<u>***Original Research Article***</u>

Estimation of gene interaction for grain yield and yield traits in *rabi* sorghum [*Sorghum bicolor* (L.) Moench]

Abstract

Generation mean analysis is the potent tool to provide information about different types of gene actions and interactions. To determine the inheritance pattern and gene action of 10 grain yield and grain related quantitative traits, six generations of the four cross combinations *viz*., BJV44 × DSMR8, BJV44 × DSMR4, PKV Kranti × DSMR8 and PKV Kranti × DSMR4 were studied employing generation mean analysis during *rabi* of 2020. Interestingly, both additive and dominant gene action were prevalent for all the traits in the cross BJV44 × DSMR8, whereas the other three crosses exhibited additive for some traits and dominant gene action for some traits. Most of the traits in the majority of the crosses displayed the duplicate type of gene interaction and realized their suitability for the population improvement program. Some crosses *viz.*, BJV44 × DSMR4 and PKV Kranti × DSMR4 exhibited complementary gene interaction and were found suitable for heterosis breeding for grain yield/plant.

Keywords; Sorghum, grain size, grain yield, genetic interaction, generation mean analysis

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] is a C_4 plant with higher photosynthetic efficiency and shows tolerance to abiotic stress (Reddy *et al*., 2009). Sorghum originated in Africa and adapted to a diverse set of environments ranging from arid and semiarid to tropical across the world. After wheat, rice, maize, barley, and sorghum is the major cereal crop with respect to production. Sorghum is significant for providing micronutrients at a low cost, in addition to serving as a food and fodder crop (Rao *et al*., 2010). As a species, Sorghum bicolor (2n = 2x =20) is categorized into five different races: *bicolor*, *caudatum*, *durra*, *guinea*, and *kafir*, as well as several intermediate classes, and it belongs to the family Poaceae, subfamily panicoideae, and tribe Andropogene. Sorghum is an often cross pollinated crop with an average of 5 to 10 *percent* cross pollination and it may exceed up to 40 percent (Barnaud *et al*., 2008).

Grain size and other grain related traits *viz.,* grain width, grain length, grain thickness, 100 grain weight, grain volume, grain density, number of grains/panicle, and days to flowering exhibited positive and significant association with grain yield (Kariyannanavar*et al,* 2022). Path analysis also showed a positive and significant direct & indirect effect on grain yield (Verma and Biradar, 2021). Therefore, a genetic study was planned and executed to know the underlying gene action, inheritance pattern, and trait heritability so that these traits can be exploited for crop improvement.

Knowledge of gene actions and the inheritance of these traits is critical to harnessing the large variability available in sorghum. Generation mean analysis informs about the relative importance of additive effects, dominance deviations, and effects due to epistatic interactions, in determining the genotypic worth of the individuals and, consequently, means genotypic values of families and generations.

Material and methods

In this study, each of the two promising varieties *viz.,* BJV44 and PKV Kranti were crossed with each of the two strong restorers on *maldandi* male sterile source *viz.,* DSMR-8 and DSMR-4 (Verma *et al.,* 2022) two generate four crosses namely, BJV44 × DSMR8, BJV44 x DSMR4, PKV Kranti × DSMR8, and PKV Kranti × DSMR4. Six generations, *i e.*, P_1, P_2, F_1, F_2, B_1, and B_2 were generated for each cross combination during *the summer* and *Kharif* seasons-2020. The F_1's of all the four crosses developed in summer-2020 and Kharif-2020, each of the F_1 was backcrossed with their P_1 and P_2 parents to develop B_1 and B_2 populations, respectively. At the same time, each F_1 advanced to produce F_2 populations. Since the development of six generations in four different crosses was time consuming process and there were not enough seeds for multiple seasons/year evaluation. Therefore, the six generations were evaluated only during the post rainy season-2020 at Botany Garden, College of Agriculture, UAS, Dharwad, Karnataka, India.

To evaluate the six generations of all the four crosses, an experiment was carried out without replications; the population size and characteristics of the parents used are given in Table 1. All the recommended packages of practices were followed to raise a healthy crop. The grain size related traits *viz.,* grain length (mm), grain width (mm), grain thickness (mm), were measured using the vernier caliper while the volume of the 100 grains was measured based on the water displacement method.

