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COMBINING ABILITY STUDIES IN OATS (*Avena sativa* L.) FOR SEED YIELD

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

Division of Plant Breeding and Genetics, S.K. University of Agricultural Sciences and Technology of Kashmir, Shalimar, Srinagar - 191 121, Jammu & Kashmir (India)
*e-mail: *sahilmushtaqdar@rediffmail.com*

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ABSTRACT

Combining ability studies in oats (*Avena sativa* L.) for seed yield was carried out to generate information on general and specific combining ability and nature and magnitude of gene effects for seed yield and their attributing traits. The experimental materials comprized of 10 diverse parents and 45 F_1 crosses (excluding reciprocals) generated through diallel mating design. The experimental material was evaluated in a randomized complete block design over 3 locations. Observations were recorded on 4 quantitative characters. Significant interactions between combining ability effects and environments were observed for all the traits. The estimates of dominance variance were higher in magnitude than their corresponding additive genetic variance in individual as well as pooled analysis indicating preponderance of non-additive gene action for all traits. Estimate of average degree of dominance revealed preponderance of over-dominance for all the traits. Parents 'SKO-207' and 'SKO-208' were identified as a good general combiner for all the traits viz., spikelets panicle^{-1}, 1000-seed weight, seed length: breadth ratio and seed yield plant^{-1}. The most promising crosses showing highly positive and significant SCA effect for seed yield were SKO-211 x SKO-213, SKO-207 x SKO-208, SKO-210 x SKO-212, SKO-209 x SKO-210, SKO-210 x SKO-213, SKO-208 x SKO-213 and SKO-208 x SKO-211.

Key words: *Avena sativa*, combining ability, GCA, SCA, seed yield

INTRODUCTION

Oats (*Avena sativa* L.), an economically important crop, belongs to the family Poaceae and ranks 6th in world cereal production following wheat, maize, rice, barley and sorghum. Oat grain has always been an important form of livestock feed. However, the amount of oats used for human consumption has increased progressively owing its dietary benefits. In fact, the health effects of oat rely mainly on the total dietary fibre and β-glucan content (Kerckhoffs *et al*., 2003). Oat protein is nearly equivalent in quality to soy protein, which as per WHO is equal to meat, milk and egg protein. The protein content of hull-less oat kernel (groat) ranges from 12 to 24%, highest among cereals (Lasztity, 1999). In many parts of the world oats is grown for grain purpose as well as for forage and fodder. Russia (countries of the former Soviet Union), US, Canada, Germany and Poland account for about 75% of the world's supply of grain oats, seed and industrial grade oats. A significant proportion of oat grain and forage, produced on smaller more remote farms around the world, including the Himalayan region, are consumed on the farm and never enter the commercial markets. A case study from Nepal covering oats showed how people in Pakistan, Afghanistan and China could benefit substantially from access to better performing cultivars in alleviating their poverty and improving human and animal nutrition (Stevens *et al*., 2000). This highlights the need for a coordinated international fodder oat network targeting resource-poor environments in relatively remote communities. The earlier attempts employed for oats improvement were largely confined to the introduction and selection of desirable lines from available germplasm. Due to continued selection much of the variability has been exhausted, so the emphasis has gradually shifted to hybridization between suitable parents so as to create genetic variability and identify desirable seggregants for use in future breeding programmes. Knowledge about the genetic systems controlling the quantitative and qualitative characters is essential to choose the most effective and efficient breeding strategy (Khodadadi *et al*., 2012). To increase productivity per unit area there is need to develop varieties which have higher grain yield potential and quality. Understanding the gene action and combining ability may help in choosing suitable breeding procedure for improving the seed yield. So, there is an urgent need to explore new technologies to boost seed yield per unit area. Keeping this in view, the present study was aimed at to estimate general and specific combining ability effects of parents and their crosses, respectively, and to study the nature and magnitude of gene action for seed yield and their attributing traits so as to identify the desirable parents and crosses for use in breeding programme.

