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Combining Ability Analysis Of Parents And Hybrids For Green Fodder Yield And Its Attributing Traits In Sweet Sorghum [*Sorghum bicolor* (L.) Moench]

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ABSTRACT

An experiment was conducted to assess the combining ability and nature of gene action in sixteen parents (4 lines and 12 testers) and forty eight F$_1$ hybrids of sweet sorghum (Sorghum bicolor (L.) Moench) with respect to green fodder yield and its components. The hybrids and their parents were evaluated in randomized block design with three replications. The magnitude of variance due to SCA was greater than GCA variance for most of the traits under study indicating predominance of non-additive gene action in the genetic control of those traits. Among parents, Line 185A and testers RSSV138-1, RSSV466 and RSSV404 emerged as good general combiners for yield and yield contributing traits. The hybrids 185A x RSSV466, 185A x RSSV138-1, PMS71A x RSSV138-1 and PMS71A x RSSV404 showed high significant sca effects for single cut forage yield and most of the yield contributing traits. These crosses could be commercially utilized after sufficient testing in All India trials.
Key words: Sweet sorghum, Combining ability, Fodder yield

INTRODUCTION

Agricultural crops and livestock play a vital role in the national economy since they fulfil the basic needs of life. Agriculture accounts for 54.6% of total employment in India and contributes 15.2% of total GDP. Livestock occupies a crucial position in Indian agriculture and directly contributes 27% of agricultural GDP. India, with 2.29% of the world land area, is maintaining about 10.71% of world's livestock population. The number of milch animals have increased from 62 million in 2000 to 83.15 million in 2012 resulting in 4.04% year-on-year growth rate of milk (Livestock census, 2012). Thus, to sustain this growth rate and for further expansion to meet the demands of ever growing human population, livestock needs sustainable supply of feed material.

The area under fodder cultivation is estimated to be about 4% of the gross cropped area which remained static for the last four decades. The available fodder production is less than the actual requirement. At present, the country faces a net deficit of 61.1% green fodder, 21.9% dry crop residues and 64% concentrate feeds (Dhananjoy, 2013). Moreover, livestock population survives to a large extent on crop residues, which are nutritionally poor.

There is an urgent need to reduce the demand and supply gap by enhancing the production and productivity of fodder crops. Forage yield in quantity alone cannot measure the feeding value of the crops. So, there is also a necessity for improving the nutritive value of forages in order to obtain a better animal performance.

In India, Sorghum (*Sorghum bicolor* (L.) Moench) is one of the most important forage crops grown widely in north western states and to a limited scale in central and southern states. Sorghum ranks first among the cereal fodder crops because of its growing ability in poor soil, faster growing habit, high yield potential, suitability to cultivate throughout the year, palatability, nutritious fodder quality, higher digestibility and various forms of its utilization. It gives uniform green fodder throughout the year and

produces tonnage of dry matter having digestible nutrients (50%), crude protein (8%), fat (2.5%) and nitrogen free extracts (45%) (Azam *et al.*, 2010). The cultivated area under different forage crops is 4.4 per cent of the total area under cultivation, of which about 2.3 m ha is under forage sorghum (Anon., 2011).

Sweet sorghum, being a well-known crop can supply food, feed, fodder, fiber and fuel. However, it has not been studied much as a fodder crop. Sweet sorghum has high biomass production, high brix percentage, short duration, low water requirement and wider adaptability (Reddy *et al.*, 2005). Sweet sorghum hybrids have been reported to produce higher sugar yield (21%) and higher grain yield (15%) than non-sweet sorghum hybrids in the rainy season indicating that there is no trade-off between grain and sugar. The palatability and quality of forage will increase by increasing the sugar content of sorghum stalk. Therefore, the important goals of sweet sorghum forage breeding programs are to increase sweetness, leafiness and juiciness in sorghum (Poehlman, 2006) which can be achieved by developing fodder varieties/hybrids in sweet sorghum with high fodder yield per unit area and time combined with superior quality. Therefore, the present study was undertaken to assess the general and specific combining ability for fodder yield and quality and to identify parents and crosses with desirable genetic effects.

