



Genetic analysis for grain and forage yield and its component traits in genus *Avena* under North western Himalayas

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Abstract

Generation mean analysis of the six populations of the two oat crosses viz., PLP-1 x *Avena sterilis* and Kent x *Avena sterilis* was chosen to study the nature and magnitude of gene effects for forage and grain yield traits. Results revealed that epistatic gene effect cannot be ignored when establishing a new breeding program to improve oat populations for various traits. The inheritance of all traits studied was controlled by additive and non-additive genetic effects, with greater values of dominance gene effect than the additive one in most cases. Biparental mating which could exploit both additive and non-additive type of gene effects was suggested for the improvement of the traits in the crosses studied.

Keywords: Epistasis, Gene action, Generation mean analysis, North western Himalayas, Oat (*Avena Sativa* L.), Scaling tests

Introduction

Oat (*Avena sativa* L.) is the sixth most important cereal crop in the world (Oliver *et al.*, 2011). Oats are grown throughout the world in the cool temperate regions, or at high altitudes in the tropics. Being an important winter forage crop, it is grown as multipurpose crop for grain, pasture, forage or as a rotation crop. Oat plantations have a comparatively low input demand of insecticides, fungicides and fertilizers due to high disease tolerance and low nourishment requirements of this crop.

In India oat is cultivated in temperate Himalayan states like Kashmir, Himachal Pradesh and Uttaranchal. It is used throughout the Himalayan region for grazing, feeding and bedding milking animals, young stock and draught animals. However, ever increasing population has led to competition between human and livestock for food. The competition for utilization of land for food grains and fodder necessities intensified efforts towards more efficient forage research and production which involves development of high yielding, fast growing, multicut with

good regeneration capacity, dual purpose, nutritious and resistant varieties of fodder crops through genetic improvement.

Breeding superior, high yielding oat varieties involves selection for multiple qualitatively and quantitatively inherited agronomic, biotic, abiotic, and quality traits that depends to a large extent on the nature of gene action involved in the control of these complex traits. Presently, most breeding approaches for oat improvement in north western Himalayas are in the domain of introduction, selection, hybridization (inter-varietal as well as interspecific) followed by pedigree, backcross, bulk and single seed descent methods. Thus, in order to isolate improved plant populations that can also then be directly utilized in molecular breeding for target gene improvement in sustainable way, the present biometrical investigation was undertaken to study the nature and magnitude of gene action for various forage and grain yield and its component traits in two cross combinations viz., PLP-1 x *Avena sterilis* and Kent x *Avena sterilis*.

Materials and Methods

Genetic material: Parental pure lines viz., PLP-1 and Kent and one local collection of wild oat (*Avena sterilis*) were selected on the basis of their diversity, resistant to powdery mildew, grain yield and fodder production. The wild ancestor of *Avena sativa* is the hexaploid wild oat (*A. sterilis*) having same genome is easily crossable with *Avena sativa* and possesses desirable traits which can be introgressed into cultivated oat through interspecific hybridization. The characteristic features of these parental lines are given in table 1.

Crosses and generations: Crosses were made between PLP-1 x *A. sterilis* and Kent x *A. sterilis* during *rabi* 2009-10 to generate F_1 seeds. The developed F_1 seeds during *rabi* 2010-11 were backcrossed simultaneously to both of the parents and also advanced for F_2 generation.

Table 1.Characteristic features of genotypes used in the present study

Genotypes	Genome	Characteristics
<i>Avena Sterilis</i>	6x=42 (Wild AACCCDD)	Earliness (136 days), high crude protein (11.81%), more 1000 grain weight (10.19 g) and forage yield.
PLP-1	6x=42 (Cultivated AACCCDD)	Good plant height (97 cm), longer growth duration (164 days), high forage yield, multi cut, good regeneration capacity and resistance to powdery mildew.
Kent	6x=42 (AACCCDD)	High forage yielding (45-50 t/ha) and high adaptability to cold climates.

