https://doi.org/10.46909/journalalse-2021-034
Available online: https://jurnalalse.com

Original Article
Journal of Applied Life Sciences and Environment
Vol. LIV, Issue 4 (188) / 2021: 389-404

STUDY OF PHENOTYPIC VARIABILITY USING THE VARIETAL DIVERSITY OF CULTIVATED FORMS OF NAKED AND HULLED OATS IN THE INTERCROPPING SYSTEM

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Received: Mar. 02, 2022. Revised: Mar. 15, 2022. Accepted: May 08, 2022. Published online: May 30, 2022

ABSTRACT. The research carried out at the Gene Bank in Suceava, Northern Romania, aimed to highlight the phenotypic variability of the germplasm of *Avena* spp. For this purpose, the morpho-productive traits and resistance to diseases, pests and weeds were analysed. Productivity, diseases and pests, days to heading and days to maturity descriptors of 46 *Avena* spp. genotypes (naked and hulled oat) with different biological statuses (36 local populations, 10 cultivars), were evaluated by testing in intercropping experiments with small grain cereals and grain legumes. The unidirectional ANOVA analysis generated values that allowed the elaboration of a hierarchy of heterogeneity in the hulled local populations, for some of the analysed characters (one thousand seeds weight/genotype, degree of attack by *Puccinia coronata* and *Oulema melanopa* and days to maturity) and these were less in naked forms. There was a high competition of *Avena* species, regarding weeds in small grain cereal variants and potentially beneficial for nitrogen symbiotic fixation by increasing naked and hulled local oat population productivity in intercropping with fava bean. The Euclidean distance classification of the oat genotypes investigated in the dendrogram distinguished the generated groups, indicating the maximum distance in cluster IV. With high heterogeneity of productivity traits, better resistance to disease and pests, and shorter maturity, members of this cluster could be used to develop genetic mixture programs.

Keywords: phenotypic variability, morphological traits, intercropping, naked and hulled cultivars.

INTRODUCTION

The existence of genetic resources in gene banks has focused mainly on conservation aspects, but in the context of climate change, the sustainability of agriculture there is an urgent need to involve under-used genetic stocks with defined traits (local populations, crop wild relatives) to exploit the potential value for the benefit of society (ECPGR, 2010). This includes adapting local populations to new management systems and establishing a mixed system of selection between farmers and breeders using the technology available for the development of evolved local breeds (Casanas *et al.,* 2017).

Because of an increase in nutrient usage efficiency and - in the case of

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legume-cereal combinations - nitrogen transfer, it was discovered that under low-input conditions intercropping systems can provide greater yields than monocropping systems (McLaughlin and Mineau, 1995; Ruijven and Berendse, 2003).

In interspecific diversity, oats (*Avena* L.) is one of the old cereal genres with many wild species and few cultivated forms, including diploid (*Avena strigosa* Screb), tetraploid (*Avena abyssinica* Hochst), hexaploid (*Avena sativa* ssp. *sativa* L., *Avena sativa* ssp. *nudisativa* (Husn.) Fruit. et Sold., *Avena byzantina* C.K. (Loskutov *et al.,* 2005) used in some regions of the globe for animal feed and human nutrition.

The study was conducted to identify genetic mixtures in order to improve the quality of agroecosystems and preserving biodiversity.

MATERIALS AND METHODS

The study was made on 46 genotypes from different oat species and biological status (25 samples of the hulled local populations, 11 samples of the naked local populations, 4 samples of the hulled cultivars, 6 samples of the naked cultivars) tested in intercropping with two species (*Vicia faba* and *Hordeum vulgare*). The oat genotypes tested are from the Suceava Gene Bank collection with origins in Romania and other European countries belonging to the species of oats hulled (*Avena sativa* ssp. *sativa, Avena byzantina, Avena strigosa, Avena abyssinica*) and naked (*Avena sativa* ssp. *nudisativa, Avena sativa* ssp. *nudisativa* var. *inermis, Avena sativa* ssp. *nudisativa* var. *chinensis*) (*Table 1*).

Table 1 - Biological material tested

Country of origin	Oat species	Number of samples of			
		local populations		cultivars	
		hulled	naked	hulled	naked
Romania	*Avena sativa* ssp. *sativa*	20	-	1	-
Sweden	*Avena sativa* ssp. *sativa*	-	-	1	-
Poland	*Avena sativa* ssp. *sativa*	-	-	1	-
	Avena sativa ssp. *nudisativa* var. *inermis*	-	1	-	-
France	*Avena sativa* ssp. *sativa*	-	-	1	-
	Avena sativa ssp. *nudisativa*	-	-	-	-
	Avena sativa ssp. *nudisativa* var. *inermis*	-	1	-	-
Germany	*Avena abyssinica*	1	-	-	-
	Avena byzantina	1	-	-	-
	Avena sativa ssp. *nudisativa*	-	-	-	1
	Avena sativa ssp. *nudisativa* var. *inermis*	-	5	-	-
	Avena sativa ssp. *nudisativa* var. *chinensis*	-	1	-	-
Bulgaria	*Avena abyssinica*	1	-	-	-
	Avena sativa ssp. *nudisativa*	-	1	-	1
Russia	*Avena byzantina*	1	-	-	-
	Avena strigosa	1	-	-	-
	Avena sativa ssp. *nudisativa* var.*inermis*	-	1	-	-
Czech	*Avena sativa* ssp. *nudisativa*	-	-	-	3
	Avena sativa ssp. *nudisativa* var.*inermis*	-	1	-	1

