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Genetic Variability, Heritability and Genetic Advance Studies for Green Forage Yield and Associated Traits in Forage Oat (*Avena sativa* L.)

D. C. Vanjare[1*], G. C. Shinde[2], S. D. Shinde[3] and V .S. Pawar[2]

[1]JRA, AICRP on Forage Crops and Utilization, [2]Department of Agricultural Botany (GPB), [3]SRA, [3]Dept. of Agriculture, Statistics, Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri, India

**Corresponding author*

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Present investigation in which forty four genotypes of forage oat were evaluated at the research field of AICRP on Forage Crops and Utilization, Mahatma Phule Krishi Vidyapeeth, Rahuri during *Rabi* 2018-19 in a RBD designs with three replications. The observations were recorded on yield and yield contributing traits *viz.,* days to 50 % flowering, plant height (cm), number of leaves /tiller, number of internodes / tiller, leaf length (cm), leaf breadth (cm), stem girth (cm), L/S ratio, dry matter content , crude protein content and green forage yield (kg/net plot). The analysis of variance revealed the significant difference among the genotypes for all the eleven characters. A wide range of variability was observed for plant height, days to 50 % flowering, leaf length, Leaf width and dry matter. The traits leaf: stem ratio, leaf width, green forage yield, stem girth, plant height, leaf length, number of leaves/tiller and number of internodes/tiller showed high heritability estimates accompanied with high genetic advance percent of mean which is due to additive gene action and direct selection for such traits is rewarding in crop improvement.

Introduction

Oats (*Avena sativa* L.) 2n = 6x = 42, is a western Mediterranean cereal crop with a moderately agricultural history, since its cultivation had started. Oat is regarded as most important cereal crop throughout the world and used as an important source of essential nutrients for human consumption (Boczkoswka and Tarczyk, 2013). Increased oat consumption is often enhanced due to nutritional attributes including antioxidants and high soluble fiber (Rasane *et al.,* 2015). The actual health benefits of oat are attributed to its high dietary fiber content (33 per cent) as compared to other cereal grains

Oat produces an abundance of excellent fodder at the time when other succulent better quality fodders are scarce and cannot be cut/grazed as a green feed, hay or silage crop. It forms an excellent combination when fed along with other cold season legumes, like berseem, Lucerne, senji, shaftal, pea and vetch. The cereal straws have similar chemical composition but oat straw is more acceptable to livestock as compared to other cereal crops. The nutritional value of oat is mainly attributed to its composition of protein, lipid and fibre (Ranhotra *et al.*, 1995).

Germplasm selected from different regions considered as the best natural resources in providing the required variation in traits to develop new oat cultivars.

Materials and Methods

The study was conducted at AICRP on Forage Crops and Utilization, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar, Maharashtra during *rabi* 2018-19. The experimental material consisted of forty four oat genotypes. Genotypes were provided by the different AICRP centers on Forage Crops and Utilization in India. The list of forty four genotypes is given in Table 1.

The experiment was laid out in randomized block design (RBD) with two replications having thirty eight genotypes with six checks. The observations were recorded on five randomly selected plants in each replication for all the characters except leaf stem ratio and green forage yield (Kg/net plot).

The data collected on individual characters were subjected to the method of analysis of variance commonly applicable to the randomized block design (Panse and Sukhatme, 1985). The phenotypic and genotypic variances were calculated using the respective mean squares from variance table (Johnson *et al.,* 1955).

The genotypic and phenotypic coefficients of variation were calculated as per Burton, (1952). Heritability in broad sense was estimated as suggested by Hanson *et al.*, (1956). The high, medium and low heritability estimates were classified on the basis of values given by Johnson *et al.*, (1955). Genetic advance (at 5 % selection intensity) was calculated using the formula given by Allard (1960)

Results and Discussion

Genetic improvement of forage yield alone is not possible through phenotypic selection because of polygenic nature and low heritability. In breeding program, the selection of parents for hybridization is largely based upon high yielding potential and genetic diversity.

The analysis of variance revealed significant genotypic differences for all eleven characters studied (Table 2). A wide range of variability was observed for plant height, days to 50 % flowering, leaf length, Leaf width and dry matter indicating sufficient amount of genetic variation among the genotypes under study presented in table 3.

High values of GCV and PCV were recorded for the traits namely, leaf/stem ratio, leaf width, stems girth and green forage yield. High estimates of heritability (b.s.) were observed for all characters studied. The highest magnitude of genetic advance per cent mean was observed for leaf: stem ratio (58.42) followed by leaf width (49.01), green forage yield (43.48), stem girth (40.78), plant height (34.18) and leaf length (28.38), number of leaves/tiller (21.89) and number of internodes/tiller (20.14).

On contrary, higher GCV and PCV values reported by Chandan *et al.*, (2013) for leaf length and days to 50 % flowering; Chauhan and Singh (2019) and Kumar *et al.*, (2004) for number of leaves and Shankar *et al.*, (2002), Kumar *et al.*, (2004), Krishna *et al.*, (2013), Bind *et al.*, (2016) for dry matter yield.