The experimental material comprising of different generations viz., P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of two crosses were evaluated in compact family randomized block design with three replications during *rabi* 2011-12 at Experimental Farm of the Department of Crop Improvement, CSKHPKV, Palampur (HP) situated at 32°6' N latitude, 76°3' E longitude at an elevation of 1290.8 m (a.m.s.l). Parents were grown in double rows of 2m length while another non segregating generations F_1 's were grown in single row of 2m length. The segregating F_2 generations were grown in four rows and BC_1 and BC_2 were grown in three rows. The row to row distance was 25 cm with plant to plant distance of 5 cm apart. Recommended package of practices were followed for raising the crop. Observations were recorded on 10 randomly taken plants in case of parents and their F_1 's, 25 in case of backcrosses (BC_1 and BC_2) and 50 plants in case of F_2 generation from each replication. Data were recorded on the following quantitative traits; days to 50 per cent flowering, plant height (cm), number of leaves per plant, number of tillers per plant, leaf: stem ratio, flag leaf area (cm²), fresh fodder yield per plant (g), dry matter (%), dry matter yield per plant (g), crude protein (%), crude protein yield per plant (g), days to maturity, seed yield per plant (g), harvest index (%) and 100-seed weight (g).

Estimation of simple scaling test (Mather, 1949), joint scaling test (Cavalli, 1952) and estimation of genic effects (Jinks and Jones, 1958) were carried out as per the procedure using SPAR1 programme (Doshi and Gupta, 1991). The adequacy of the additive - dominance model was tested using the ABC scaling test (Mather, 1949), incorporating the weighted least square method (Hayman, 1960).

Results and Discussion

The nature and magnitude of genetic variation present in population is elucidated by genetic analysis of the quantitative traits. The predominance of additive gene effects signifies the development of homozygous lines while dominance gene effects are used for exploitation of hybrid vigour. The estimates of joint scaling test and

the magnitudes of components of genetic variation for the traits examined are presented in table 2. The results of scaling tests revealed that additive-dominance model was fit in cross Kent x *A. sterilis* for days to 50% flowering, plant height, tillers per plant, leaves per plant, leaf: stem ratio, green fodder yield per plant and dry matter yield per plant which suggested the absence of epistasis in this cross as was reported earlier (Dogra et al., 2003) for majority of traits in oat. In the cross combination PLP-1 x *A. sterilis* failure of additive dominance model was reported for all traits except leaves per plant and green fodder yield per plant, thereby indicating presence of non allelic interactions for remaining traits in this cross; therefore six parameter model was used for estimation of gene effects. The estimated values of dominance component, was found to be predominant over additive component, for majority of characters in both crosses indicating additive as a decisive type of gene action, hence breeding strategy in above crosses should be hybridization followed by deferring selection to later generations. For days to 50% flowering additive component in positive direction was predominant in both the crosses. These crosses can be profitably used for developing late flowering genotypes through simple selection even in early generations. In case of days to maturity significant dominance genic effects in negative direction and additive gene effects in positive direction were observed in both the crosses. The cross combination Kent x *A. sterilis* mainly positive additive gene effect was predominant for plant height. The cross can be exploited even in early generation through simple recurrent selection for tallness. In case of leaf stem ratio, preponderance of dominance gene component was observed in both cross combinations. Besides dominance gene effects additive gene effect in negative direction was also found in cross combination PLP-1 x *Avena sterilis* for control of this forage trait. Significant positive dominance effect was observed in cross combination PLP-1 x *A. sterilis* for flag leaf area which indicates that selection in later generations will be fruitful to increase biomass production.

