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Research Note

Estimates of genetic variability, heritability and genetic advance of oat (*Avena sativa* L.) genotypes for green fodder yield

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Abstract

Genetic variability was estimated among 34 genotypes of M_6 generation were derived from oat genotypes Kent and JO-1 during *rabi* 2010 at All India Co-ordinated Research Project on Forage crops, Seed Breeding Farm, JNKVV, Jabalpur (M.P). The materials for the present study comprises of genotypes which were selected on the basis of performance for fodder yield and yield contributing characters in M_5 generation. In JO-1 population, the genotype JMO-187 and in Kent population the genotype JMO-429 recorded maximum total green fodder yield. High phenotypic and genotypic coefficient of variation was recorded for crude protein yield followed by leaf area, total dry matter yield and total green fodder yield which indicated the presence of ample amount of variation for these characters. High values of heritability coupled with high expected genetic advance were observed for the characters *viz.*, leaf area and axis length suggesting the scope for selection.

Key words:
Oat, GCV, PCV, Heritability, Variability

Oat (*Avena sativa* L.) is an important forage annual crop of *rabi* season belongs to family Poaceae and ranks sixth in production among all cereal crops next to wheat, maize, rice, barley and sorghum in the world scene. The genus *Avena* is large and diverse containing both wild and cultivated polyploidy series with a basic chromosome number of n=7. Three naturally occurring ploidy levels are known with the genus, diploids (2n=2x=14), tetraploid (2x=4x=28) and hexaploid (2n=6x=42). Oat (2n=6x=42) is a natural allopolyploid evolved through cycles of interspecific hybridization and polyploidization combining three distinct genomes. Availability of the genetic variability for the component characters was a major asset for initiating a fruitful crop improvement program. Oat is a multipurpose cereal crop grown worldwide for human food and animal feed. The nutritive value of oat forage is high and dry matter digestibility is in excess of 75 per cent when fed to dairy cattle (Burgess *et al.* 1972). The cereal straws have almost similar chemical composition but oat straws have more digestible organic matter and metabolizable energy (Cuddeford, 1995). In India, it is used as green fodder, hay and silage for animals. It has excellent growth habit, quick recovery after cutting and provides good quality herbage. Oat is considered to be a nutritious source of protein, carbohydrate, fibre, vitamins, and minerals as well as of compounds with beneficial effects on health.

Yield is a complex character which mainly depends upon several component characters, so that selection of genotypes based on yield component is not effective but based on component character is more effective. Thus, variability in genotypes for yield and yield contributing characters forms the basic factor to be considered while making selection of parents since estimate of genetic parameters are useful to breeder for designing an effective breeding programme. Hence, present investigation was undertaken to know the GCV, PCV, heritability and genetic advance for various yield contributing characters in oat genotypes.

The present investigation was conducted at All India Co-ordinated Research Project on Forage Crops, Seed Breeding Farm, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P) during the *rabi* 2010-2011.Thirty four varieties of oat were treated with different doses (150, 200, 300 and 400 Gy) of gamma rays at Gamma chamber JNKVV, Jabalpur (M.P) and response to the different doses of gamma rays in M_1 and onward generations were recorded. Thirty two mutant progenies generated by treating different varieties with different doses were selected from M_5 generation and was forwarded to M_6 generation along with two check varieties for the present study. The total treatments are mentioned below:

Treatments	Variety	Mutagenic Treatment (Gy)	Treatments	Variety	Mutagenic Treatment (Gy)
T_1	JO-1	Control	T_{18}	JMO -448	200
T_2	JMO -220	300	T_{19}	JMO -189	300
T_3	JMO	300	T_{20}	JMO	300

	-222			-193	
T_4	JMO -14	300	T_{21}	JMO -194	300
T_5	JMO -41	300	T_{22}	JMO -197	300
T_6	JMO -42	300	T_{23}	JMO -199	300
T_7	JMO -54	200	T_{24}	Kent	Control
T_8	JMO -56	200	T_{25}	JMO -425	300
T_9	JMO -71	200	T_{26}	JMO -424	300
T_{10}	JMO -75	200	T_{27}	JMO -421	300
T_{11}	JMO -79	200	T_{28}	JMO -419	300
T_{12}	JMO -131	200	T_{29}	JMO -415	300
T_{13}	JMO -139	200	T_{30}	JMO -413	300
T_{14}	JMO -149	400	T_{31}	JMO -407	300
T_{15}	JMO -159	300	T_{32}	JMO -404	300
T_{16}	JMO -158	300	T_{33}	JMO -401	300
T_{17}	JMO -187	300	T_{34}	JMO -429	300

Thirty two mutant varieties along with two checks (JO-1 and Kent) were sown in Randomized Complete Block Design with three replications during *rabi* 2010. Each plot was maintained with the size of 3 x 10 m^2 and having three rows for each treatment in each replication. The distance between rows and plants was maintained as 30 cm and 5 cm respectively. The following observations were recorded on five tagged plants in M_6 generation. Leaves plant^{-1}, tillers plant^{-1}, leaf area (cm^2), leaf stem ratio, axis length (cm), total dry matter yield (kg), dry matter yield day^{-1} (kg), crude protein yield (kg), crude protein yield day^{-1} (kg) and total green fodder yield (kg). The statistical analysis was done by the method given by Panse and Sukhatme (1954).