Results and Discussion

Adequacy of additive-dominance model

Scaling tests were run to evaluate the effectiveness of the additive dominance model for the inheritance of traits relevant to grain size and grain yield. Except for grain density in PKV Kranti × DSMR4, the entire studied trait's scaling test values were found to be significantly different from zero, indicating the presence of nonallelic gene interaction and the inadequacy of the additive dominance model for the inheritance of these traits (Table 2). Whereas, for the grain density in the cross PKV Kranti × DSMR4 the additive dominant model was found to be adequate (Koubisy, 2019 and Feltaous *et al*., 2020).

Gene effects

The nature and extent of the gene effects influencing the genetic control of the traits under study were determined using the six parameter model. Except for grain density in PKV Kranti × DSMR4, the estimated mean effect parameter [m], which measures the contribution from the overall mean as well as the locus effects and interactions of the fixed loci, was found to be significant for all traits in all the four crosses. This finding suggests that these characters are quantitatively inherited and highlights the significance of non-allelic interactions. For grain length in BJV44 x DSMR4, grain density in BJV44 × DSMR8, and grain width in BJV44 × DSMR4 & PKV Kranti × DSMR4, the additive [d] gene effect was observed to be negative and significant. The results for grain volume in PKV Kranti × DSMR4, grain weight in BJV44 × DSMR8 and PKV Kranti × DSMR4, grain width in PKV Kranti × DSMR8, and grain density in BJV44 x DSMR4 were all found to be non-significant.

For days to flowering, 100 grain weight, grain yield/plant, grain width, grain length, grain thickness, grain volume, grains/panicle, and plant height in all the crosses, the dominance effect [h] was found to be significant. While it wasn't significant for grain density in PKV Kranti × DSMR8, for grain breadth and thickness in PKV Kranti × DSMR4, respectively. Days to flowering, grain yield/plant, grain length, grain thickness, grains/panicle, and plant height exhibited significant additive × additive interaction [i] in all the crosses. Except PKV Kranti ×

DSMR4, the additive × additive interaction [i] was found to be significant for 100 grain weight and volume in all the crosses. For grain density, the crosses PKV Kranti × DSMR8 and BJV44 × DSMR8 were recorded significant and the rest of the crosses were non significant for grain density. The additive × additive interaction [i] was found to be important for grain width in the BJV44 × DSMR8 and BJV44 × DSMR4, but not in other crosses. It's interesting to note that the additive × dominance interaction [j] was significant for grain yield/plant and grains/panicle in all four crosses.

For days to flowering, grain yield/plant, 100 grain weight, grain breadth, grain thickness, 100 grain volume, grains/panicle, and plant height, the dominance × dominance interaction [l] effect was observed significant in all the examined crosses. While it was significant in all crosses other than PKV Kranti ×DSMR8 for grain length. The dominance × dominance interaction [l] effect was significant in all crosses other than PKV Kranti × DSMR4 for grain thickness and grain density. For the majority of the crosses, it was discovered that dominance × dominance interaction [l] effects were greater than additive × dominance [j] and additive × additive interactions [i]. These results are in harmony with the earlier reports of Gaddameedi *et al*., 2018 and Rokade *et al*., 2021.

Types of epistasis

Based on the signs of dominance [h] and dominance × dominance [l] interaction, the type of epistasis is determined. The epistasis is a complementary type when these effects are in the same direction; if not, it is a duplicate type. A duplicate type of interaction was involved for most of the traits in all crosses(Table 3). It's interesting to note that duplicate gene interaction was present in all the traits of the BJV44 × DSMR8 cross (Mohammed *et al*., 2018).

Information about gene action, inheritance patterns, and heritability is very helpful for improving traits and, ultimately, yield. To determine the genotypic values of the individuals and, subsequently, the mean genotypic values of families and generations, Hayman's generation means analysis gives information on the relative relevance of the additive effect, dominance effect, and non-allelic gene interactions. Based on the significant values of all the scales and joint scale tests for all the traits in all the crosses except for grain density in PKV Kranti × DSMR4 for the grain density, the current study demonstrated the existence of epistasis.