Table 2. Estimates of scaling tests and genic effects in oat for cross PLP- 1 x *Avena sterilis*

Traits → Parameters	Days to 50 % flowering	Plant height	Leaves per plant	Tillers per plant	Leaf: stem ratio	Flag leaf area	Green fodder yield per plant	Dry matter %
A ↓	0.67±3.28	-10.33**±3.61	-10.00*±4.92	-3.67±2.06	-0.23**±0.07	-3.33±3.11	-41.67**±8.33	-2.03±3.34
B	-6.67*±2.91	16.33**±3.67	-12.67±6.80	-3.67±2.16	-0.03±0.06	12.67**±2.16	-10.00±25.17	12.37**±2.91
C	9.33±7.46	7.33±8.96	-3.33±9.68	-8.00*±3.16	-0.14±0.16	8.00±7.71	35.00±42.39	-18.67*±7.04
D	7.67*±3.13	0.67±4.63	9.67±5.04	-0.33±1.83	0.06±0.06	-0.67±4.08	43.33±23.33	-14.50**±3.60
[m]	132.33**±1.4	99.00**±2.08	46.33**±1.86	11.33**±0.67	0.55**±0.03	18.67**±1.86	180.00**±10.0	20.13**±1.58
[d]	7.00** ±1.16	-10.67**±2.03	3.00±3.42	-0.33±1.25	-0.07**±0.02	0.67±1.70	-16.67±12.02	-5.17**±1.74
[h]	-11.33±6.68	-6.33±9.41	9.00**±10.56	3.67*±3.75	0.12'±0.13	8.67*±8.23	65.83**±47.	32.73**±7.37
[i]	-15.33*±6.25	-1.33 ±9.26	19.33±10.08	0.67±3.65	-0.12±0.12	1.33±8.17	-86.67±46.67	29.00**±7.21
[j]	3.67*±1.68	-13.33**±2.53	1.33±3.73	0.00±1.47	-0.10**±0.03	-8.00**±1.79	-15.83±12.56	-7.20**±2.09
[l]	21.33* ±8.78	-4.67 ±12.08	-42.0*±16.75	6.67* ±2.91	-0.38*±0.18	-10.67±10.28	-138.33*±64.10	-39.33**±9.90
X ²	11.26*	29.18**	7.29	9.53*	20.40**	37.61**	-	30.37**
Type of interaction	Duplicate	Complementary	Duplicate	Complementary	Duplicate	Duplicate	Duplicate	Duplicate

Traits → Parameters	Dry matter yield per plant	Crude protein content	Crude protein yield per plant	Days to maturity	Seed yield per plant	1000 seed weight	Harvest index
A ↓	-14.59*±5.27	1.31±1.49	-3.31*±1.68	-7.33±4.07	0.23±2.43	-0.01±0.46	1.07±1.71
B	15.37*±6.69	-14.47**±0.80	-5.04**±0.46	-30.00**±4.00	-2.29±2.46	-8.97**±0.56	10.51**±2.81
C	-25.99±13.90	-1.57±2.88	-4.14*±1.96	28.67**±6.74	93.23**±7.89	-14.90**±1.13	11.41*±5.09
D	-13.38±7.36	5.80**±1.53	2.11±1.24	33.00**±3.54	47.65**±3.63	-2.96**±0.60	-0.08±2.50
[m]	36.17**±3.23	12.23**±0.67	4.42**±0.47	167.33**±1.33	58.26**±1.75	2.32**±0.26	27.37**±1.09
[d]	-11.88**±3.5	7.21**±0.73	0.95±0.83	24.33**±2.33	19.29**±0.98	1.21**±0.30	-0.51±1.22
[h]	38.15*±14.95	-8.62*±3.10	-1.49±2.51	-49.00**±7.38	-100.05**±7.49	4.15**±1.22	0.60*±5.16
[i]	26.76±14.72	-11.59**±3.06	-4.21±2.49	-66.00**±7.09	-95.29**±7.26	5.91**±1.19	0.17±4.99
[j]	-14.98**±4.1	7.89**±0.79	0.87±0.86	11.33**±2.57	1.26±1.29	4.48**±0.35	-4.72**±1.48
[l]	-27.53±19.84	24.75**±4.10	12.57**±3.84	103.33**±11.51	97.36**±8.82	3.07±1.64	11.76±7.05
X ²	16.88**	367.26**	121.47**	103.41**	173.69**	342.40**	16.33**
Type of interaction	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Complementary	Complementary

