FULL LENGTH ARTICLE   **OPEN ACCESS**

Estimation of genetic components of variance for yield and its contributing characters in forage sorghum [*Sorghum bicolor* (L.) Moench]

Pankaj Kumar[1], Girish Chandra[2], Bhim Jyoti[1], Anupama Singh[3], Santosh Magadum[3], P K Shrotria[3] and N K Singh[3]
[1] VCSG, UUHF CoF Ranichauri, Tehri Garhwal, 249199, Uttarakhand
[2] Department of Life Science, SGRR University, Dehradun- 248001
3G.B.P.U.A.T., Pantnagar, U.S. Nagar- 234 527, Uttarakhand
Email: vaidya.pankaj4@gmail.com

ABSTRACT
The investigation was carried out to study the variability and component of genetic variance of parents and their crosses made by five sudan grass pollinators with ten cytoplasmic male sterile lines in a line x tester mating design. The sufficient inherent variability was present among the genotypes. The σ² gca was significant for most of the characters, however, the ratio of σ² gca / σ² sca revealed preponderance of non-additive gene action in plant height and green fodder yield, where additive gene action was more with σ² gca / σ² sca ratio being more than unity. The genetic control of yield and its components were observed to be under non-additive gene action predominantly. The components of variance and average degree of dominance ($\sqrt{\sigma^2_D} / \sqrt{\sigma^2_A}$) which was more than unity for most of the characters, where the preponderance of additive gene action seems to be more important for plant height, leaf length, green fodder yield and dry fodder yield. Both the additive and non-additive gene actions to be responsible for inheritance of forage yield and its components in sorghum. The sufficient divergence was present between lines and testers, thereby satisfying the choice of parental material for heterosis study.
KEY WORDS: *variability, cytoplasmic male sterile, gca and sca*

INTRODUCTION
Sorghum (*Sorghum bicolor* (L.) Moench) is the third most important cereal crop of the country and world's fifth most important cereal, after wheat, rice, maize and barley [1 -4]. Sorghum is one crop species that can survive in harsh climatic conditions of arid environments contains both cultivated and wild races and possesses a significant amount of genetic diversity for agronomic traits of importance [5-6]. It is commonly used as a source of grain food, syrup, fuel, and feed for livestock [7-8].
Genetic improvement of quantitative traits depends on the nature and amount of variability present in the genetic stocks and extend to which the desirable traits are heritable. The wide range of genetic variability possess in Indian sorghum. However, the improvement work in land races did not achieve an appreciable increase in their yielding ability. Assessment of genetic variability therefore becomes an essential prerequisite for identifying potential parents for hybridization. Diverse parents are expected to yield higher frequency of the heterotic hybrids in addition to generating a broad spectrum of variability in segregating generations [2]. The average performance of a line in hybrid combinations referred as general combining ability (GCA), and it is due to the additive portion of genetic variance. Whereas, the deviation from expectation on the basis of average performance is due to dominance and epistasis or non-additive genetic variance referred as specific combining ability [9]. Additive variance (σ^2A) due to the average effects of alleles (additive effects, same locus) and dominance variance (σ^2D) due to interaction of average effects of alleles (dominance effects, same locus) [10].

MATERIALS AND METHODS
The field experiments for present investigation were conducted at the Instructional Dairy Farm of the G.B. Pant University of Agriculture and Technology, Pantnagar (U.S. Nagar), India during *Kharif* seasons 2012 and 2013. The experimental materials consisted fifty F_1 crosses developed through line x tester mating fashion [11] between ten diverse *Sorghum bicolor* type CMS lines (female), five *Sorghum sudanense /Sorghum bicolor* type forage sorghum pollinators (male) and three checks. The experimental material was planted in randomized block design with three replications. Observations were recorded on plant height, leaves per plant, leaf length, leaf width, stem diameter, number of tillers per plant, leaf: stem ratio, green fodder yield and dry fodder yield. The analysis was processed by the software Windostat 9.2 from Hyderabad. Combining ability analysis in line x tester mating design was carried out following the method developed by Kempthorne (1957) and later on modified by Arunachalam (1974). This design is related to North Carolina Design II of Comstock and Robinson (1952). The following statistical analysis was carried for line x tester analysis utilizing the procedure of Kempthorne (1957) as per the Singh and Chaudhary (1977).

