cluster II		Cluster III	
Estimators	Min-Max	Average	Min-Max	Average	Min-Max	Average
No. pods/genotype	2.00-80.00	32.05	23.00-159.00	89.54	98.00-242.00	144.73
No. seeds/genotype	3.00-137.00	59.35	125.00-278.00	181.05	254.00-539.00	326.27
Yield (g)/genotype	2.04-155.10	55.57	70.21-256.20	161.01	165.54-341.40	239.49
One thousand seeds weight (g)/genotype	344.2-1453.30	896.24	561.68-1375.10	880.02	514.75-890.20	717.66
Botrytis fabae (%)/plants	0.00-10.00	1.33	0.00-4.08	0.69	0.00-4.06	1.17
Aphys fabae (%)/plants	0.00-40.00	4.69	0.00-4.08	0.27	0.00-3.00	0.27
*Uromyces viciae fabae (%)/*plants	0.00-10.00	1.10	0.00-0.00	0.00	0.00-3.00	0.27
Ascochyta fabae (%)/plants	0.00-15.00	1.67	0.00-4.59	0.47	0.00-3.40	0.68
Bruchus rufimanus (%)/seeds	0.00-45.90	13.90	2.1-29.5	11.39	3.70-13.00	8.25
Ascochyta fabae (%)/seeds	0.00-56.60	22.20	3.1-31.4	14.43	3.70-15.00	10.24

The Ward Linkage dendrogram (Figure 3) built on the Euclidean distance showed the maximum distance in cluster III represented by the following members: 4 obsolete cultivars/var. minor (SVGB-15592, SVGB-15596, SVGB-15608, SVGB-50), 1 obsolete cultivar/var. aequina (SVGB-39), 3 local populations/var. major (SVGB-294, SVGB-10543, SVGB-142), inbreed line/var. aequina (SVGB 15587), 1 inbreed line/var. major (SVGB 15580). Therefore, the members of this cluster have a high heterogeneity of productivity descriptors, the degree of attack of diseases and pests on plants and seeds, and can be used in the development of varietal mixtures and protective crops.

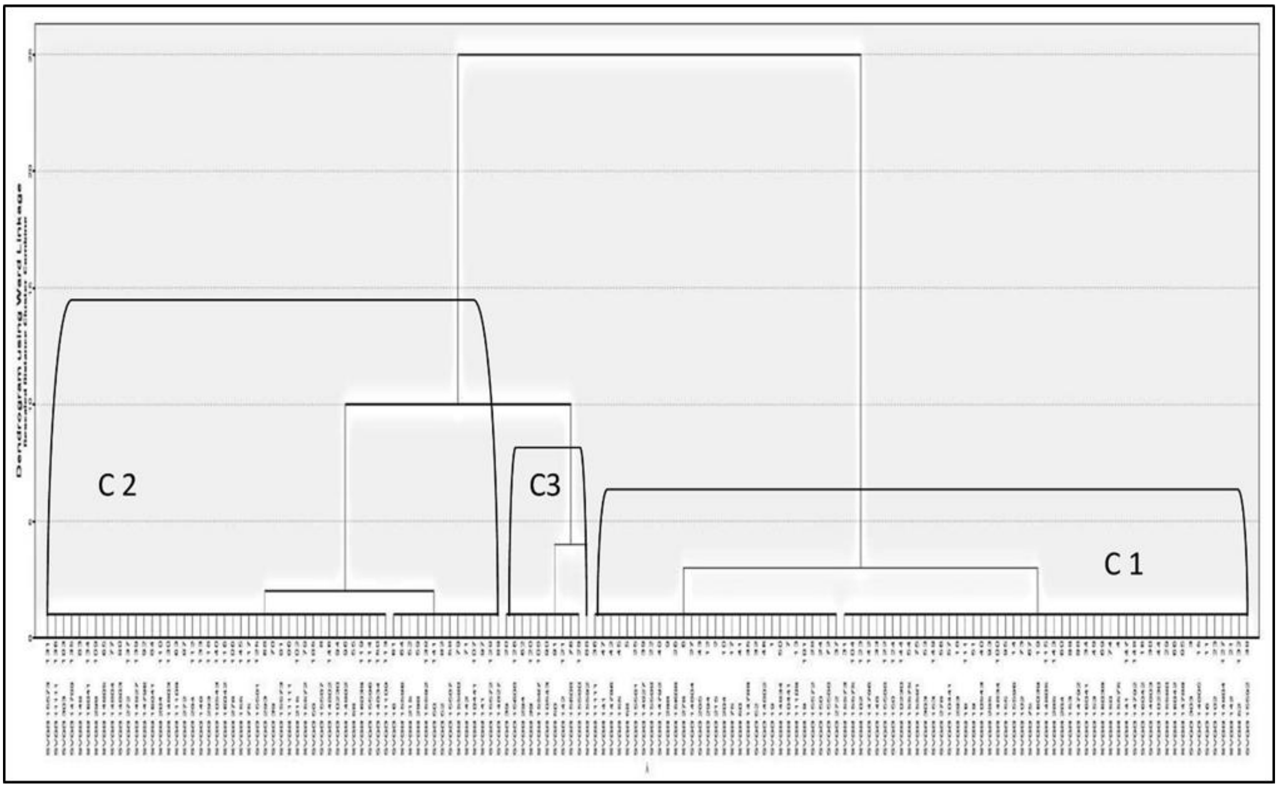

Figure 3. Dendogram Ward based on Euclidean distance using the data from three experiments and ten agro-morphological traits

CONCLUSIONS

Our study, evidentiated a sufficiently large phenotypic variability for the tested germplasm, highlighting a hierarchy of heterogeneity especially in local populations and less in varieties and lines obsolete inbred in intercropped cultures and monocultures, chemically treated.

The incidence of diseases and pests was limited in the two experimental systems, statistically highlighting the local populations in the intercropping system by a variable susceptibility to rust (*Uromyces viciae fabae*), aphids (*Aphys fabae*), anthracnose (*Ascochyta fabae*) on plants and seeds and faba bean weevil attack on seeds (*Bruchus rufimanus*) in both culture systems.

Germplasm of *Vicia faba* showed poor competition for weeds and potentially beneficial for fixing symbiotic nitrogen by increasing oat productivity in the faba bean version of both intercropping experiments being recommended as a protective crop in association with oats or barley in any agricultural exploitation.

The classification of the productivity descriptors, diseases and pests in the dendogram using the distance of the Pearson correlation showed similarities between yield and its components in both culture systems and a link between the degree of aphid attacks and anthracnose in the intercropped culture system being the most influential quantitative variables of the phenological expression that resulted from the interaction between the genotypes and the environmental conditions.

The classification of faba bean genotypes studied in the dendogram using Euclidean distance differentiated the formed clusters, highlighting the maximum distance in cluster III, its members having maximum values of productivity traits and minimum values of disease and pest attacks compared to the other two clusters. Therefore, the identified genotypes in this cluster (4 obsolete cultivars/ var. minor - SVGB-15592, SVGB-15608, SVGB-50, SVGB-15596, 1 obsolete cultivars/ var. aequina - SVGB-39, 3 local populations/ var. major - SVGB-294, SVGB-10543, SVGB-142, 1 inbreed line/var. aequina - SVGB 15587, 1 inbreed line/var. major - SVGB 15580) could be used in the development of genetic mixtures thus contributing to the sustainability of crop production and environmental protection.

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