MATERIALS AND METHODS

The basic material for the present study consisted of 10 elite lines of oats viz., SKO-204, SKO-205, SABZAAR, SKO-207, SKO-208, SKO-209, SKO-210, SKO-211, SKO-212 and SKO-213 available at Division of Plant Breeding and Genetics (PBG), SKUAST-K, Shalimar. Forty five F_1 crosses (excluding reciprocals) were generated through a 10 x 10 diallel mating design during *rabi* 2009-10 at SKUAST-K, Shalimar Srinagar (J&K). The final experimental material comprizing of 10 parents and their 45 F_1's were evaluated during *rabi* season 2010-11 at three locations namely Experimental Farm of the Division of PBG, SKUAST-K, Shalimar, Mountain Research Centre for Field Crops, Khudwani Anantnag and FOA, Wadura, Sopore. The data were subjected to statistical and biometrical analysis separately for the individual environment as well as pooled over environments. The experiment was laid out in a completely randomized block design with 3 replications and each treatment was sown in 2 rows each of 1 m length. Plant spacing was maintained at 30 cm x 10 cm. The observations were recorded on four quantitative characters viz., spikelets panicle^{-1}, 1000-seed weight, seed length: breadth ratio and seed yield plant^{-1}. Data were subjected to the 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 (Griffing, 1956).

RESULTS AND DISCUSSION

The combining ability analysis carried out in individual environments and for the data pooled over environments revealed significant mean squares for general and specific combining ability for all the traits studied (Table 1). 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. Significant gca x environment and sca x environment mean squares were observed for the all traits suggesting that gca and sca were influenced by the environmental variations. Estimates of G x E interaction indicated that dominance x environment interaction (σ^2DL) variance and that of additive x environment interaction (σ^2AL) were significant for all characters. Average degree of dominance (σ^2D/ σ^2A)$^{0.5}$ revealed preponderance of over-dominance for all traits in individual environments and in the data pooled over environments indicating that the set of material used was diverse and contained contrasting alleles in most of the cases in dispersion phase, which on combination through hybridization increased heterozygosity in individual environments and in the data pooled over environments. Similar results have been reported by several workers which reveal that seed characters viz., spikelets panicle^{-1}, 1000-seed weight, seed length: breadth ratio and seed yield plant^{-1} have greater importance in non-additive gene effects (Ajmal *et al.,* 2004; Nassimi *et al.,* 2006; Kakani *et al.,* 2007; Khan *et al.,* 2007; Singh and Shrotria, 2008; Akram *et al.,* 2011).

Table 1: Analysis of variance for combining ability and estimates of components of variance for seed yield and its attributing traits in oats (*Avena sativa* L)

Source of variation	d.f.	Mean square			
		Spike lets panicle^{-1}	1000-seed weight (g)	Seed length: breadth ratio	Seed yield (g plant^{-1})
GCA	9	1911.677**	61.617**	0.732**	5.466**
SCA	45	2190.882**	14.106**	0.371**	4.236**
Environments	2	2324.651**	2198.798**	11.495*	271.0323**
GCA x Environment	18	361.443**	9.151**	13.837**	94.354**
SCA x Environment	90	369.282**	3.918**	9.205**	45.390**
Pooled	324	0.743	2.301	0.198	1.447
σ^2A	-	106.162 ± 0.272	12.516 ± 0.574	0.246 ± 0.023	0.964 ± 0.012
σ^2D	-	730.046 ± 4.411	16.934 ± 0.866	0.349 ± 0.866	2.331 ± 0.043
σ^2AL	-	30.058 ± 0.574	2.320 ± 1.210	3.304 ± 1.210	10.408 ± 1.033
σ^2DL	-	368.359 ± 2.812	3.617 ± 1.713	7.984 ± 1.713	89.942 ± 4.612