MATERIAL AND METHODS

The present investigation involving four lines, twelve testers and forty eight crosses. Four lines, namely 185A, ICS38A, 24A, PMS71A were crossed on to each of the twelve testers PMS130, KR135, SSV74, SSVV84, NSSV14, RSSV138-1, RSSV404, RSSV466, IS18542, 6NRL, BNM16, UK81 in line x tester fashion to produce forty eight F_1 hybrids during rabi season of 2015 at Indian Institute of Millets Research, Hyderabad. The forty eight F_1 hybrids along with their corresponding sixteen parents were sown in randomized block design with three replications at AICRP on Forage Crops, ARI, Rajendranagar during kharif, 2016. Each entry was raised in two rows of 4 m length with a spacing of 30 cm between the rows and 10 cm between the plants with in the row. All the recommended agronomical practices under AICRP on sorghum were followed and plant protection measures were applied as and when required to ensure good crop. The observations were recorded on five randomly selected plants per each entry in each replication for days to 50 per cent flowering, plant height (cm), number of leaves per plant, leaf length (cm), leaf breadth (cm), leaf to stem ratio, sugar brix (%), green fodder yield (t/ha), dry matter content (%), dry fodder yield (t/ha), ADF, NDF and CP (%). Mean of five plants for each entry for each character was calculated and the data was analyzed statistically using the software WINDOSTAT version 8.1.

RESULTS AND DISCUSSION

Analysis of variance for combining ability revealed that parents and crosses differed significantly for all the characters studied (Table 1). The mean squares due to lines and testers were significant for most of the characters. Estimates of mean squares for lines and testers revealed the presence of great deal of diversity among the parents with respect to fodder yield and yield contributing traits. The mean squares due to Lines vs Testers were significant for all the characters. This revealed that lines and testers interacted and pronounced different heterotic effects. This could be due to the fact that parents used in this investigation had considerable genetic variability. Analysis of variance for combining ability for yield and yield components indicated that general combining ability (GCA) and specific combining ability (SCA) mean squares were highly significant for all the characters.

The estimates of variances due to combining ability revealed that σ^2gca was highly significant for all the characters except ADF. σ^2sca was highly significant for all the characters. However, the magnitude of *sca* variance is higher than that of *gca* variance for all the traits under study except days to 50 per cent flowering (Mohammed, 2009), sugar brix (Umakanth *et al*, 2012) and dry matter content (Table 2) and revealed that non additive gene action was predominant in the inheritance of fodder yield and its component traits. Similar observations were also reported by Bhatt and Bhasketi (2011), Kamdi *et al*. (2011), Akbari *et al.* (2013) and Tariq *et al.* (2014). The general combining ability effects of lines and testers are presented in the Table 3. Among the parents, 185A, RSSV138-1, RSSV404 and RSSV466 were identified as the good general combiners for majority of the characters. 185A showed significant *gca* effects in desirable direction for days to 50 per cent flowering, leaf breadth, crude protein and green fodder yield. RSSV138-1 showed high significant desirable *gca* effects for plant height, number of leaves, leaf length, leaf breadth, green fodder yield, dry fodder yield, dry matter content, sugar brix and ADF. RSSV404 showed high significant desirable *gca* effects for plant height, number of leaves, leaf to stem ratio, green fodder yield, dry fodder yield, dry matter content, ADF, NDF and crude protein. RSSV466 showed high significant desirable *gca* effects for days to 50 per cent flowering, plant height, leaf breadth, green fodder yield, dry fodder yield and crude protein.

High *gca* values of parents 185A, RSSV138-1, RSSV404 and RSSV466 for fodder yield and its component traits indicated that these parents had favourable gene, therefore may be used in forage sorghum

improvement programme.The specific combining ability effects of hybrids for forage yield and component characters are presented in the Table 4. For days to 50 per cent flowering, among 48 crosses twenty two crosses recorded negative *sca* effects. The highest negative significant *sca* effects was recorded by the cross 185A x IS18542 that involves Low x Low *gca* effect and may give desirable transgressive segregants. Similar findings were reported by Kamdi *et al.* (2011).

For plant height, nineteen crosses recorded significant positive *sca* effects of which, the cross 185A x RSSV466 recorded highest positive *sca* effect followed by 27A x SSV84, 185A x 6NRL, 185A x RSSV138-1. The highest significant positive *sca* effect of the cross 185A x RSSV466 resulted from Low x High parental *gca* effects indicating the presence of dominance and complementary gene action.

Nine crosses recorded significant *sca* effects for number of leaves per plant of which 185A x RSSV138-1 recorded highest positive *sca* effect followed by ICS38A x IS18542, 185A x RSSV466. The parents involved in the cross combinations were low x high, high x high and low x low general combiner indicating the presence of dominance or complementary gene action, addititive x additive type gene action.

For leaf length, four crosses recorded significant *sca* effect of which 185A x RSSV138-1 recorded highest positive *sca* effect followed by ICS38A x IS18542, ICS38A x NSSV14 and 185A x RSSV466. The parents involved in the cross combinations were low x high and low x low general combiner indicating the presence of dominance or complementary gene action and additive x additive type gene action.

For leaf breadth, eighteen crosses recorded significant *sca* effects in which cross 27A x PMS130 recorded highest positive *sca* effect followed by 27A x NSSV14 and 185A x NSSV14. The parents involved in the first two cross combinations were low x low general combiners and low x high general combiners in another cross.