Table 2 - The experimental design for intercropping system

No. Plot	Oat species	No. Plot	Oat species	No. Plot	Oat species	No. Plot	Oat species	No. Plot	Oat species
1	*Avena sativa* ssp. *sativa* HLP	10	*Avena sativa*-ssp. *sativa* HLP	19	*Avena abyssinica* HLP	28	*Avena sativa* ssp. *sativa* HLP	37	*Avena sativa* ssp. *sativa* HLP
2	*Avena sativa* ssp. *sativa* HLP	11	*Avena sativa* ssp. *nudisativa* var. *inermis* NLP	20	*Avena sativa* ssp. *sativa* HLP	29	*Avena sativa* ssp. *nudisativa* NAC	38	*Avena sativa* ssp. *nudisativa* var. *inermis* NLP
3	*Avena sativa* ssp. *nudisativa* NAC	12	*Avena sativa* ssp. *sativa* HLP	21	*Avena sativa* ssp. *nudisativa* var. *inermis* NLP	30	*Avena sativa* ssp. *sativa* HLP	39	*Avena sativa* ssp. *sativa* HLP
4	*Avena sativa* ssp. *sativa* HLP	13	*Avena byzantina* HLP	22	*Avena sativa* ssp. *sativa* HAC	31	*Avena sativa* ssp. *sativa* HLP	40	*Avena sativa* ssp. *nudisativa* var. *inermis* NLP
5	*Avena sativa* ssp. *nudisativa* var. *chinensis* NLP	14	*Avena nudisativa* ssp. *inermis* NAC	23	*Avena byzantina* HLP	32	*Avena sativa* ssp. *sativa* HAC	41	*Avena sativa* ssp. *sativa* HLP
6	*Avena sativa* ssp. *sativa* HAC	15	*Avena sativa* ssp. *sativa* HLP	24	*Avena sativa* ssp. *sativa* HLP	33	*Avena sativa* ssp. *nudisativa* var. *inermis* NLP	42	*Avena sativa* ssp. *nudisativa* var. *inermis* NLP
7	*Avena sativa* ssp. *sativa* HLP	16	*Avena strygosa* HLP	25	*Avena sativa* ssp. *nudisativa* NAC	34	*Avena abyssinica* HLP	43	*Avena sativa* ssp. *sativa* HLP
8	*Avena sativa* ssp. *Sativa* HLP	17	*Avena sativa* ssp. *sativa* HAC	26	*Avena sativa* ssp. *sativa* HLP	35	*Avena sativa* ssp. *sativa* HLP	44	*Avena sativa ssp. nudisativa* var. *inermis* NLP
9	*Avena sativa* ssp. *nudisativa* NAC	18	*Avena sativa* ssp. *nudisativa* var. *inermis* NLP	27	*Avena sativa* ssp. *nudisativa* NLP	36	*Avena sativa* ssp. *nudisativa* NAC	45	*Avena sativa* ssp. *sativa* HLP
46	*Avena sativa* ssp. *nudisativa* var. *inermis* NLP								

Legend: HLP - hulled local population, NLP - naked local population, HAC - hulled cultivar, NAC - naked cultivar.

The experimental design for intercropping system *(Table 2)* was accomplished in 2 blocks with 46 plots, in consecutive order (1 - 46). Each plot had 6 rows of 1.5 m length labelled thus: plot 1 (V_1 - 2 rows *Avena* spp., V_2 - 1 row *Avena* spp., 1 row *Vicia faba*, V_3 - 1 row *Avena* spp., 1 row *Hordeum vulgare*), plot 2 (V_1, V_2, V_3) … to the plot 46 (V_1, V_2, V_3).

In the intercropping oat with fava bean and barley, there were no chemical treatments, and manual ploughing was carried out.

The estimation of the phenotypic variability was made based on the specific morpho-physiological descriptors: yield/ genotype, 1000 seed weight, degree of attack of foliar diseases: *Septoria* leaf blotch (*Septoria avenae* f. sp. *avenae* %), crown rust (*Puccinia coronata* f. sp. *avenae* %), degree of attack of oat leaf beetle (*Oulema melanopa* %) on plants, days to heading, days to maturity. In order to evaluate the behaviour of *Avena* spp. in terms of competition with weeds species, their distribution was determined and studied in each variant.

The main climatic parameters of the two years of study were similar in terms of temperature, but the precipitation differed a lot in April (31.2 mm), May (33.9 mm) and July (21.1 mm), the difference being of 63.6 mm throughout the vegetation period of the oats *(Table 3)*.

Table 3 - Air temperature and rainfall during the growing season

Year / Month	March	April	May	June	July	August	Average / Total
Temperature (°C)							
2019	6,1	9,3	14,3	20,8	19,2	20,4	15,02
2020	4,8	8,2	13,6	19	19,5	19,1	14,03
Deviation	1,3	1,1	0,7	1,8	-0,3	1,3	0,99
Rainfall (mm)							
2019	18,8	36,6	118,9	149,6	30,1	46	400
2020	17,7	5,4	85	140,1	51,2	37	336,4
Deviation	1,1	31,2	33,9	9,5	-21,1	9	63,6

Statistical analyses

For all mentioned descriptors were calculated average (x), variation amplitude (min-max), F-ANOVA test (p/0.05), and LSD test (p/0.05) using SPSS 26.

RESULTS AND DISCUSSION

Tests performed on the studied oat germplasm showed a clear differentiation of the productivity traits. The average values obtained highlighted the high yield genotype that was recorded in variant V_2 in 2019 for hulled (91.73 g/m) and naked local populations (69.21 g/m) (*Table 4*). Due to the small amounts of rainfall from May to June (85.0 - 140.1 mm; *Table 1*) in the phenophases of elongation of the straw and flowering-heading low average values of the yield/genotype were noticed in 2020, in hulled local populations (49.11 g/m) and naked local populations (20.5 g/m) compared to 2019, an aspect also specified by Bîlteanu G. *et al.* 1991.

In addition, in the two years of testing, the one-thousand-seeds weight as a productivity element showed a greater variation of the average values and amplitudes (min-max) within the oat hulled local populations, in comparison with the naked ones (*Table 4*). The hydric stress in April of 2020 (5.4 mm) during the emergence period and in June

(140.1 mm) during the flowering-heading phenophase determined in the case of hulled local populations a variable number of seedlings with a large number of inflorescences and kernels with a lower degree of grain roundedness (average/2020; V_1 - 28.48, V_2 - 25.12; V_3 - 23.92) compared to 2019 (average; V_1 - 31.30, V_2 - 30.32; V_3 - 30.80).