RESULTS AND DISCUSSION
Analysis of variance
The results of analysis of variance revealed that the mean squares for genotypes, with respect to all the characters, were highly significant for pooled over years analysis (Table 1). Thereby, indicating that sufficient inherent variability is present among the genotypes (parents as well as crosses) for all the characters.
Genetic improvement of any crop is largely depends on the extent of genetic variability and its judicious exploitation through suitable breeding techniques, various parameters may be used for assessing the inherent genetic variability. The analysis of variance, mean values and their range of variation for different characters have used as the parameters for assessing the extent of genetic variability. Highly significant estimates of genotype mean squares supported with wide range of mean values for all the characters under study, suggest substantial inherent genetic variability in the experimental material (lines, tester and crosses). It was also apparent that the experimental material has the ability to utilize effectively the existing environments for the expression of characters of economic importance in forage sorghum.
In the earlier reports also, sufficient genetic variability for fodder yields and components traits in sorghum have been reported. Yield being the complex trait and influenced by the environment, exhibited a lot of variability and wide range of means for both green and dry fodder yields in the present investigation, which is in conformity with earlier findings [15-19].
In pooled analysis over years**,** significant differences were observed for most of the characters except stem diameter, green and dry fodder yield. Variance due to parents was highly significant for all the traits and when it was partitioned in to variance due to lines, testers and line *vs.* tester, it was found that lines differ significantly for all the traits; testers differ significantly also for all the traits except for leaf area, whereas line *vs.* tester differ significantly for all the traits except leaf area and number of tillers per plant. Variance due to crosses was also significant for all the characters, whereas amongst its components *viz.,* line, tester and line x tester, the difference due to lines was significant for leaf length, leaf width, leaf area and number of tillers per plant while variance due to tester was found to be significant for all the characters, number of leaves per plant, leaf width, number of tillers per plant and leaf/stem ratio. Variance due to line x tester interaction was significant for all the characters. The variance due to parent *vs.* crosses was significant for all the characters.
Year x parent interaction showed significance for plant height, green and dry fodder yield. Further partitioning of year x parent interaction indicated that variance due to year x line interaction was significant for green and dry fodder yield, whereas year x tester interaction was significant for number of leaves per plant and green fodder yield. Higher order interaction like year x line x tester was found to be significant for all the characters except number of leaves per plant, leaf length, leaf width, leaf area, stem diameter and leaf/stem ratio. Year x parent *vs.* cross interaction was found to show significance for leaf length and number of tillers per plant.
In this investigation, highly significant mean squares for line *vs.* tester for most of the characters except for leaf area and number of tillers per plant indicated appropriate choice of parental material (line and tester) for the study of variance through line x tester analysis. Further, based on the study of means of lines and testers for various characters, it was also found that there was great difference in the mean values of line and tester for the important traits of forage sorghum such as plant height, leaf length, leaf area, stem diameter, green fodder yield and dry fodder yield. This indicates sufficient divergence between lines and testers, thereby satisfying the choice of parental material for heterosis

study. Further, the testers used in the study are sorghum x sudan grass derivatives with varied and high amount of heterosis already fixed in them.

Pooled analysis of variance over years for combining ability indicated that variance due to lines was significant for leaf length, leaf width, leaf area and number of tillers per plant, thereby indicating significant contribution of lines towards combining ability for these traits. Mean squares due to tester were also significant for, plant height, leaf length, leaf area, stem diameter, green and dry fodder yield. The single degree of freedom comparison for parents *vs.* hybrids, which indicates average heterosis, was significant for all the characters clearly suggested considerable amount of average heterosis in the hybrids (Table 2). This reflected the presence of adequate genetic variability in the experimental material. Similar finding has been reported [20].