The gene effect [m] revealed that all the traits in all the crosses were inherited quantitatively and exhibited the importance of epistasis. Significant [d] additive effects indicate the prospect of improvement by selection in early segregating generations for the majority of traits in the majority of crosses. Similar to this, a significant dominance impact [h] implies delaying the selection for later generations to achieve homozygosity. The findings suggested that both additive and dominant effects contributed to the inheritance of the traits under study, raising the possibility that selection for desirable traits may be effective in early generations. However, it is preferable to postpone selection for later segregating generations.

The significance of additive × dominance [j] and dominance × dominance [l] gene interactions showed that additive × dominance, dominance and non allelic interactions have a significant influence on the traits. Therefore, it is recommended to postpone selection for subsequent segregating generations until populations achieve homozygosity. According to the current research, all types of epistasis, including additive, dominance, and dominance-dominance, played a part in the expression of all the traits studied. In the current study, it is advised to postpone selection for the majority of the traits in the majority of crosses, and interestingly for all the traits in the cross BJV 44 × DSMR8 because these were exhibiting duplicate kind of epistasis. According to this study, duplicate epistasis exists for the majority of the traits, which would reduce the range of variability (Kearsy and Pooni, 1996). Delaying selection until homozygosity is reached would be preferable to take advantage of transgressive segregants. However, it is recommended to use heterosis breeding for traits that demonstrate complementary gene interaction (Table 3). To increase grain yield/plant, it would be desirable to take advantage of heterosis in the crosses BJV44 × DSMR4 and PKV Kranti × DSMR4 in further breeding program.

Conclusion

The results of the current study showed that almost all traits are significantly influenced by the additive, dominance, and interaction components. Heterosis breeding can be used to exploit the crosses exhibiting complementary gene interaction, while reciprocal and biparental mating approaches can be used to accumulate favorable genes in crosses for traits that exhibit duplicate gene interaction. The findings of this study may be useful for future research on grain yield and attributes connected to grain size.

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Table 1: Parents used and population size of the different generations of different crosses

Cross-1: BJV44 × DSMR8			**Cross-2: BJV44 x DSMR4**	
Sl. No	**Generation**	**Population Size**	**Generation**	**Population Size**
1	P_1 (BJV-44- High grain yield and quality)	20	P_1 (BJV-44- High grain yield and quality)	20
2	P_2 (DSMR-4- Strong restorer and bold seeds)	20	P_2 (DSMR-4- Strong restorer and bold seeds)	20
3	F_1	20	F_1	20
4	F_2	453	F_2	453
5	B_1	158	B_1	158
6	B_2	157	B_2	157
Cross-3: PKV Kranti × DSMR8			**Cross-4: PKV Kranti × DSMR4**	
1	P_1 (PKV Kranti- High grain yield and quality)	20	P_1 (PKV Kranti- High grain yield and quality)	30
2	P_2 (DSMR-8- Strong restorer and bold seeds)	22	P_2 (DSMR-4- Strong restorer and bold seeds)	24
3	F_1	19	F_1	22
4	F_2	455	F_2	453
5	B_1	156	B_1	156
6	B_2	154	B_2	158