The analysis of variance revealed highly significant differences for all characters suggesting the presence of high genetic variability among the genotype assessed (Table 1). These results are in conformity with the findings of Bibi *et al.* (2012) who reported that all genotypes differ significantly with respect to leaves plant^{-1}, tillers plant^{-1}, leaf area, leaf stem ratio, axis length, total dry matter yield, dry matter yield day^{-1}, crude protein yield, crude protein yield day^{-1} and total green fodder yield.

Phenotypic coefficient of variation (PCV) was higher in magnitude than that of genotypic coefficient of variation (GCV) for crude protein yield (25.45 and 20.25) followed by leaf area (24.46 and 21.10), total dry matter yield (23.44 and 19.41) and total green fodder yield (21.24 and 15.38) indicating the substantial modifying effect of environment in the expression of these traits (Table 3). Similar to these results, Krishna *et al.* (2013) also observed that estimates of GCV was smaller than that of PCV suggesting influence of environment on them. Bibi *et al.* (2012) recorded that PCV was slightly greater than GCV for number of leaves plant^{-1}, leaf area and number of tillers plant^{-1} indicating influence of environment on them.

Heritability is the index of transmissibility of characters from parents. It need to be studied in order to determine extent to which the observed variation is inherited. High heritability estimates were observed for leaf area (85.90), axis length (82.30), crude protein yield (79.50) and leaves plant^{-1} (73.80) which indicated that there is scope for improvement through individual plant selection.

Leaf area and crude protein yield showed high estimates of heritability with high genetic advance. These results are in conformity with the findings of Sangwan *et al.* (2012) who observed that high heritability with high genetic advance for tillers plant^{-1} and green fodder yield. Singh and Singh (2010) also recorded that, the heritability and genetic advance were high for characters like tillers plant^{-1}, green fodder yield and dry matter yield. These results indicated the scope for selection in these characters.

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Table 1. Analysis of variance for fodder yield and its components in oat

Source of Variation	d.f	Leaves plant^{-1}	Tillers plant^{-1}	Leaf area (cm^2)	Leaf stem ratio	Axis length (cm)	Total dry matter yield (kg)	Dry matter yield day^{-1} (kg)	Crude protein yield (kg)	Crude protein yield day^{-1} (kg)	Total green fodder yield (kg)
Replication	2	0.34	10.52	10.59	0.0001	0.55	1100.38	0.012	0.0008	0.00001	170.58
Genotype	33	80.44**	8.94**	25930.05**	00.006**	77.99**	50.16**	00.012**	00.033**	00.00003**	680.51**
Error	66	0.14	0.24	0.676	0.0007	0.70	0.68	0.012	0.0001	0.00003	0.48

*,** Significant at 5% and 1% level respectively

Table 2. Genetic parameters of variation for fodder yield and its components in oat

Character	Range		Mean	Coefficient of variation (%)		Heritability broad sense (%)	Genetic Advance as % of mean
	Min.	Max.		GCV	PCV		
Leaves plant^{-1}	5.73	12.46	9.09	7.22	9.78	73.80	40.16
Tillers plant^{-1}	6.00	13.06	9.53	10.25	15.64	65.50	18.45
Leaf area (cm^2)	95.88	217.24	156.56	21.10	24.56	85.90	42.46
Leaf stem ratio	0.66	0.84	0.75	6.05	7.05	73.80	10.72
Axis length (cm)	30.50	52.55	41.52	13.47	16.36	82.30	27.39
Total dry matter yield (kg)	3.25	8.27	5.76	19.41	23.44	68.50	33.10
Dry matter yield day^{-1} (kg)	0.033	0.291	0.162	15.06	20.45	73.60	34.05
Crude protein yield (kg)	0.25	0.65	0.45	20.25	25.45	79.50	39.29
Crude protein yield day^{-1} (kg)	0.002	0.018	0.01	14.73	19.95	73.80	13.90
Total green fodder yield (kg)	21.45	43.66	32.55	15.38	21.24	72.40	31.35