Table 1: Analysis of variance for simple RBD with respect to different characters during the pooled over years

Source of variation	df	Plant Height (cm)	No. of Leaves Plant^{-1}	Leaf Length (cm)	Leaf Width (cm)	Leaf Area (cm^2)	Stem Diameter (cm)	No. of Tillers plant^{-1}	Leaf-Stem Ratio	Green Fodder Yield (kg plot^{-1})	Dry Fodder Yield (kg plot^{-1})
Replication	2	249.90	0.63	1.81	0.33	1628.01	0.02	0.10	0.001	21.07	1.90
Treatment	67	5900.25**	4.37**	214.00**	2.64**	19676.00**	0.13**	1.26**	0.011**	232.24**	10.69**
Error	134	55.71	1.07	8.59	0.26	1391.23	0.02	0.17	0.001	12.79	0.94
SEm ±		3.02	0.42	1.19	0.21	15.12	0.06	0.06	0.17	0.012	1.45
CV %		4.08	7.27	3.19	6.79	7.63	9.27	9.27	13.29	8.30	10.86
CD at 1 %		11.16	1.55	4.38	0.76	55.79	0.23	0.23	0.62	0.05	5.35
CD at 5 %		8.48	1.18	3.33	0.56	42.36	0.18	0.18	0.47	0.03	4.06

*p< 5% and **<*p*1% levels of probability, respectively

Table 2: Analysis of variance for combining ability pooled over years

Source of Variation	df	Plant Height (cm)	No. of Leaves Plant^{-1}	Leaf Length (cm)	Leaf Width (cm)	Leaf Area (cm^2)	Stem Diameter (cm)	No. of tillers plant^{-1}	Leaf-Stem Ratio	Green Fodder Yield (Kg plot^{-1})	Dry Fodder Yield (Kg/plot^{-1})
Replicates	2	137.14	0.28	4.03	0.44	2060.73	0.01	0.35	0.0001	8.12	1.10
Years	1	806.45**	69.22**	75.40**	5.93**	43987.39**	0.02	2.29**	0.0083**	4.38	0.80
Replication x year	2	40.26	0.37	5.90	0.12	766.31	0.03	0.001	0.0008	6.76	0.05
Crosses	49	2259.65**	3.51**	93.90**	2.23**	13423.56**	0.11**	1.28**	0.0110**	68.64**	3.54**
Line	9	1676.84	3.45	180.21**	4.03*	24314.85*	0.09	2.37*	0.0126	73.53	5.08
Tester	4	15089.30**	4.23	351.07**	2.86	26074.71*	0.35*	1.89	0.0148	271.39**	8.14*
Line x Tester	36	979.83**	3.44**	43.75**	1.71**	9295.05**	0.09**	0.93**	0.0101**	44.89**	2.64**
Year x Crosses	49	117.64**	0.94	12.94**	0.22	1307.18	0.02	0.37**	0.0007	39.30**	2.83**
Year x Line	9	138.67	1.21	17.54	0.33	2693.53*	0.03	0.46	0.0006	35.35	4.55
Year x Tester	4	240.90	2.29*	23.55	0.32	350.03	0.01	0.91*	0.0017*	81.21	4.42
Year x Line x Tester	36	98.69**	0.73	10.61	0.18	1066.94	0.02	0.28**	0.0006	35.63**	2.22**
Error	196	43.23	1.27	7.61	0.27	1433.85	0.02	0.15	0.0009	6.87	0.61
Total	299	421.81	1.80	22.82	0.60	3520.00	0.04	0.38	0.0025	22.30	1.46
Variance											
GCA		162.49**	-0.014	4.71**	0.04	343.22**	0.003*	0.02	0.0001	2.33	0.04
SCA		146.86**	0.453**	5.52**	0.26	1371.35**	0.011**	0.11**	0.002**	1.54	0.07
GCA/SCA		1.11	0.031	0.85	0.15	0.25	0.27	0.18	0.05	1.51	0.57

