

Genetic analysis for fodder yield and other important traits in oats (*Avena sativa* L.)

Mushtaq Ahmad*, Gul Zaffar, S. D. Mir, S. M. Razvi, Z. A. Dar and Shahida Iqbal

Division of Genetics and Plant Breeding, Sher-e-Kashmir University of Agricultural Sciences and Technology Shalimar Campus, Srinagar 191 121, J & K

(Received: April 2013; Revised: November 2013; Accepted: December 2013)

Abstract

The parents and 45 F₁ crosses (excluding reciprocals) of forage oats (*Avena sativa* L.) were analyzed genetically to generate information on combining ability (general and specific), nature and magnitude of gene effects for forage yield and their attributing traits. The estimates of dominance variance were higher in magnitude than their corresponding additive genetic variance indicating preponderance of non-additive gene action except for days to 50% flowering. None of the parents was found to be a good general combiner simultaneously for all traits. However, SKO-208 was identified as a good general combiner for most of the traits. The most promising crosses that revealed highly positive and significant SCA effect for forage yield were SKO212, SKO213, SKO204 x SKO208, SKO204 x SKO211, SKO210 x SKO211 and SKO207 x SKO 210.

Key words: Forage oats, combining ability, GCA, SCA.

In many parts of the world oats (*Avena sativa* L.) is grown for use as grain as well as for forage and fodder, straw for bedding, hay, haylage, silage and chaff. Oats occupies a prominent place among *rabi* fodders in India. It provides a high tonnage of nutritious green fodders. It has a wider adaptability, particularly in western and north western regions of the country because of its excellent growing habitat's, quick re-growth and better nutritional value. As per national estimate, by 2015 and 2025 A.D., sixty crores animals will need 1097 and 1170 million tonnes of green fodder, respectively. Deficiency of green fodder will be about 64.9% and for dry fodders it may go to up to 24.9% in 2025 A.D. [1].

In J & K state livestock population is about 7.8 million but fodder production is not sufficient to meet the requirements of a burgeoning live stock population. Cultivation of high yielding fodder oat cultivar Sabzaar developed for temperate climatic conditions of Kashmir valley has helped in enhancing forage productivity but in order to further increase the productivity *per* unit area there is need to develop varieties having higher forage yield potential and quality. Understanding the gene action and combining ability may help in choosing suitable breeding procedure for improvement of forage oat [2-5]. Therefore, there is an urgent need of exploiting new research technologies to boost forage yield in terms of higher yield of green fodder and dry matter per unit area. The present investigation was carried out to estimate general and specific combining ability effects of parents and their crosses, and to study the nature and magnitude of gene action for forage yield and their attributing traits.

The basic material for the present study consisted 10 diverse genotypes of oats (*Avena sativa* L.) viz., SKO-204, SKO-205, SABZAAR, SKO-207, SKO-208, SKO-209, SKO-210, SKO-211, SKO-212, and SKO-213 selected from the germplasm collection maintained at Division of Plant Breeding and Genetics, SKUAST-K, Shalimar. Forty five F₁ crosses (excluding reciprocals) were generated through a 10 x 10 diallel mating design in *rabi* 2009-10 at SKUAST-K, Shalimar and were evaluated alongwith 10 parents. The experiment was laid out in a completely randomized

*Corresponding author's e-mails: sahilmuhtaqqdar@rediffmail.com

block design with three replications at three random locations, namely, experimental farm (E_1), Shalimar, Mountain Research Centre for Field Crops, Khudwani Anantnag (E_2) and FOA (E_3), Wadura, during *rabi* 2010-11 and each treatment was sown in 2 rows each of 4 meter length. Row to row and plant to plant spacing was maintained at 30 and 10 cm. The observations were recorded on 8 quantitative characters. Data were subjected to analysis of variance to find significant differences among genotypes for the recorded data. After obtaining the significant differences, data were further analyzed for gca and sca using model-1 and method-II [3].