The ANOVA F factor, emphasises significantly high values (*Table 4*) statistically differentiating local hulled populations by naked local populations through a high heterogeneity of productivity traits (one-thousand- seeds weight/genotype, F (2, 72) - 8.346) in the all variants by 2020. The LSD test values show statistically significant differences in the hulled local populations for the one-thousand-seeds weight/genotype between the three types of variants (V_1, V_2, V_3), (p-0.000*).

Regarding the susceptibility to *Puccinia coronata*, average values of 3.52 in V_1 and 0.60 in V_2 for hulled genotypes and average values of 3.27 in V_1 and 0.09 in V_2 for naked genotypes compared to the V_3 variant where both genotypes were immune, were observed in 2020.

In the 2020 intercropping system, the ANOVA F factor highlighted a large variation in the degree of attack of crown rust compared to 2019 at hulled local populations [F (2,72) = 10.096; p = 0.000] and naked local populations [F (2,30) = 3.401; p = 0.047].

Referring to the resistance to *Septoria avenae*, high values of variation amplitude (0-15 %) (*Table 4*) were determined in the variants with oat (V_1) and fava bean (V_2) for the naked local populations.

Concerning the resistance to *Oulema melanopa*, an amplitude of attack degree of 0-15%, in the V_3 variant and 0-10% in the V_1 and V_2 variants in 2019 in the hulled local populations (*Table 4*), were noticed.

The degree of attack variability was statistically significant with a high value of the ANOVA factor [F (2, 72) = 4.301, p = 0.017]. LSD test values show significant statistical differences (p-0.000*) in attack variability between variants V_1 and V_3.

In 2020 in the intercropping system, at hulled local populations, the descriptor, days to maturity in V_1 and V_3 variants shows high values of the variation amplitude (134.02-141.00) in comparison with V_2, 134.00-138.00 (*Table 4*).

The ANOVA F factor for the descriptor days to maturity had high statistical values [F (2, 72) =3.564, p = 0.031], the values of the LSD post hoc test show a statistically significant difference (p = 0.000*) between V_2 and V_3.

Table 4. Values of morpho-physiological descriptors for hulled and naked local populations in intercropping experiment system

Genotypes	Hulled local populations						Naked local populations					
Tested years	**2019**			**2020**			**2019**			**2020**		
No.samples	25			25			11			11		
Variants	V_1	V_2	V_3	V_1	V_2	V_3	V_1	V_2	V_3	V_1	V_2	V_3
Descriptors	**Yield / genotype (g/m)**											
Average	89.08	91.73	87.09	36.63	49.11	37.20	62.47	69.21	68.70	14.3	20.5	18.5
Minimum	18.45	16.70	27.80	11.38	5.42	7.26	10.05	10.50	12.30	2.40	1.25	2.56
Maximum	156.0	175.1	215.6	116.6	154.2	137.2	95.4	142.4	173.3	34.38	86.46	83.77
F-ANOVA (p = 0.05)	F (2,72) = 0.082, p = 0.922			F (2,72) = 1.116, p = 0.333			F (2,30)-0.071, p = 0.932			F (2,30)-0.241, p = 0.787		
LSD (p = 0.05)	0.81	0.81	0.86 0.68	0.19	0.19	0.21 0.95	0.73	0.73	0.75 0.97	0.50	0.50	0.65 0.82
Descriptors	**1000 Seed weight / genotype (g)**											
Average	31.30	30.32	30.80	28.48	25.12	23.92	23.15	23.70	24.69	22.82	21.20	20.57
Minimum	14.5	14.7	13.20	22.42	17.60	12.10	19.20	19.20	22.30	13.30	12.60	11.70
Maximum	40.50	37.20	39.20	37.00	35.00	31.00	27.50	27.70	30.00	28.81	28.20	26.50
F-ANOVA (p = 0.05)	F (2,72) = 0.155, p = 0.857			F (2,72) = 8.346, p = 0.001			F (2,30)-0.945, p = 0.400			F (2,30)-0.674, p = 0.517		
LSD p(0.05)	0.58	0.58	0.77 0.78	0.00*	0.00*	0.00* 0.30	0.62	0.62	0.18 0.39	0.42	0.42	0.26 0.75
Disease	**Septoria avenae f.sp. avenae %**											
Average	0.52	0.76	0.28	1.52	0.92	1.80	1.81	1.36	1.09	1.72	2.00	1.36
Minimum	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Maximum	3.00	10.00	3.00	5.00	5.00	10.00	15.00	15.00	10.00	10.00	5.00	5.00
F-ANOVA (p = 0.05)	F (2,72) = 0.674, p = 0.513			F (2,72) = 1.399, p = 0.253			F (2,30)-0.090, p = 0.914			F (2,30)-0.182, p = 0.834		
LSD p(0.05)	0.56	0.56		0.26	0.26	0.60 0.10	0.79	0.79	0.67 0.87	0.79	0.79	0.73 0.52