*p< 5% and **<*p*1% levels of probability, respectively

Table 3: Components of variance for various characters during pooled over years

Genetic component	Plant height (cm)	No. of leaves plant^{-1}	Leaf length (cm)	Leaf width (cm)	Leaf area (cm^2)	Stem diameter (cm)	No. of tillers plant^{-1}	Leaf-Stem Ratio	Green fodder yield (kg/plot^{-1})	Dry fodder yield (kg/plot^{-1})
σ^2 GCA	162.4900**	-0.0140	4.7100**	0.0400	343.2200*	0.0030*	0.0200	0.0001	2.3300	0.0400
σ^2 SCA	146.8600**	0.4500**	5.5200**	0.2600	1371.3500**	0.0110**	0.1100**	0.0020**	1.5400	0.0700

σ² GCA/σ² SCA	1.1100	0.0300	0.8500	0.1500	0.2500	0.3000	0.1800	0.0500	1.5100	0.5700
σ² A (F=1)	324.9800	-0.0280	9.4200	0.0700	686.4400	0.0060	0.0400	0.0001	4.6600	0.0800
σ² D (F=1)	146.8600	0.4530	5.5200	0.2600	1371.3500	0.0100	0.1100	0.0010	1.5400	0.0700
σ²A/σ² D	2.2100	-0.0620	1.7000	0.2800	0.5000	0.5500	0.3300	0.0850	3.0200	1.0900
Degree of dominance (σ²D/σ² A)$^{1/2}$	0.6700	4.0300	0.7600	1.2000	1.4100	1.3500	1.7500	3.4250	0.5700	0.9600
σ² A (F=0)	649.9700	-0.0560	18.8400	0.1400	1372.8800	0.0120	0.0700	0.0003	9.3200	0.1500
σ² D (F=0)	587.4300	1.8110	22.0900	1.0200	5485.4000	0.0430	0.4300	0.0060	6.1800	0.2800
σ²A/σ² D	1.1100	-0.0310	0.8500	0.1400	0.2500	0.2730	0.1600	0.0430	1.5100	0.5400
Degree of dominance (σ²D/σ² A)$^{1/2}$	0.9500	5.7000	1.0800	0.6900	2.0000	1.9100	2.4800	4.8430	0.8100	1.3600

*p< 5% and **<p1% levels of probability, respectively

Significant variance due to line x tester interaction observed for all the characters suggest the presence of significant *sca* effects for the crosses besides indication of presence of inter allelic interaction. Present results for significance of line x tester interaction are also in accordance with [21-23].

Estimation of components of variance

Estimates of *gca* variance (σ² *gca*), *sca* variance (σ² *sca*), additive variance (σ²$_A$), dominance variance (σ²$_D$) and average degree of dominance (√σ²$_D$ / √σ²$_A$) on the basis of pooled analysis over years (Table 3). The estimates for components of genetic variance *i.e.* σ²$_A$ and σ²$_D$ were computed from the variance of combining ability calculated on the basis of the covariance of half sib and full sib as suggested by Kempthorne (1957). The estimates of variance due to combining ability revealed that σ² *gca* was significant for all the characters except leaf width, number of leaves per plant, green fodder yield and dry fodder yield. However, the ratio of σ² *gca* / σ² *sca* revealed the preponderance of non-additive gene action plant height and green fodder yield, where additive gene action was more with σ² *gca* / σ² *sca* ratio being more than unity. Both the additive and non-additive gene actions have been reported to be responsible for inheritance of forage yield and its components in sorghum [24-26]. Some reports have also indicated that additive genetic variance existed in substantial amount in sorghum populations along with non-additive gene action for green fodder and its components [27-28]. The magnitude of ratio of *gca/sca* variance was much lower (< 4) indicating that relative importance of non-additive gene action in controlling forage yield. In the present investigation also the genetic control of yield and its components, have been observed to be under non-additive gene action predominantly as compared to additive gene action [29].