Table.1 List of forty four forage oat genotypes

S.N.	Genotype	Origin	S.N.	Genotype	Origin
1	OL-1861-1	Ludhiana	**23**	HFO-225	Hisar
2	OL-1802	Ludhiana	**24**	HFO-417	Hisar
3	OL-1842	Ludhiana	**25**	OL-1866	Ludhiana
4	HFO-619	Hisar	**26**	UPO-16-4	Pantnagar
5	NDO-1102	Faizabad	**27**	HFO-514	Hisar
6	OS-377	Hisar	**28**	OL-1873	Ludhiana
7	JO-10-501	Jabalpur	**29**	OL-1804-1	Ludhiana
8	OL-1769	Ludhiana	**30**	SKO-229	Srinagar
9	OL-1876	Ludhiana	**31**	JO-04-19	Jabalpur
10	JO-05-7	Jabalpur	**32**	HFO-607	Hisar
11	OL-1869	Ludhiana	**33**	JO-4-321	Jabalpur
12	OL-1871	Ludhiana	**34**	OL-1862	Ludhiana
13	OL-1766-1	Ludhiana	**35**	OL-1769-1	Ludhiana
14	OL-1861-1	Ludhiana	**36**	OS-424	Hisar
15	HFO-611	Hisar	**37**	RSO-8	Rahuri
16	JO-05-301	Jabalpur	**38**	RSO-60	Rahuri
17	HFO-609	Hisar	**39**	JHO-822 (Ch)	Jhansi
18	SKO-225	Srinagar	**40**	OS-6(Ch)	Hisar
19	OS-432	Hisar	**41**	UPO-212 (Ch)	Pantnagar
20	HFO-610	Hisar	**42**	Kent (Ch)	Hisar
21	UPO-10-3	Pantnagar	**43**	RO-19 (Ch)	Rahuri
22	PLP-18	Palampur	**44**	RO-11-1 (Ch)	Rahuri

Table.2 Analysis of variance for eleven characters of forty four oat genotypes

Sr.No.	Character	Replication	Genotypes	Error
	DF	**2**	**43**	**86**
1	Days to 50 % flowering	10.098**	143.511**	1.741
2	Plant height (cm)	23.058**	644.569**	3.149
3	Number of of leaves/tiller	1.475**	1.615**	0.184
4	Number of internodes/tiller	5.638**	1.274**	0.195
5	Leaf length (cm)	1.935	85.708**	3.920
6	Leaf width (cm)	0.0396	0.329**	0.020
7	Stem girth (cm)	0.0423	0.614**	0.018
8	Leaf: stem ratio	0.0254*	0.151**	0.007
9	Dry matter content (%)	9.412**	9.486**	1.108
10	Crude protein content (%)	0.066	2.098**	0.091
11	Green forage yield (kg/net plot)	0.144**	0.913**	0.0276

*, ** = significant at 5% and 1 % levels, respectively

Table.3 Estimates of variability parameters for green forage yield and its contributing characters in 44 forage oat genotypes

Sr. No.	Character	Mean	Range	Genotypic variance	Phenotypic variance	GCV	PCV	Heritability (bs) h²	Genetic Advance	Genetic Advance % of Mean
1	Days to 50 % flowering	77.01	64.67-93.33	47.26	49.00	8.93	9.09	96.40	13.91	18.06
2	Plant height (cm)	87.49	50.07-108.67	213.81	216.96	16.71	16.84	98.50	29.90	34.18
3	No. of leaves/tiller	5.52	4.27-6.60	0.48	0.66	12.51	14.72	72.20	1.21	21.89
4	No. of internodes/tiller	4.94	3.80-5.87	0.36	0.55	12.14	15.08	64.90	1.00	20.14
5	Leaf length (cm)	35.44	24.41-52.05	27.26	31.18	14.73	15.76	87.40	10.06	28.38
6	Leaf width (cm)	1.24	0.61-2.03	0.10	0.12	25.96	28.32	84.00	0.61	49.01
7	Stem girth (cm)	2.15	1.22-2.79	0.20	0.22	20.70	21.64	91.50	0.88	40.78
8	Leaf: stem ratio	0.71	0.35-1.63	0.05	0.06	30.57	32.96	86.00	0.42	58.42
9	Dry matter (%)	18.95	14.10-22.19	2.79	3.90	8.82	10.42	71.60	2.91	15.38
10	Crude Protein (%)	9.94	8.31-12.18	0.67	0.76	8.23	8.77	88.00	1.58	15.90
11	Green forage yield (kg/net plot)	2.46	1.13-3.34	0.30	0.32	22.07	23.08	91.50	1.07	43.48

The traits leaf: stem ratio, leaf width, green forage yield, stem girth, plant height, leaf length, number of leaves/tiller and number of internodes/tiller showed high heritability estimates accompanied with high genetic advance percent of mean whereas, days to 50 % flowering, crude protein content and dry matter content had high heritability estimates accompanied with moderate genetic advance percent of mean which is due to additive gene action and direct selection for such traits is rewarding in crop improvement. Similar results of high estimates of heritability coupled with high genetic advance percent of mean were in accordance with Pundir *et al.*, (2001) for number of leaves, leaf length, leaf width, green forage yield; Kapoor, *et al.*, (2011) for plant height and leaf length, Jaipal and Shekhawat (2016) for leaf stem ratio, leaf length, green forage yield; Wagh *et al.*, (2018) for leaf length, leaf width, plant height, number of leaves leaf stem ratio, stem girth and green forage yield and Chauhan and Singh (2019) for number of leaves, plant height, stem girth and green forage yield.

In conclusion the mean sum of squares due to genotype was highly significant for all the characters studied. The characters *viz.*, leaf/stem ratio, leaf width, stem girth, and green forage yield showed high estimates of GCV and PCV indicating ample variability for these characters.

The traits leaf: stem ratio, leaf width, green forage yield, stem girth, plant height, leaf length, number of leaves/tiller and number of internodes/tiller showed high heritability estimates accompanied with high genetic advance percent of mean which is due to additive gene action and direct selection for such traits is rewarding in crop improvement.

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