Genotypes	Hulled local populations						Naked local populations					
Disease	**Puccinia coronata (%)**											
Average	15.24	16.24	14.92	3.52	0.60	0.00	22.45	22.54	21.63	3.27	0.09	0.00
Minimum	0.00	0.00	0.00	0.00	0.00	0.00	1.00	1.00	1.00	0.00	0.00	0.00
Maximum	60.00	60.00	60.00	20.00	3.00	0.00	50.00	50.00	50.00	20.00	1.00	0.00
F-ANOVA (p = 0.05)	F (2,72) = 0.035, p = 0.966			F (2,72) = 10.096, p = 0.000			F (2,30)-0.006, p = 0.994			F (2,30)-3.401, p = 0.047		
LSD p(0.05)	0.84	0.84	0.95 0.80	0.00*	0.00*	0.00* 0.47	0.99	0.99	0.93 0.92	0.03*	0.03*	0.65 0.82
Pest	**Oulema melanopa (%)**											
Average	2.40	1.32	0.48	1.60	1.08	0.80	3.00	1.27	2.54	2.18	0.72	0.81
Minimum	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Maximum	10.00	10.00	5.00	10.00	5.00	5.00	10.00	5.00	10.00	5.00	5.00	5.00
F-ANOVA (p = 0.05)	F (2,72) = 4.301, p = 0.017			F (2,72) = 1.217, p = 0.302			F (2,30)-0.879, p = 0.426			F (2,30)-2.829, p = 0.075		
LSD p(0.05)	0.10	0.10	0.00* 0.20	0.32	0.32	0.12 0.59	0.21	0.21	0.73 0.35	0.04*	0.04*	0.05 0.89
Descriptors	**Days to heading**											
Average	75.76	75.76	75.76	77.56	77.28	76.92	74.81	74.81	74.81	75.72	75.72	75.72
Minimum	71.00	71.00	71.00	72.00	72.00	72.00	71.00	71.00	71.00	72.00	72.00	72.00
Maximum	78.00	78.00	78.00	82.00	82.00	81.00	77.00	77.00	77.00	80.00	80.00	80.00
F-ANOVA (p = 0.05)	F (2,72) = 0.000, p = 1.000			F (2,72) = 1.217, p = 0.302			F (2,30)-0.000, p = 1.000			F (2,30)-0.000, p = 1.000		
LSD p(0.05)	1.00	1.00	1.00 1.00	0.72	0.72	0.42 0.65	1.00	1.00	1.00 1.00	1.00	1.00	1.00 1.00
Descriptor	**Days to maturity**											
Average	125.7	125.7	125.7	137.8	136.7	138.4	124.8	124.8	124.8	138.8	137.1	138.8
Minimum	121.0	121.0	121.0	134.0	134.0	134.0	121.0	121.0	121.0	134.0	134.0	134.0
Maximum	128.0	128.0	128.0	141.0	138.0	141.0	127.0	127.0	127.0	141.0	138.0	141.0
F-ANOVA (p = 0.05)	F (2,72) = 0.000, p = 1.000			F (2,72) = 3.654, p = 0.031			F (2,30)-0.000, p = 1.000			F (2,30)-1.831, p = 0.178		
LSD p(0.05)	1.00	1.00	1.00 1.00	0.09	0.09	0.34 0.00*	1.00	1.00	1.00 1.00	0.10	0.10	1.00 0.10

Variants: V_1 - *Avena* spp.-*Avena* spp.; V_2 - *Avena*-*Vicia faba*; V_3 - *Avena* spp.-*Hordeum vulgare*

Fig. 1 and *Fig. 2* show the average values of the agronomic descriptors analysed in 2019 and 2020 in intercropping experiments for 25 samples of hulled local populations and 11 samples of naked local populations. In the hulled local populations (*Fig. 1*) there is a variability of productivity, the attack degree of oat leaf beetle and crown rust in the two years, their high values being recorded in 2019. In the case of the naked local populations (*Fig. 2*), the productivity traits and the attack degree of the crown rust showed variability in the two years of testing, with high values in 2019. Also, it is highlighted in both the hulled and naked local populations a variation of the descriptor days to maturity in the two years; the genotypes studied having a late maturity in 2020.

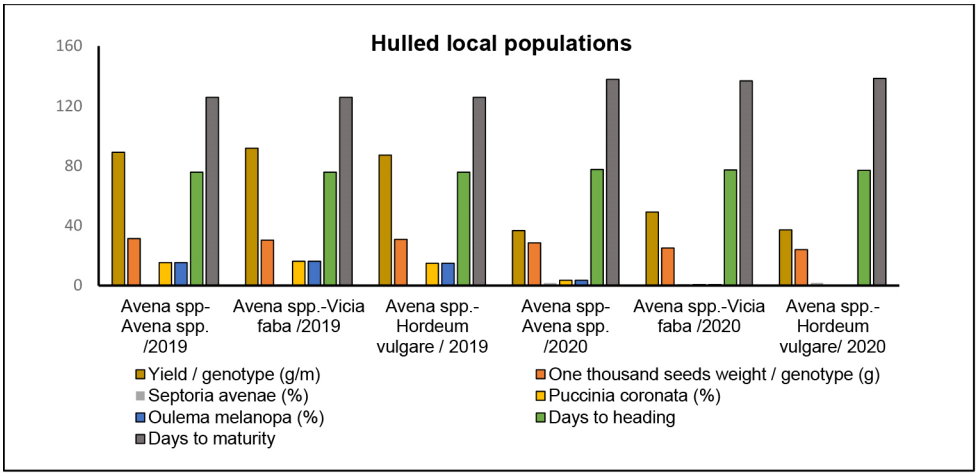

Figure 1 - Influence of the intercropping system on the variability of productivity traits, disease and pest in the hulled oat local populations

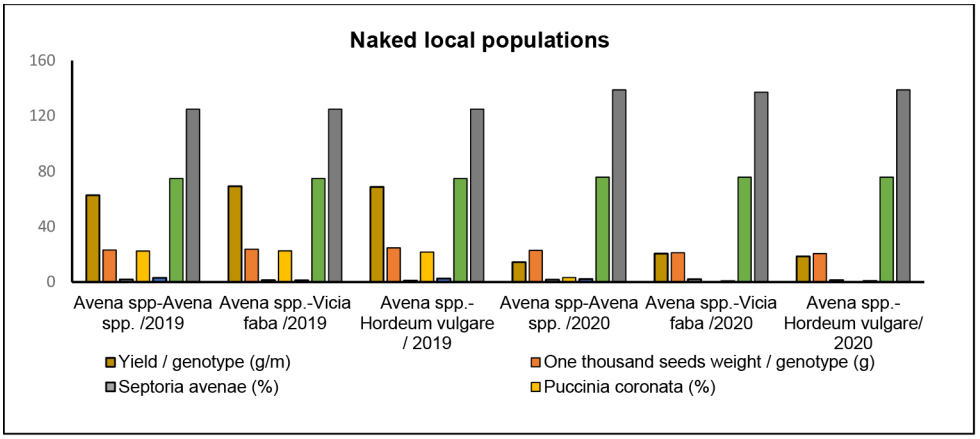

Figure 2 - Influence of the intercropping system on the variability of productivity traits, disease and pest in the naked oat local populations

The hulled cultivars (150.40 g/m) and naked cultivars (97.64 g/m) sown in 2019, in the intercropping system, recorded high values of the average yield/genotype, in V_1 (*Table 4*).