Estimation of components of variance (additive variance from *gca* and dominance variance from *sca* variance), and subsequent estimation of average degree of dominance (√σ²$_D$ / √σ²$_A$) which was more than unity for most of the characters during pooled analysis, further indicate the preponderance of dominance gene action for most of the traits except plant height, leaf length, green fodder yield and dry fodder yield, where, additive gene action seems to be more important. also reported the similar findings in forage sorghum [30-31].

CONCLUSION

Genetic improvement of any crop is largely depends on the extent of genetic variability. In this study the degree of dominance was greater than unity and both the additive and non-additive gene actions were responsible for inheritance of forage yield and its components in sorghum. The sufficient divergence was present between lines and testers, thereby satisfying the choice of parental material for heterosis study and essential prerequisite for identifying potential parents for hybridization.

REFERENCES
1. FAO (2004). Production year book 2002 No. 56. FAO Stat. Ser 176 – Food and Agriculture Organization of the United Nations, Rome, Italy.
2. Chavan ,S.K., Mahajan, R.C., Fatak, S.U. (2010). Genetic variability studies in sorghum. Karnataka Journal of Agricultural Science 23 (2): 322-323.
3. Kumar, A.A., Reddy, B.V.S., Sharma, H.C., Hash, C.T., Rao, P.S., Ramaia, B., Reddy, P.S. (2011). Recent advances in sorghum genetic enhancement research at ICRISAT. American Journal of Plant Science 2: 589–600.

4. Motlhaodi, T., Geleta, M., Bryngelsson, T., Fatih, M., Chite, S., Ortiz, R. (2014). Genetic diversity in ex-situ conserved sorghum accessions of Botswana as estimated by microsatellite markers. Australian Journal of Crop Science 8 (1): 35-43.

5. Hart, G., Schertz, K., Peng, Y., Syed, N. (2001). Genetic mapping of *Sorghum bicolor* (L.) Moench QTLs that control variation in tillering and other morphological character. Theoretical and Applied Genetics 103: 1232-1242.

6. Ritter, K.B., McIntyre, C.L., Godwin, I.D., Jordan, D.R., Chapman, S.C. (2007). An Assessment of the Genetic Relationship between Sweet and Grain Sorghums, within *Sorghum bicolor ssp. bicolor* (L.) Moench, Using AFLP Markers. Euphytica 157: 161-176.

7. Ferraris, R. (1981). Early assessment of sweet sorghum as an agro-industrial crop I varietal evaluation. Australian Journal of Experimental Agriculture and Animal Husbandry 21: 75-82.

8. Lekgari, A., Dweikat, I. (2014). Assessment of genetic variability of 142 sweet sorghum germplasm of diverse origin with molecular and morphological markers. Open Journal of Ecology 4: 371-393.

9. Sprague, G.F., Tatum, L.A. (1942). General and specific combining ability in single crosses in corn. Journal of American Society Agronomy 34: 923-932.

10. Halluer, A.R., Carena, M.J., Miranda Filho, J.B. (2010). Quantitative genetics in Maize Breeding. Springer ISBN: 978-1-4419-0765-3, XVI, 664p. (http://www.springer.com/978-1-4419-0765-3).

11. Kempthorne, D. (1957). An introduction to genetic statistics. John Wiley & Sons. New York. pp 468-471.

12. Arunachalam, V. (1974). The fallacy behind the use of a modified line x tester design. Indian Journal of Genetics 34: 280-287.