Table 2: Scaling test and gene effects for grain yield and grain related traits

Cross	BJV44 × DSMR8	BJV 44 × DSMR-4	PKV Kranti × DSMR8	PKV Kranti × DSMR4
1. Days to flowering				
Scaling test				
A	2.51**±0.48	0.28±0.46	1.55*±0.44	3.30**±0.43
B	-0.16±0.50	5.36**±0.47	-5.73**±0.52	3.26**±0.48
C	-3.55**±0.81	3.58**±0.82	3.07**±0.83	8.72**±0.81
D	-2.95**±0.25	-1.03**±0.31	3.63**±0.30	1.08**±0.35
Joint Scaling test	237.31**	171.29**	136.42**	270.88**
Genetic parameters				
m	67.28**±0.09	64.40**±0.13	69.55**±0.12	66.31**±0.14
d	2.99**±0.17	2.51**±0.19	4.96**±0.18	4.86**±0.21
h	4.50**±0.61	-1.64*±0.70	-7.24**±0.69	-5.34**±0.76
i	5.89**±0.49	2.06**±0.62	-7.25**±0.60	-2.16**±0.70
j	2.67**±0.55	-5.08**±0.57	7.27**±0.59	0.04±0.56
l	-8.23**±1.06	-7.70**±1.11	11.43**±1.09	-4.40**±1.17
2. Grain yield per plant (g)				
Scaling test				
A	55.15**±1.24	-15.14**±1.21	23.28**±1.36	6.22**±1.12
B	32.30**±1.26	-5.73**±1.29	-29.97**±1.29	-1.45±1.19
C	14.99**±2.17	-31.51**±2.21	50.78**±2.35	-18.43**±2.00
D	-36.24**±0.79	-5.32**±0.72	28.74**±0.82	-11.60**±0.74
Joint Scaling test	3240.99**	255.16**	2626.16**	287.83**
Genetic parameters				
m	92.52**±0.31	71.19**±0.29	118.56**±0.32	86.81**±0.28
d	11.79**±0.50	8.52**±0.43	31.66**±0.50	21.01**±0.48
h	88.01**±1.82	40.92**±1.71	-19.53**±1.91	50.75**±1.70
i	72.47**±1.58	10.64**±1.43	-57.48**±1.63	23.21**±1.49
j	22.85**±1.43	-9.41**±1.39	53.24**±1.47	7.66**±1.32
l	-159.93**±2.95	10.22**±2.80	64.17**±3.09	-27.98**±2.77
3. 100 grain weight (g)				
Scaling test				
A	0.589**±0.097	0.758**±0.118	1.807**±0.094	0.359**±0.085
B	0.620**±0.102	0.276*±0.119	0.857**±0.093	0.449**±0.089
C	-0.686**±0.172	-0.151±0.202	-0.169±0.151	0.836**±0.127
D	-0.947**±0.068	-0.592**±0.061	-1.417**±0.063	0.014±0.058
Joint Scaling test	214.96**	117.75**	717.07**	56.14**
Genetic parameters				
m	3.578**±0.028	3.681**±0.023	3.946**±0.025	4.311**±0.021
d	0.041±0.039	0.167**±0.039	0.659**±0.039	0.040±0.040
h	1.621**±0.150	0.701**±0.151	2.297**±0.138	-0.476**±0.125
i	1.894**±0.135	1.185**±0.121	2.833**±0.126	-0.027±0.115
j	-0.03±0.13	0.48**±0.13	0.95**±0.13	-0.09±0.12
l	-3.103**±0.231	-2.219**±0.255	-5.498**±0.216	-0.781**±0.204

Contd….

Cross	**BJV44 × DSMR8**	**BJV 44 × DSMR-4**	**PKV Kranti × DSMR8**	**PKV Kranti × DSMR4**
4. Grain width (mm)				
Scaling test				
A	0.654**±0.046	0.110*±0.048	-0.184**±0.048	-0.111*±0.045
B	0.398**±0.045	0.102*±0.049	-0.128**±0.044	-0.147**±0.045
C	0.180*±0.080	0.063±0.078	-0.326**±0.079	-0.292**±0.078
D	-0.436**±0.028	-0.074**±0.022	-0.007±0.027	-0.017±0.026
Joint Scaling test	367.25**	14.67**	20.11**	15.34**
Genetic parameters				
m	3.862**±0.011	4.228**±0.008	4.109**±0.011	4.199**±0.010
d	0.060**±0.017	-0.098**±0.016	-0.009±0.017	-0.040*±0.017
h	0.683**±0.065	0.402**±0.057	0.231**±0.064	0.098±0.062
i	0.872**±0.056	0.148**±0.044	0.013±0.055	0.034±0.052
j	0.26**±0.05	0.01±0.06	-0.05±0.05	0.04±0.05
l	-1.925**±0.105	-0.360**±0.100	0.299**±0.105	0.224*±0.104
5. Grain length (mm)				
Scaling test				
A	0.497**±0.057	0.154*±0.085	-0.229**±0.059	-0.067±0.055
B	0.173**±0.057	0.127±0.082	-0.360**±0.055	-0.101*±0.059
C	-0.369**±0.101	-0.424**±0.157	-0.974**±0.098	-1.440**±0.099
D	-0.519**±0.036	-0.352**±0.053	-0.193**±0.035	-0.636**±0.033
Joint Scaling test	243.09**	44.63**	104.72**	440.79**
Genetic parameters				
m	4.692**±0.014	4.887**±0.023	4.883**±0.014	4.599**±0.012
d	0.238**±0.021	-0.086**±0.028	0.179**±0.022	0.064**±0.021
h	1.132**±0.083	0.821**±0.124	0.895**±0.081	1.328**±0.078
i	1.038**±0.072	0.704**±0.106	0.385**±0.070	1.272**±0.065
j	0.32**±0.07	0.027±0.09	0.14*±0.07	0.03±0.06
l	-1.707**±0.132	-0.985**±0.192	0.203±0.132	-1.103**±0.131
6. Grain thickness				
Scaling test				
A	0.457**±0.044	0.259**±0.052	0.239**±0.046	0.058±0.046
B	0.199**±0.044	0.001±0.057	-0.105*±0.047	-0.026±0.053
C	0.098±0.076	-0.243*±0.094	-0.425**±0.078	-0.107±0.084
D	-0.279**±0.025	-0.251**±0.028	-0.280**±0.024	-0.070*±0.027
Joint Scaling test	190.87**	100.38**	192.69**	9.67*
Genetic parameters				
m	2.753**±0.010	2.758**±0.011	2.851**±0.008	2.841**±0.010
d	0.161**±0.016	0.101**±0.018	0.299**±0.017	0.167**±0.018
h	0.389**±0.060	0.470**±0.070	0.551**±0.059	-0.081±0.065
i	0.558**±0.050	0.503**±0.057	0.559**±0.047	0.140*±0.054
j	0.26**±0.05	0.26**±0.06	0.34**±0.05	0.08±0.05
l	-1.214**±0.099	-0.762**±0.119	-0.693**±0.103	-0.172±0.111