*, **indicate significance at 5 and 1% levels, respectively

General combining ability effects

None of the parents revealed significant and desirable gca effects for all the traits (Table 2), SKO-208, SKO-210, SKO-207 and SKO-213 for spike lets panicle^{-1}; SKO-207, SKO-204, SKO-205 and SKO-211 for 1000-seed weight (g); SKO-209, SABZAAR, SKO-205 and SKO-208 for seed length breath ratio; SKO-207, SKO-208 and SKO-212 for seed yield plant^{-1}. SKO-208 shows significant and desirable gca effects for three traits viz., spikelets panicle^{-1}, seed length breadth ratio and seed yield plant^{-1}. SKO-207 showed significant and desirable gca effects for three traits viz., spikelets panicle^{-1}, 1000-seed weight and for seed yield plant^{-1}. The parents with desirable GCA for maximum traits could be utilized in the seed yield improvement breeding programme. These populations could then serve as a source for isolation of new desirable lines. According to Langham (1961), genotypes with high gca possess genes capable of expressing high phenotypic effects but are prevented from doing so by the retarding effect of residual genetic background (RGB). Likewise genotypes with low gca possess low genes capable of expressing extremely low phenotypic effects but are again prevented from doing so by enhancing effect of residual genetic background (RGB).

Specific combining ability effects

The estimates of sca effects of 45 crosses for various traits revealed that none of the cross combination possessed high sca effects for all the traits studied (Table 3). The magnitude of sca effects is of vital importance in selecting cross combinations with higher probability of generating transgressive

Table 2: Pooled analysis for general combining ability effects for forage attributing traits in oats

Parents	Spike lets panicle^{-1}	1000-seed weight (g)	Seed length: breadth ratio	Seed yield (g plant^{-1})
SKO-204	-10.052**	3.493**	-0.699**	-3.048**
SKO-205	-2.728**	1.604**	0.122*	-3.354**
SABZAR	-0.691**	-4.785**	0.127**	-2.067**
SKO-207	4.115**	11.446**	-0.528**	6.674**
SKO-208	12.670**	-3.267**	0.277**	4.776**
SKO-209	-0.450**	-5.527**	0.373**	-0.104
SKO-210	6.263**	-2.841**	-0.669**	-0.687**
SKO-211	-0.969**	1.391**	0.374**	-2.270**
SKO-212	-11.756**	-4.350**	-0.566**	0.924**
SKO-213	3.596**	-10.119**	- 0.598**	-0.844**
S.E. (g i)	±0.136	±0.287	±0.041	±0.190
S. E. (gi – gj)	0.203	0.428	0.083	0.283
Parents with desirable gca effects (No.)	4	4	4	3

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

Table 3: Pooled analysis for specific combining ability effects for forage yield and its attributing traits in oats (*Avena sativa* L.)