The hydric stress of May-June 2020 manifested in the phenophase of straw elongation and flowering-heading affected the yield/genotype in the case of varieties as well, noting low values in the hulled cultivars (87.21) and naked cultivars (24.40) compared to 2019.

In 2020, in the hulled cultivars as in the case of the hulled local populations, there was a variability of the descriptor, one thousand weight seeds under the influence of water stress in April, June from the phenophases of emergence, flowering-heading highlighted by the higher value of ANOVA factor [F (2.9) - 3.151; p-0.052] compared to 2019. The values (0.04*) LSD test showed statistically significant differences between V_1 and V_3 (*Table 5*).

Concerning the susceptibility to *Puccinia coronata*, the naked cultivars were sown in the intercropping system in 2020, showing the variability of the average values in the three variants as follows: 6.00 in V_1, 0.66 in V_2, 0.00 in V_3. Also, the ANOVA F factor, emphasises high values statistically (*Table 5*) [F (2, 15)-16.404, p-0.000] in 2020, values (0.000*) LSD test showed significant differences between all variants.

The presence of *Oulema melanopa* on plants in the intercropping system caused a variability of the degree of attack in both years of testing in naked cultivars with amplitude values of 0-10% in V_1 and 0-3% in V_2 (*Table 5).*

The ANOVA F factor had significantly high values (*Table 5*) in naked cultivars from variants 2019 [F (2, 15)-3.509, p-0.056] and 2020 [F (2, 15)-4.953, p-0.022]. LSD test values show significant differences of attack variability between variants: V_1 and V_3 for the year 2019 (p-0.020*) and V_1, V_2, V_3 from 2020 (p- 0.01 *).

Fig. 3 and *Fig. 4* show the average values of the agronomic descriptors analysed in two consecutive years (2019, 2020) in intercropping experiments for four samples of hulled cultivars and six samples of naked cultivars. In the hulled cultivars (*Fig. 3*) there is variability in productivity, the attack degree of oat leaf beetle and crown rust, days to maturity in both years, their high values of productivity and degree of attack of *Oulema melanopa* being recorded in 2019. In the case of the naked cultivars (*Fig. 4*), the productivity traits and the attack degree of the crown rust, days to maturity showed variability in the two years of testing, with high values in 2019 for crown rust and productivity. Also, it is highlighted in both the hulled and naked cultivars a variability of the descriptor days to maturity in the two years, with the genotypes studied having a late maturity in 2020. The behaviour of the oat genotypes in association with two genera (*Vicia faba* and *Hordeum vulgare*) in the intercropping systems in 2019 and 2020) was characterised by:

- poor plant competition in the variants *Avena* spp.-*Vicia faba,* with weed species (*Table 5*);

- increased the oats yields in V_2 (*Avena* spp.-*Vicia faba*) by fixing symbiotic nitrogen at hulled local populations 91.73 g in 2019; 49.11 g in 2020 and naked local populations 69.21 g in 2019 and 20.5 in 2020) *(Table 6*).

Table 5 - Values of morpho–physiological descriptors for hulled and naked cultivars from intercropping experiment system.

Genotypes	Hulled cultivars						Naked cultivars					
Tested years	**2019**			**2020**			**2019**			**2020**		
No.samples	4			4			6			6		
Variants	V_1	V_2	V_3	V_1	V_2	V_3	V_1	V_2	V_3	V_1	V_2	V_3
Descriptors	**Yield / genotype (g/m)**											
Average	150.40	121.80	124.47	87.21	19.23	55.39	97.64	96.71	86.25	24.40	23.47	18.44
Minimum	44.15	30.30	26.00	32.73	17.52	27.06	54.75	78.70	50.80	5.02	9.07	3.45
Maximum	221.9	187.8	189.5	159.3	190.3	79.48	169.4	123.8	162.2	85.64	44.19	30.29
F-ANOVA (p = 0.05)	*F (2,9) = 0.191, p = 0.829*			*F (2,9) = 0.941, p = 0.425*			*F (2,15) = 0.263, p = 0.772*			*F (2,15) = 0.147, p = 0.864*		
LSD ***p = (0.05)***	0.58	0.58	0.62 0.95	0.59	0.59	0.44 0.20	0.91	0.91	0.57 0.51	0.93	0.93	0.62 0.67
Descriptors	**1000 Seed weight / genotype (g)**											
Average	38.85	39.32	39.97	35.95	31.00	29.77	27.66	29.36	27.78	27.12	24.81	25.50
Minimum	37.00	34.80	37.30	33.10	27.80	24.50	25.00	25.40	24.20	22.70	20.40	20.30
Maximum	40.60	45.90	42.40	39.81	34.80	26.00	29.70	37.10	30.60	33.00	30.90	31.60
F-ANOVA (p = 0.05)	F (2,9) = 0.104, p = 0.902			F (2,9) = 3.151, p = 0.052			F (2,15) = 0.657, p = 0.533			F (2,15) = 0.549, p = 0.589		
LSD ***P = (0.05)***	0.85	0.82	0.66 0.79	0.09	0.09	0.04* 0.65	0.32	0.32	0.94 0.35	0.32	0.32	0.48 0.76
Disease	***Septoria avenae* f.sp. *avenae* (%)**											
Average	1.25	0.75	1.25	1.50	2.75	0.00	1.66	2.00	2.00	2.83	1.16	0.83
Minimum	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Maximum	5.00	3.00	5.00	3.00	10.00	0.00	3.00	10.00	5.00	5.00	3.00	3.00
***F-ANOVA* (p = 0.05)**	F (2,9) = *0.068*, p = *0.935*			F (2,9) = *0.856*, p = *0.457*			*F (2,15) = 0.030*, p = *0.970*			*F (2,15) = 2.684*, p = *0.101*		
LSD ***p(0.05)***	0.75	0.75	1.00 0.75	0.56	0.56	0.49 0.22	0.83	0.83	0.83 1.00	0.09	0.09	0.04* 0.72