Contd….

Cross	**BJV44 × DSMR8**	**BJV 44 × DSMR-4**	**PKV Kranti × DSMR8**	**PKV Kranti × DSMR4**
7. 100 grain volume				
Scaling test				
A	1.072**±0.078	0.710**±0.079	0.706**±0.083	-0.438**±0.068
B	0.529**±0.076	0.034±0.075	0.042±0.077	-0.409**±0.080
C	-0.441**±0.128	-0.169±0.139	-0.575**±0.146	-0.719**±0.098
D	-1.021**±0.048	-0.456**±0.062	-0.661**±0.052	0.064±0.057
Joint Scaling test	515.50**	117.39**	218.06**	90.65**
Genetic parameters				
m	2.962**±0.018	3.108**±0.025	3.429**±0.021	3.608**±0.019
d	0.323**±0.032	0.157**±0.036	0.468**±0.029	0.065±0.043
h	1.861**±0.109	0.766**±0.133	1.299**±0.119	-1.197**±0.118
i	2.043**±0.096	0.912**±0.124	1.322**±0.103	-0.128±0.113
j	0.54**±0.09	0.68**±0.01	0.66**±0.09	-0.03±0.10
l	-3.644**±0.180	-1.655**±0.201	-2.070**±0.187	0.975**±0.197
8. Grain density				
Scaling test				
A	-0.159**±0.030	0.059*±0.032	0.255**±0.021	0.010±0.015
B	0.026±0.030	-0.591**±0.037	0.221**±0.020	0.022±0.016
C	0.029±0.061	-0.530**±0.058	0.304**±0.036	0.009±0.029
D	0.081**±0.022	0.001±0.017	-0.086**±0.012	-0.012±0.012
Joint Scaling test	62.12**	292.94**	207.02**	6.15^{NS}
Genetic parameters				
m	1.212**±0.009	1.206**±0.007	1.194**±0.005	
d	-0.099**±0.011	0.017±0.011	0.020*±0.008	
h	-0.187**±0.049	-0.419**±0.043	0.026±0.029	
i	-0.162**±0.043	-0.003±0.035	0.172**±0.025	
j	-0.18**±0.03	0.65**±0.04	0.03±0.02	
l	0.295**±0.076	0.536**±0.072	-0.648**±0.048	
9. Number of grains per panicle				
Scaling test				
A	1023.84**±22.47	-815.65**±73.16	-560.40**±22.45	-79.82**±22.45
B	452.24**±22.08	-390.23**±63.58	-1291.58**±21.26	-322.04**±23.70
C	309.68**±38.15	-855.67**±123.55	1422.39**±38.17	-930.88**±38.67
D	-583.20**±13.36	175.10**±37.17	1637.19**±12.84	-264.51**±13.77
Joint Scaling test	3200.74**	132.99**	17689.97**	772.81**
Genetic parameters				
m	2467.63**±5.22	1968.45**±14.92	3058.92**±5.129	2035.32**±5.03
d	263.86**±8.32	156.23**22.15	398.41**±7.72	462.04**±9.40
h	1752.53**±31.12	747.56**±91.93	-1967.17**±30.31	1419.97**±32.11
i	1166.40**±26.71	-350.21**±74.34	-3274.37**±25.68	529.02**±27.55
j	571.60**±26.24	-425.41**±71.58	731.17**±25.23	242.22**±26.20
l	-2642.47**±50.63	1556.09**±152.04	5126.35**±49.11	-127.15*±53.94