13. Comstock, R.E., Robinson, H.R. (1952). Genetic parameters, their estimation and significance. Proceedings of 6th International Grasslands Congress 1: 284-191.

14. Singh, R.K., Chaudhary, B.D. (1977). Biometrical methods in quantitative genetics analysis. Kalyani Publishers, Ludhiana.

15. Muhammad, D. (1990). Grain yield forage yield and forage quality among different sorghum types under irrigated and dry land condition. Dissertation Abstract International Science and Engineering 50 (7): 2685.

16. Mehndiratta, P.D., Hooda, P.V., Sindhu, B.S., Satija, D.R. (1993). Expliotation of hybrid vigour in inter specific fodder sorghum. Crop Improvement Society of India. pp 40-41.

17. Desai, S.A., Shrotria, P.K., Singh, R. (2000). Variability and heterosis for forage yield and its components in inter-specific crosses of forage sorghum. Karnataka Journal of Agricultural Science 13 (2): 315-320.

18. Jain, S.K., Patel, P.R. (2012). Genetic variability in land races of forage sorghum [*Sorghum bicolor* (L.) Moench] collected from different geographical origin of India. International Journal of Agricultural science. 4 (2): 182-185.

19. Paliwal, A. (2012). Studies on combining ability and heterosis in forage sorghum [*Sorghum bicolor* (L.) Moench] hybrids developed on alternate cytoplasms. Ph.D. thesis submitted to G.B. Pant University of Agriculture and Technology, Pantnagar, US Nagar, Uttarakhand India.

20. Sharma, H., Sharma, V. (2006). Heterosis in sorghum {*Sorghum bicolor* (L.) Moench}. Agricultural Science Digest 26 (4): 245 – 248.

21. Manickam, S., Das, L.D.V. (1995). Combining ability analysis for forage characters in sorghum {*Sorghum bicolor* (L.) Moench}. Annals of Agricultural Research 16 (1): 49-52.

22. Agrawal, M., Singh, R., Shrotria, P.K. (2005). Combining ability analysis for forage yieldd and quality characters in sorghum {*Sorghum bicolor* (L.) Moench}. Forage Research 31(1): 8-11.

23. Maarouf, I., Mohammed Nunha, H.T. (2008). Heterosis and combining ability for quality traits in forage sorghum. Australian Journal of Basic and Applied Sciences 2 (1): 99-104.

24. Dangi, O.P., Paroda, R.S. (1978). Combining ability analysis for yield and its components in forage sorghum. Indian Journal of Agricultural Science 48: 287-290.

25. Patel, J.R. (1980). Heterosis and combining ability studies in forage sorghum. Ph. D. Thesis. Gujarat Agricultural University, Anand Campus, Anand.

26. Pathak, H.C., Sanghi, A.K. (1992). Combining ability and heterosis, studies in forage sorghum {*Sorghum bicolor* (L.) Moench} across environments. Indian Journal of Genetics 52 (1): 75-85.

27. Kambal, A.E., Webstar, O.J. (1965). Estimates of general and specific combining ability in grain sorghum (*Sorghum vulgare* Pers.). Crop Science 5: 521-523.

28. Kulkarni, N., Sreeramulu, C. (1973). Combining ability and heterosis for sorghum fodder yield. Andhra Agricultural Journal 20: 1-20.

29. Maarouf, I.M. (2009). Line x tester analysis across locations and years in Sudanese x exotic lines of forage sorghum. Journal Plant Breeding and Crop Science 1(9): 311-319.

30. Kadam, D.E., Patil, F.B., Bhor, T.J., Harner, P.N. (2001). Line x tester analysis in sweet sorghum hybrids. Journal of Maharatra Agricultural University 25 (3): 318-319.

31. Kenga, R., Alabi, S.O., Gupta, S.C. (2004). Combining ability studies in tropical sorghum (*Sorghum bicolor* (L.) Moench). Field Crop Research 88: 251-260.