Genotypes	Hulled cultivars						Naked cultivars					
Disease	***Puccinia coronata (%)***											
Average	6.50	6.00	7.00	21.00	0.75	0.00	11.00	13.50	12.33	6.00	0.66	0.00
Minimum	3.00	1.00	3.00	0.00	0.00	0.00	1.00	1.00	1.00	0.00	0.00	0.00
Maximum	10.00	10.00	10.00	80.00	3.00	0.00	25.00	25.00	20.00	10.00	3.00	0.00
***F-ANOVA* (p = 0.05)**	F (2,9) = *0.059*, p = *0.943*			F (2,9) = *1.084*, p = *0.379*			*F (2,15) = 0.127*, p = *0.881*			*F (2,15) = 16.404*, p = *0.000*		
LSD	0.86	0.86	0.86	0.24	0.24	0.22	0.62	0.62	0.79	0.00*	0.00*	0.00*
p(0.05)			0.73			0.97			0.81			0.57
Pest	***Oulema melanopa (%)***											
Average	4.50	0.00	2.50	2.25	0.75	0.75	3.16	0.50	0.00	4.00	0.66	0.50
Minimum	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Maximum	10.00	0.00	10.00	3.00	3.00	3.00	10.00	3.00	0.00	10.00	3.00	3.00
***F-ANOVA* (p = 0.05)**	F (2,9) = *1.430*, p = *0.289*			F (2,9) = *1.333*, p = *0.311*			*F (2,15) = 3.509*, p = 0.056			*F (2,15) = 4.953*, p = *0.022*		
LSD	0.12	0.12	0.42	0.19	0.19	0.19	0.56	0.56	0.02*	0.01*	0.01*	0.01*
(p = 0.05)			0.37			1.00			0.70			0.89
Descriptors	**Days to heading**											
Average	73.75	73.75	73.75	73.50	73.75	73.50	75.33	75.33	75.33	75.33	75.00	74.50
Minimum	73.00	73.00	73.00	72.00	72.00	72.00	73.00	73.00	73.00	74.00	74.00	73.00
Maximum	76.00	76.00	76.00	76.00	76.00	76.00	77.00	77.00	77.00	74.50	73.00	76.00
F-ANOVA (p = 0.05)	*F (2,9) = 0.000, p = 1.000*			*F (2,9) = 0.024, p = 0.976*			*F (2,15) = 0.000, p = 1.000*			*F (2,15) = 0.549, p = 0.589*		
LSD	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.68	0.68	0.31
(p = 0.05)			1.00			0.85			1.00			0.54
Descriptor	**Days to maturity**											
Average	12.7	123.7	123.7	137.0	136.2	137.0	125.3	125.5	125.3	137.6	136.6	137.5
Minimum	123.0	123.0	123.0	134.0	134.0	134.0	123.0	123.0	123.0	134.0	134.0	134.0
Maximum	126.0	126.0	126.0	141.0	138.0	141.0	127.0	127.0	127.0	141.0	138.0	141.0
F-ANOVA (p = 0.05)	*F (2,9) = 0.000, p = 1.000*			*F (2,9) = 0.111, p = 0.896*			*F (2,15) = 0.000, p = 1.000*			*F (2,15) = 0.287, p = 0.755*		
LSD	1.00	1.00	1.00	0.69	0.69	1.00	1.00	1.00	1.00	0.49	0.49	0.90
p(0.05)			1.00			0.69			1.00			0.56

Variants: V_1 - *Avena* spp.-*Avena* spp.; V_2 - *Avena-Vicia faba*; V_3 - *Avena* spp.- *Hordeum vulgare*

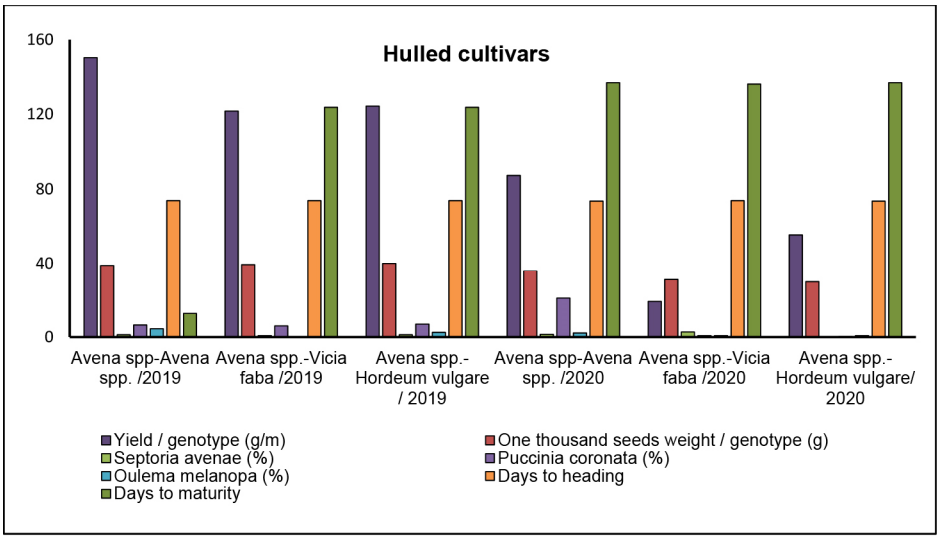

Figure 3 - Influence of the intercropping system on the variability of productivity traits, disease and pest in the hulled oat cultivars.