Contd….

Cross	**BJV44 × DSMR8**	**BJV 44 × DSMR-4**	**PKV Kranti × DSMR8**	**PKV Kranti × DSMR4**
10. Plant height				
Scaling test				
A	21.84**±1.41	-17.99**±1.96	31.31**±1.69	-20.25**±1.56
B	-3.70*±1.46	-9.92**±2.09	-14.20**±162	-22.38**±1.76
C	58.25**±2.32	-9.00**±3.28	25.21**±2.77	-74.04**±2.69
D	20.06**±0.79	9.45**±1.11	4.05**±0.85	-15.71**±0.93
Joint Scaling test	1205.93**	125.73**	690.91**	823.51**
Genetic parameters				
m	270.38**±0.28	262.27**±0.40	270.44**±0.31	253.41**±0.33
d	32.39**±0.55	20.39**±0.77	46.34**±0.59	33.00**±0.66
h	-51.35**±1.87	-10.12**±2.64	-29.45**±2.11	40.17**±2.19
i	-40.11**±1.57	-18.90**±2.23	-8.10**±1.70	31.41**±1.85
j	25.54**±1.69	-8.07**±2.43	45.51±1.84	2.13±1.96
l	21.98**±3.20	46.80**±4.49	-9.02*±3.64	11.22**±3.76

Table 3: Different gene interaction for the traits under study in four different crosses

Sl. No.	**Crosses** **Characters**	**BJV44 × DSMR8**	**BJV 44 × DSMR-4**	**PKV Kranti × DSMR8**	**PKV Kranti × DSMR4**
1.	Days to flowering	Duplicate	Complementary	Duplicate	Complementary
2.	Grain yield / plant (g)	Duplicate	Complementary	Duplicate	Duplicate
3.	100 grain weight (g)	Duplicate	Duplicate	Duplicate	Complementary
4.	Grains/ panicle	Duplicate	Complementary	Duplicate	Duplicate
5.	100 grains volume (cc)	Duplicate	Duplicate	Duplicate	Duplicate
6.	Grain density	Duplicate	Duplicate	Duplicate	**No interaction**
7.	Grain length (mm)	Duplicate	Duplicate	Complementary	Duplicate
8.	Grain width (mm)	Duplicate	Duplicate	Complementary	Complementary
9.	Grain thickness (mm)	Duplicate	Duplicate	Duplicate	Complementary
10.	Plant height (cm)	Duplicate	Duplicate	Complementary	complementary

Table 4: Gene actions recorded for the different traits in different crosses

Traits	BJV44 × DSMR8	BJV 44 × DSMR-4	PKV Kranti × DSMR8	PKV Kranti × DSMR4
Days to flowering	A and D	D	D	D
Grain yield per plant	A and D	A and D	D	A and D
100 grain weight	A and D	A and D	A and D	D
Grain width	A and D	D	D	D
Grain length	A and D	D	A and D	A and D
Grain thickness	A and D	A and D	A and D	D
100 Grain volume	A and D	A and D	A and D	D
Grain density	A and D	D	A and D	*
Number of grains per panicle	A and D	A and D	D	A and D
Plant height	D	D	D	D

***** Trait showed absence of non allelic interaction.

Where,

A- Additive gene action, D- Dominance gene action and A & D- both Additive and Dominance gene action.