Crosses	Spikelets panicle^{-1}	1000-seed weight (g)	Seed length: breadth ratio	Seed yield (g plant^{-1})
SKO-204 x SKO-205	5.582**	-11.411**	0.446	-4.122**
SKO-204 x SABZAR	14.767**	-5.543**	-0.766**	9.132**
SKO-204 x SKO-207	6.072**	7.321**	0.389	9.521**
SKO-204 x SKO-208	5.609**	-1.231	-2.768**	-2.334**
SKO-204 x SKO-209	-1.363**	3.345**	0.569*	5.675**
SKO-204 x SKO-210	-1.296**	-11.444**	-0.364	5.678**
SKO-204 x SKO-211	3.489**	5.231**	0.828**	7.321**
SKO-204 x SKO-212	-7.150**	-8.974**	0.240	5.231**
SKO-204 x SKO-213	25.369**	13.443**	-0.298	-4.302**
SKO-205 x SABZAR	8.887**	9.221**	-0.645*	11.721**
SKO-205 x SKO-207	6.415**	-8.204**	0.423	-3.244**
SKO-205 x SKO-208	0.396	3.213**	-4.673**	7.532**
SKO-205 x SKO-209	-0.354	-14.112**	0.644**	-5.111**
SKO-205 x SKO-210	-23.067**	7.121**	-0.578*	-2.743**
SKO-205 x SKO-211	52.276**	12.934**	0.640*	-1.332**
SKO-205 x SKO-212	-0.363	-2.999**	-0.520*	9.508**
SKO-205 x SKO-213	19.489**	-1.721	0.578*	-0.166
SABZAR x SKO-207	-4.066**	-3.122**	-0.456	3.694**
SABZAR x SKO-208	-0.418	2.167*	-3.632**	6.972**
SABZAR x SKO-209	14.832**	7.143**	0.789**	4.582**
SABZAR x SKO–210	27.785**	-2.431*	-0.765*	-2.273**
SABZAR x SKO-211	-16.428**	-7.457**	0.456	-2.370**
SABZAR x SKO-212	44.711**	7.486**	2.445**	9.332**
SABZAR x SKO-213	-2.215**	-0.679	-1.578**	-12.322*8
SKO-207 x SKO-208	21.109**	6.353**	-0.435	18.635**
SKO-207 x SKO-209	-1.863**	-1.145	0.459	-1.180
SKO-207 x SKO-210	28.980**	-2.156**	1.421**	6.342**
SKO-207 x SKO-211	14.434**	-1.512	0.321**	1.295*
SKO-207 x SKO-212	44.128**	2.180*	0.925**	-1.234
SKO-207 x SKO-213	-22.354**	8.321**	1.543**	-6.764**
SKO-208 x SKO-209	20.674**	-0.019	-2.622**	-4.543**
SKO-208 x SKO-210	8.628**	-1.745	-0.711*	-0.921
SKO-208 x SKO-211	1.082*	-3.423**	-4.465**	10.340**
SKO-208 x SKO-212	-28.002**	-0.806	0.388	-0.933
SKO-208 x SKO-213	2.739**	-0.411	-4.456**	12.834**
SKO-209 x SKO-210	30.656**	16.623**	0.721*	14.675**
SKO-209 x SKO-211	24.776**	-2.745	0.455	2.999**
SKO-209 x SKO-212	-11.641**	6.914**	-0.754*	2.274**
SKO-209 x SKO-213	-5.789**	4.967**	0.540*	-2.046**
SKO-210 x SKO-211	-7.604**	-1.974*	0.530*	-2.616**
SKO-210 x SKO-212	6.535**	6.675**	2.980**	18.672**
SKO-210 x SKO-213	18.387**	-1.231	0.789**	12.345**
SKO-211 x SKO-212	7.322**	5.911**	-0.674*	-6.847**
SKO-211 x SKO-213	-6.159**	1.549	0.412	27.980**
SKO-212 x SKO-213	48.424**	-2.933**	-0.123	0.764
S. E (sij)	±0.411	±0.966	±0.255	±0.639
S. E (sij – sik)	±0.674	±1.420	±0.082	±0.940
Crosses with desirable SCA effects (No.)	27	19	16	24

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

segregates. Significant yield performance in specific crosses was due to the combinations on the basis of their *per se* performance and sca effects. For spikelets panicle^{-1}, desirable cross combinations were

SKO-204 x SKO-208, SKO-204 x SKO-211 and SKO-205 x SKO-211, SKO-212 x SKO-213. For 1000-seed weight and seed length: breadth ratio, the desirable cross combinations were SKO-209 x SKO- 210, SKO-204 x SKO-213, SKO-205 x SKO- 211 and SKO-210 x SKO-212, SABZAR x SKO-212 and SKO-207 x SKO-213. For seed yield plant^{-1}, the desirable cross combinations were SKO-211 x SKO-213, SKO-207 x SKO-208, SKO-210 x SKO-212, SKO-209 x SKO-210, SKO-210 x SKO-213, SKO-205 x SABZAAR SKO-208 x SKO-213 and SKO-208 x SKO-211.

Conclusion: In cross combinations, SKO-211 x SKO-213, SKO-207 x SKO-208, SKO-210 x SKO-212, SKO-209 x SKO-210, SKO-210 x SKO-213, SKO-205 x SABZAAR, SKO-208 x SKO-213 and SKO-208 x SKO-211 having significant sca effects for green fodder yield plant^{-1} need further evaluation in segregating generations to identify desirable transgressive segregants. Based on the present study, it may be concluded that greater magnitude of non-additive genetic component of variance relative to additive component favours heterosis breeding, but in absence of commercial exploitation of heterosis diallel selective mating system can be utilized for the release of additive component of variance (by breaking linkage blocks) for exploitation through selection procedures**.** SKO-207 and SKO-208, identified as putative parents based on their gca (general combining ability) effects, sca (specific combining ability) effects and *per se* performance, could be utilized in seed yield improvement breeding programme. The results indicate that by using the correct breeding of parents and selection procedures, seed yield can be improved.

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