Analysis of variance for general and specific combining ability and their interaction with the environment for the revealed that traits mean squares due to environments were significant for all the traits, which revealed that environments taken under study were diverse. The significance of the variances resulting from gca x environments and sca x environments pointed out that gca and sca effects also exhibited interaction with environments for all the traits. The estimates of variance due to dominance deviation (σ^2D) were much higher than the corresponding additive genetic variance σ^2A for all the traits, indicating preponderance of non additive gene action as compared to additive gene action in individual environments and in pooled analysis indicating that breeding methods like bi-parental mating or inter-mating

or recurrent selection are suggested, after which selection could be practiced to identify better performing progenies for these characters except days to 50% flowering for which simple selection would bring about desired improvement. Aaverage degree of dominance $(\sigma^2D/\sigma^2)^{0.5}$ revealed preponderance of over dominance for most of the traits except days to 50 per cent flowering in individual environments and in pooled analysis, indicating that the present set of materials was diverse and contained contrasting alleles in most of the cases in the dispersion phase, which on combination through hybridization increased heterozygosity in the individual environments as well as for the data pooled over environments except days to 50% flowering which exhibited dominance. The present findings are in agreement with reports published earlier [6-8].

General combining ability effects

The estimates of GCA effects of parents (Table 1), revealed that none of the parents showed significant GCA effects in the desired direction simultaneously for all the traits studied. As none of the parents was a good general combiner for all the traits studied, SKO-204, SKO-212, SKO-205 and SKO-211 were good combiners for green fodder yield and dry matter yield. SKO-208 was be a good general combiner for most of the traits. The above mentioned parents have good potential for improving the respective characters and

Table 1. Pooled analysis for general combining ability effects for forage yield and other important traits in oats

Parents	Days to 50% flowering	No of leaves/plant	No. of tillers m^{-1}	Culm diameter (cm)	Plant height (cm)	Leaf stem ratio	Dry matter yield $plant^{-1}$ (g)	Green fodder yield $plant^{-1}$ (g)
SKO-204	-2.674**	-1.889**	-5.604**	-0.250*	4.365**	5.226**	-0.171**	0.999**
SKO-205	2.131**	-1.889**	-3.465**	0.074	-0.450**	8.530**	-0.170**	0.874**
SABZAAR	-13.359**	-1.148*	8.026**	-0.481**	5.254**	-15.589**	-0.256**	-1.321**
SKO-207	4.039**	3.389**	10.304***	0.130	-3.246**	-9.775**	-0.127**	-0.326**
SKO-208	-0.730**	1.907**	-4.094**	0.944**	-1.783**	8.147**	0.213**	-0.312**
SKO-209	-0.267*	-0.963*	-8.113**	-0.157	-1.839**	11.719**	-0.229**	-1.221**
SKO-210	4.548**	-0.962*	-1.363**	0.259*	7.263**	-9.246**	-0.175**	-0.914**
SKO-211	2.465**	0.148	5.878**	0.511**	3.420**	-7.065**	0.265**	0.841**
SKO-212	2.169**	2.093**	6.433**	-0.611**	3.161**	7.121**	0.141**	1.875**
SKO-213	1.678**	-0.685	11.6723**	0.204**	-13.144**	-4.668**	0.276**	-0.256**
S.E. (g i)	± 0.112	± 0.477	± 0.172	± 0.107	± 0.158	± 0.558	± 0.001	± 0.008
S. E. (g i – g j)	0.167	0.711	0.257	0.159	0.236	0.833	0.002	0.012
No. of parents showing desirable gca effects	4	3	5	4	5	5	4	4

*, ** Significant at 5 and 1 per cent level, respectively

Table 2. Pooled analysis for specific combining ability effects for some promising crosses of forage yield and other important traits in oats