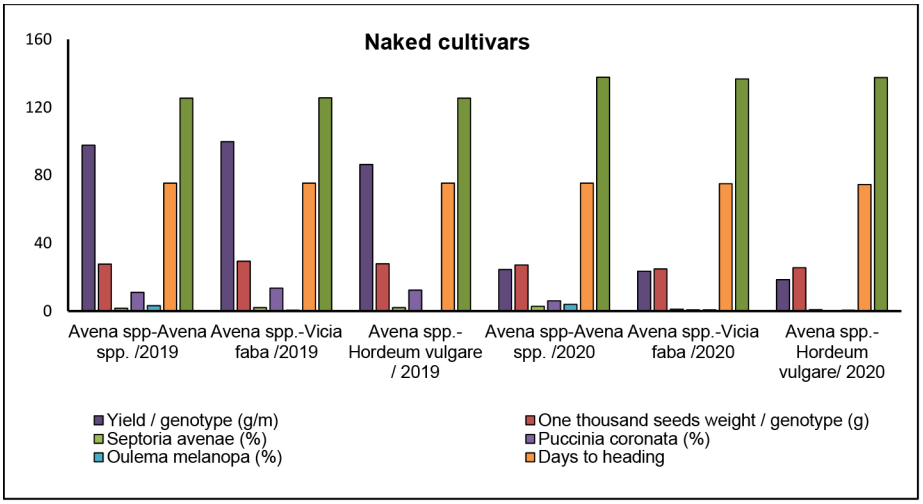

Figure 4 - Influence of the intercropping system on the variability of productivity traits, disease and pest in the naked oat cultivars.

Similar studies have analysed the increased nutritional potential of the soil (Rodriguez *et al.,* 2020).

Avena spp. genotypes tested were analysed hierarchically by the Ward variance method. Based on the studied criteria, genotypes grouped in five clusters with 20 to 114 members (*Table 7*). These values were in line with the results of another researcher in domain such as Demirkol *et al*. (2019).

Table 6 - The behaviour of *Avena* ssp. related to weed presence and yield/genotype in intercropping system

Experimental years	Intercropping 2019			Intercropping 2020		
Variables	*Avena* spp. *Avena* spp.	*Avena* spp. *Vicia faba*	*Avena* spp. *Hordeum* spp.	*Avena* spp. *Avena* spp.	*Avena* spp. *Vicia faba*	*Avena* spp. *Hordeum*
Number of weed species	14	16	14	10	13	11
Average yield (g)/ hulled local population	89.08	91.73	87.09	36.63	49.11	37.20
Average yield (g)/ naked local population	62.47	69.21	68.70	14.3	20.5	18.5
Average yield (g)/ hulled cultivars	150.40	121.80	124.47	87.21	19.23	55.39
Average yield (g)/ naked cultivars	97.64	96.71	86.25	24.40	23.47	18.44

Table 7 - Cluster membership on *Avena* spp. accessions tested in three variants of intercropping system

No. of cluster	No. of members	No. of genotypes	Local populations		Advanced cultivars	
			Hulled	Naked	Hulled	Naked
Cluster I	48	26	15	4	4	3
Cluster II	47	25	16	4	2	3
Cluster III	47	25	12	5	6	2
Cluster IV	114	41	21	11	3	6
Cluster V	20	10	4	5	1	0

The amplitude of variation (min-max) and the average values of the 5 clusters showed that in cluster 4, these estimators indicated a high heterogeneity of the morpho-physiological characters, the genotypes tested being classified based on the Euclidean distance into a large group of members (114) with high phenotypic variability compared to the other clusters (*Table 8*).

The Ward Linkage dendrogram (*Fig. 5*) showed the maximum Euclidian distance in cluster IV. Out of the 41 genotypes included in this cluster are highlighted in the three intercropping variants from two consecutive years (2019 and 2020) the following: two hulled local populations/*Avena abyssinica*-SVGB-18444, SVGB-17197, 1 hulled local populations/ *Avena sativa* ssp. *sativa* -SVGB-7260, 1 naked local population/ *Avena sativa* ssp. *nudisativa* var. *inermis* -SVGB-184147. As a result, these accessions have a great variety in productivity characteristics, disease and pest attack severity, and days to maturity. They can also be utilized to create hybrid types and drought-resistant crops in dry places.

Table 8 - Various traits range values in clusters

Cluster I		Cluster II		Cluster III		Cluster IV		Cluster V	
Min Max	Average	Min Max	Average	Min Max	Average	Min Max	Average	Min Max	Average
Yield/genotype (g/m)									
108.75 221.90	145.17	35.00 71.19	53.89	73.40 116.70	90.54	1.25 44.80	19.48	16.50 104.80	64.20
One-thousand-seeds weight/genotype (g)									
24.50 45.90	33.25	13.20 37.00	25.61	23.10 39.20	29.89	11.70 37.30	24.49	19.20 39.81	29.22
***Septoria avenae* (%)/ plants**									
0.00 15.00	1.60	0.00 10.00	1.83	0.00 15.00	1.04	0.00 10.00	1.13	0.00 0.00	0.00
***Puccinia coronata* (%)/ plants**									
0.00 50.00	12.88	0.00 25.00	4.43	0.00 25.00	7.00	0.00 30.00	2.46	40.00 80.00	51.25
***Oulema melanopa* (%)/ plants**									
0.00 10.00	2.15	0.00 10.00	1.66	0.00 10.00	1.19	0.00 10.00	1.25	0.00 10.00	1.20
Days to heading									
73.00 80.00	75.63	72.00 81.00	76.79	71.00 80.00	75.72	71.00 82.00	75.67	71.00 77.00	74.65
Days to maturity									
123.00 141.00	126.77	123.0 141.0	131.94	121.00 138.00	127.53	121.00 141.00	136.03	121.00 134.00	125.15