*P≤0.05; and **P≤0.01

Table 3. Estimates of scaling tests and genic effects in oat for cross Kent x *Avena Sterilis*

Traits → Parameters	Days to 50 % flowering	Plant height	Leaves per plant	Tillers per plant	Leaf: stem ratio	Flag leaf area	Green fodder yield per plant	Dry matter %
A ↓	-3.67±2.73	18.33*±7.77	-3.67±6.57	-1.00±1.92	-0.05±0.08	-3.33±3.76	13.33±13.01	-0.40±3.14
B	-3.00 ±4.15	-6.00±7.72	-11.67±8.23	-0.67±1.56	-0.05±0.06	31.33**±2.49	-30.00±26.25	4.03*±1.57
C	4.00±12.63	4.33±8.88	-17.33±13.40	-3.67±2.77	-0.05±0.15	48.67**±5.13	-16.67±29.67	-3.43±8.92
D	5.33±6.22	-4.00±5.38	-1.00±6.60	-1.00±1.49	0.03±0.08	10.33**±2.49	0.00±18.86	-3.53±4.34
[m]	128.33**±2.96	103.33**±1.33	42.33**±2.60	11.00**±0.58	0.53**±0.03	29.33**±0.88	166.67**±6.67	24.50**±2.1
[d]	5.00 ±1.89	10.67*±4.67	9.67*±4.06	1.67±0.94	0.03±0.04	-4.33*±1.76	-46.67**±13.3	-2.53*±1.07
[h]	-7.33±12.63	-1.17±11.32	0.67±13.86	2.83*±3.08	0.02*±0.16	-19.00**±5.33	48.33*±38.27	7.88**±8.80
[i]	-	8.00±10.75	-	-	-	-20.67**±4.99	-	7.07±8.67
[j]	-	12.17*±5.06	-	-	-	-17.33**±1.89	-	-2.22±1.67
[l]	-	-20.33±20.67	-	-	-	-7.33±8.72	-	-10.70±9.90
X ²	3.34	7.02	4.14	1.83	3.73	218.24**	2.70	7.88*
Type of interaction	-	Complementary	-	-	-	Complementary	-	Duplicate

Traits → Parameters	Dry matter yield per plant	Crude protein %	Crude protein yield per plant	Days to maturity	Seed yield per plant	1000 seed weight	Harvest index
A ↓	1.83±3.36	5.65**±0.50	3.86**±1.17	-7.00±3.99	-32.07**±2.07	0.30±0.70	0.82±2.63
B	-1.23±6.85	-1.96±2.20	-0.83±1.14	-13.00**±3.87	-16.99**±1.95	-4.81**±0.51	4.99±2.11
C	-11.07±7.19	2.27*±1.12	0.37±1.50	20.00**±5.12	56.61**±5.81	-0.26±0.66	6.10*±3.40
D	-5.83±3.81	-0.71±1.14	-1.33*±0.65	20.00**±2.62	52.84**±2.91	2.12**±0.37	0.59±2.00
[m]	41.07**±1.24	12.54**±0.18	5.15**±0.19	159.33**±0.67	58.93**±1.35	5.04**±0.05	27.19**±0.69
[d]	16.37**±2.90	3.67**±1.08	3.72**±0.52	14.67**±2.26	15.12**±1.09	-0.79*±0.35	-1.39±1.45
[h]	4.67±8.06	0.72±2.32	1.95±1.45	-26.67**±5.69	-95.40**±5.92	-7.79**±0.80	-1.46*±4.13
[i]	-	1.41±2.28	2.67*±1.30	-40.00**±5.25	-105.68**±5.83	-4.25**±0.73	-1.19±4.01
[j]	-	3.80**±1.10	2.35**±0.81	3.00±2.36	-7.54**±1.31	2.56**±0.38	-2.08±1.62
[l]	-	-5.10±4.45	-5.70**±2.56	60.00**±10.39	154.75**±7.25	8.76**±1.56	-4.62±6.71
X ²	4.84	187.93**	25.56**	65.39**	500.87**	123.99**	7.95*
Type of interaction	-	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Complementary