Parents	Days to 50% flowering	No of leaves/plant	No. of tillers m ⁻¹	Culm diameter (cm)	Plant height (cm)	Leaf stem ratio	Dry matter yield plant ⁻¹ (g)	Green fodder yield plant ⁻¹ (g)
SKO-204xSKO-208	-2.016*	0.608	-7.051**	-0.487	9.443**	-3.263**	1.131**	5.656**
SKO-204xSKO-209	3.431**	2.923**	0.189	-0.811*	3.165	8.653**	0.633**	3.163**
SKO-204xSKO-211	3.282**	-1.633**	19.439**	1.765**	-6.316*	-12.949**	1.125**	5.623**
SKO-205xSKO-208	-5.996**	-2.392**	-4.524**	-0.170	-7.187*	7.366**	0.533**	2.666**
SKO-205xSKO-210	2.015*	-1.811*	-9.949**	1.848**	4.322**	-7.275**	0.352**	1.762**
SKO-205xSKO-211	-3.857**	1.700*	6.078**	-0.997*	5.387*	-5.452**	0.521**	2.765**
SABZAARxSKO-207	-8.162**	2.534*	17.588**	-2.800**	8.350**	-6.793**	0.561**	2.804**
SABZAARxSKO-210	-4.783**	-2.515*	17.115**	2.737**	-5.604*	-6.097**	0.273**	1.365**
SKO-207xSKO-208	-1.041**	-1.330	16.041**	2.552**	9.165**	-13.763**	0.470**	2.352**
SKO-207xSKO-210	-1.292	-0.867	5.949**	0.904*	6.230*	-6.414**	0.943**	4.713**
SKO-208xSKO-209	-1.709*	1.237	1.458*	2.395**	-1.869	-11.066**	0.449**	2.244**
SKO-209xSKO-212	-4.940**	-1.052	-5.292**	-0.939*	-3.480	-6.852**	0.746**	3.731**
SKO-210xSKO-211	5.726**	2.997**	6.282**	-1.589**	8.119**	-8.257**	1.000**	5.000**
SKO-210xSKO-212	-9.977**	5.497**	4.041**	-0.911*	6.600**	-5.776**	0.181**	0.907**
SKO-212xSKO-213	-3.560**	3.219**	-3.505**	-0.811*	18.119**	-2.268*	1.294**	6.469**

*, ** Significant at 5 and 1 per cent level, respectively

may be used in a multiple crossing program to synthesize a dynamic population with most of the favourable genes for amelioration of forage yield and could be utilising extensively in the forage breeding programme to accelerate the pace of genetic improvement for isolation of new desirable lines

Specific combining ability effects

Eight cross combinations possessed significant sca effects for all the traits (Table 2). The cross combinations viz., SKO212 x SKO213, SKO204 x SKO208, SKO204 x SKO211, SKO210 x SKO211, SKO207 x SKO210, SKO204 x SKO209, SKO209 x SKO212, SKO205 x SKO211, SKO205 x SKO208, SABZAAR x SKO207, SKO207 x SKO208 and SKO208 x SKO209 exhibited high and significant sca effects for green fodder yield plant⁻¹. These cross combinations need further evaluation in segregations to identify desirable transgressive segregants in the advanced generations. The magnitude of sca effects is of vital importance in selecting cross combinations with higher probability of generating transgressive segregates. Significant yield performance in specific crosses was due to the combinations on the basis of their *per se* performance and sca effects.

References

1. **Anonymous.** 2001. Govt of India, Planning Commission.
2. **Griffing B.** 1956b. Concept of general and specific combining ability in relation to dialled crossing systems. Australian J. Biol. Sci., **9**: 463-493.
3. **Iqbal M., Navabi A., Salmon D. F., Yang R. C., Murdoch B. M., Moore S. S. and Spaner D.** 2007. Genetic analysis of flowering and maturity time in high latitude spring wheat. Euphytica, **154**: 207-218.
4. **Topal A., Aydin C. and Akgiin N.** 2004. Diallel cross analysis in durum wheat (*Triticum durum* Desf.): identification of best parents for some kernel physical features. Field crop Res., **87**: 1.
5. **Sprague G. F. and Tatum L. A.** 1942. General versus specific combining ability in single crosses of corn. J Am. Soc. Agron., **34**: 923-932.
6. **Stuber C.W.** 1994. Heterosis in plant breeding. Plant Breed Rev., **12**: 227-2.
7. **Ahmad M., Zaffar G., Mir S. D., Dar Z. A. and Iqbal S.** 2013. Combining ability studies in oats (*Avena sativa* L.) for seed yield. Appl. Biol. Res., **15**:1-6.
8. **Çifci1 E. A. and Yaǎdy K.** 2010. Combining Ability of Agronomic Traits of bread wheat in F₁ and F₂ generations. J. Agril. Fac. Uludag Univ., **24**: 85-92.
9. **Singh R. K. and Shrotria P. K.** 2008. Combining ability analysis for forage yield and its components in forage sorghum. Forage Research, **34**: 79-82.