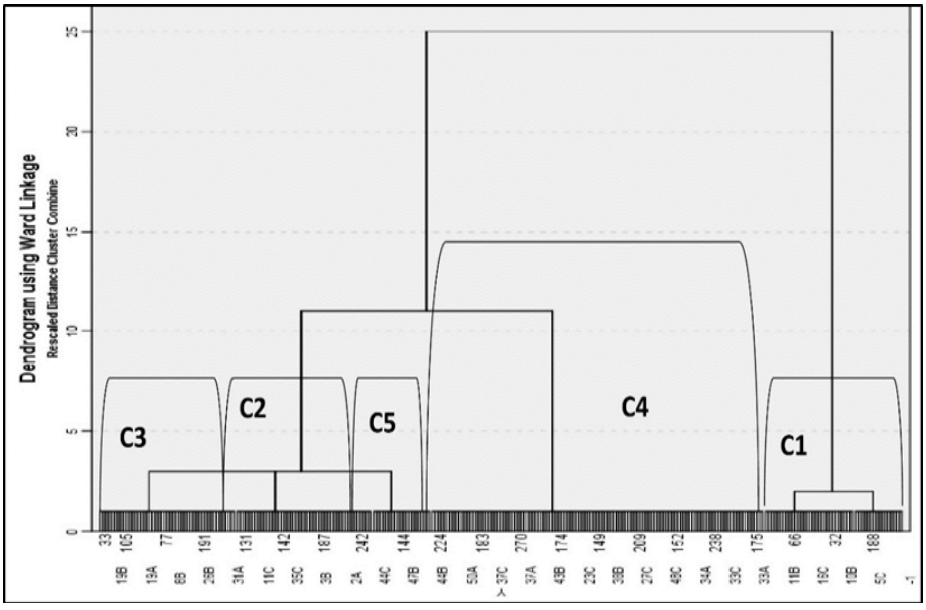

Figure 5 - Dendrogram Ward is based on Euclidean distance and includes data from three intercropping experiment types as well as seven agromorphological variables.

Local hulled populations (SVGB-18444, SVGB-17197) of the *Avena abyssinica* species with diversity centres in Ethiopia can be used in breeding programmes as gene sources for early varieties (Trofimovskaya *et al.,* 1976, Frey KJ, 1991), to improve productivity, (Kanan *et al.,* 1996), resistance to some diseases (Sebesta *et. al.,* 2000). In this respect, in the intercropping experiment with three variants was highlighted by the following characteristics: yield/genotype (20.98-54.7 g in 2020; 10.47-28.3 g in 2019) and one-thousand-seeds weight/ genotype (17.60-35.70g in 2020; 20.60-27.77g in 2019); vegetation period of 121-123 days at maturity in 2020, 136 days at maturity in 2019; resistance to *Septoria avenae* (degree of attack = 0% in 2020, 3 % in 2019).

Naked local population (SVGB-18417) of the *Avena sativa* ssp. *nudisativa* var. *inermis* species with its diversity centre in China/Mongolia can be used in breeding programmes as gene sources for creation of varieties with naked grain adapted to the climatic conditions in our country (Murariu *et al.,* 2017). In the intercropping system with two years of testing, this access was characterised by: yield/genotype (10.75 /2019; 12.95/2020); thousand-seeds weight/ genotype (12.5 /2019; 20.7/2020), *Septoria avenae* (degree of attack = 0% in 2020, 3 % in 2019); *Puccinia coronata* (degree of attack = 1 % in 2020, 0 % in 2019); *Oulema melanopa* (degree of attack 3 % in 2020, 0 % in 2019); days to maturity (126/2020; 141/2019).

The local hulled population (SVGB-7260) of the *Avena sativa* ssp. *sativa* species from Hodosa, Harghita County, Romania tested in three experimental variants was highlighted by: yield /genotype (9.36 in 2019; 33.25 in 2020); one-thousand-seeds weight/ genotype (22.83 in 2019; 31.07 in 2020); *Septoria avenae* (degree of attack 3 % in 2020, 0 % in 2019); *Puccinia coronata* (degree of attack = 1% in 2019/ 2020); *Oulema melanopa* (degree of attack = 3 %/ 2020/ 2019); days to maturity (124 in 2020; 141 in 2019).

CONCLUSIONS

The varietal mixture of oat germplasm tested in two consecutive years of intercropping with barley and fava bean showed significant phenotypic variability for a series of descriptors like one-thousand-seeds weight, crown rust, oat leaf beetle and days to maturity.

The water intake was different from the emergence and flowering-heading phenophases. The two years (2020 - dry year, 2019 - normal year) of testing determined a hierarchy of heterogeneity, especially for the hulled oat local populations to some analysed traits (one thousand seeds weight, crown rust, days to maturity) and of naked cultivars for oat leaf beetle.

The germplasm of *Avena* spp. showed high weed competition in variants with cereals (oat, barley) and could be useful for symbiotic nitrogen fixation by increasing oat productivity in the fava bean and oat variant for the naked and hulled local population, making it recommended for cultivation in conjunction with grain legumes in any agricultural exploitation.

The identified genotypes in this cluster (2 hulled local populations/*Avena*

abyssinica- SVGB-18444, SVGB-17197, 1 hulled local populations/ *Avena sativa* ssp. *sativa* -SVGB-7260, 1 naked local population/ *Avena sativa* ssp. *nudisativa* var. *inermis* -SVGB-18417) could be utilized to produce genetic combinations for the intercropping system, contributing to the long-term viability of low-input crop production in small-scale agricultural systems and environmental protection in dry areas, in breeding programmes as gene sources for early varieties.

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