*P≤0.05; and **P≤0.01

Genetic analysis in oat

In present study both the cross combinations had mainly or predominantly dominance gene effects as reported earlier (Dwivedi *et al.*, 1984; Singh *et al.*, 1985). In these crosses selection at latter generations would be promising for improvement of forage yield. For dry matter yield dominance gene effect was predominant than additive component for genetic control of the trait in both the cross combinations. The values of additive gene effects were found to be significant and positive for both the crosses in case of crude protein percent. In case of crude protein yield per plant, the only gene effect was additive component and that too was found only in Kent $\times$ *A. sterilis* cross combination in desired direction. Thus, for more crude protein yield per plant simple selection in early generations will be feasible for its improvement. Grain yield is a complex character and main aim of oat breeding. In both of the cross combinations significant positive additive component was observed for genetic control of this trait as reported earlier (Sood *et al.*, 2006). Further, for this trait in present study, mainly additive $\times$ additive non-allelic interaction genic effects were noticed in both the crosses, as observed earlier by De koeyer and Stuthman (1998). For 1000 grain weight positive additive gene effect in cross combination PLP-1 $\times$ *A. sterilis* and negative additive gene effect in cross combination Kent $\times$ *A. sterilis* were found significant.

Epistatic components of gene action *i.e.*, *i* (additive $\times$ additive), *j* (additive $\times$ dominance) and *l* (dominance $\times$ dominance) in cross combination PLP-1 $\times$ *A. sterilis* for days to 50% flowering, leaf:stem ratio, crude protein per cent, days to maturity, dry matter per cent and seed yield per plant and in cross combination Kent $\times$ *A. sterilis* for flag leaf area, crude protein percent, crude protein yield per plant, days to maturity and 1000 seed weight were found to be significant (Table 3). Preponderance of non-additive gene action and higher order interactions for these traits indicate the quantitative nature of inheritance of the traits. Breeding strategies like diallel selective mating or biparental matting's in early segregating generations followed by recurrent selection might be appropriate approach towards genetic improvement of these traits. Additive $\times$ additive type of epistatic gene effects were highly significant for seed yield per plant, days to maturity and 1000 seed weight in both cross combinations. Dominance $\times$ dominance type of digenic interactions were found significant in both cross combinations for crude protein yield per plant, days to maturity and seed yield per plant. The epistatic effect of additive $\times$ dominance was highly significant for flag leaf area, crude protein % and 1000 seed weight in both of

cross combinations. The negative additive $\times$ additive (*i*) and additive $\times$ dominance (*j*) estimates shows the gene pairs responsible for seed yield per plant, green fodder yield per plant, plant height, days to 50% flowering, crude protein percent, days to maturity etc, are in dispersion form (Mather and Jinks, 1977) suggesting gene contribution of both the parents. Complementary type of gene action was observed for plant height, tillers per plant, 100 seed weight, and harvest index in cross PLP-1 $\times$ *A. sterilis* and plant height, flag leaf area, harvest index in cross Kent $\times$ *A. sterilis* (Table 3). The breeding strategy should be selection in early generation by adopting bi-parental matings for isolation of transgressive segregants.

Conclusion

In the present study complex nature of gene effects was observed for the traits studied indicating that simple selection procedure may not play important role for improvement of these traits. It was observed that magnitude of additive gene effects were small relative to the corresponding dominance effect in most cases, suggesting that pedigree selection method as a useful breeding program for oat improvement in present situation. Further, the present study indicates that all three kinds of gene effects (*d*, *h* and interactions) were involved in the inheritance of studied traits. Thus, plants selected in early segregating generations may not breed true and emphasizes that selection at later segregating generations may show good results for such multiplicative gene effects.

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