For sugar brix, twenty crosses recorded significant *sca* effects in desirable direction. PMS71A x RSSV466 recorded highest positive *sca* effect followed by 27A x RSSV138-1, 27A x SSV74 and 185A x RSSV138-1. The parents involved in these cross combinations were Low x High general combiners indicated the presence of complementary epistasis gene action in the direction of additive effects of the good performer. These crosses could be exploited for progeny selection.

For leaf to stem ratio, fifteen crosses recorded significant *sca* effects in desirable direction. The cross PMS71A x IS18542 recorded highest positive *sca* effect followed by ICS38A x BNM16, PMS71A x PMS130 and 27A x RSSV466. The parents involved in the cross combinations were low x high, high x high and low x low general combiner indicating the presence of dominance or complementary gene action, addititive x additive type gene action.

For green fodder yield, eleven crosses recorded significant *sca* effects in desirable direction. PMS71A x RSSV138-1 recorded highest positive *sca* effect followed by ICS38A x PMS130 and 185A x RSSV466. Though the crosses exhibited high *sca* effects with good per se performance the parents involved in these cross combinations include Low x High, Low x Low and High x High general combining parents. The crosses PMS71A x RSSV138-1 and 185A x RSSV466 resulted by involvement of Low x High and High x High general combining parents respectively indicating the presence of dominance or complementary gene action in the direction of additive effects of the good performer. The significant positive *sca* effect in the cross ICS38A x PMS130 involves parents with Low x Low general combining effects. Such low combining parents are highly responsible to heterozygosity due to non-additive gene effect. Hence such crosses could be utilized for hybrid breeding programme.

For dry fodder yield, twelve crosses recorded significant *sca* effects in desirable direction. The cross ICS38A X PMS130 displayed highest positive *sca* effect followed by PMS71A X RSSV466, 185A x RSSV466. The crosses exhibited highly significant positive *sca* effects involving Low x High, Low x Low and High x High general combiners indicating the presence of additive x additive, dominance or complementary gene action. These combinations could transfer transgressive segregants in their later generation.

Fourteen crosses recorded significant *sca* effects in desirable direction for dry matter content. The cross combination 185A x RSSV138-1 recorded highest positive *sca* effect followed by ICS38A x 6NRL, 27A x SSV74 and 27A x RSSV138-1. These crosses exhibited highly significant positive *sca* effects involving Low x High general combiners indicating the presence of dominance or complementary gene action.

For ADF, seventeen crosses exhibited significant *sca* effects in desirable direction. ICS38A x RSSV138-1 ICS38A x IS18542, 27A x BNM16 and 27A x NSSV14 recorded higher negative *sca* effects. Among these, the former three crosses resulted from Low x Low general combiners and are highly responsible to heterozygosity due to non- additive gene effect. Hence such crosses could be utilized for hybrid breeding programme.

For NDF, fifteen crosses recorded significant negative *sca* effects. 185A x NSSV14 recorded highest negative *sca* effect followed by 27A x RSSV138-1, 27A x SSV84 and ICS38A x 6NRL. The parents involved in these cross combinations include Low x Low and Low x High general combiners respectively, indicating the presence of additive x additive, dominance or complementary gene action.

Twenty four crosses recorded significant positive *sca* effects for crude protein. The cross 185A x SSV74 recorded highest positive *sca* effect followed by PMS71A x RSSV138-1, 27A x 6NRL resulted due to High x Low, Low x Low and Low x High general combiners rrespectively, indicating the presence of additive x additive, dominance or complementary gene action.

CONCLUSION

High GCA values of the parents RSSV138-1, RSSV466, RSSV404 and 185A for forage yield and its contributing traits like plant height, number of leaves per plant, leaf length, leaf breadth indicated that these parents had favourable genes, therefore could be better choices for improvement of forage yield and component traits through hybridization.

Overall, the cross combinations 185A x RSSV466, 185A x RSSV138-1, PMS71A x RSSV138-1 and PMS71A x RSSV404 exhibited highly significant SCA effects coupled with high *per se* performance for green fodder yield, dry fodder yield and other yield contributing characters *viz.*, days to 50 per cent flowering, plant height, number of leaves per plant, leaf length and leaf breadth. These combinations were derived from High x High and Low x High combiners indicating the presence of complementary or dominance gene action in the direction of additive effects of good performer. So these cross combinations could be used in forage sorghum improvement programme.

Table 1 Analysis of variance for yield, yield components and quality traits in sweet sorghum.

Source of variation	d.f.	Days to 50% flowering	Plant height	No of leaves /plant	Leaf length	Leaf breadth	Sugar brix	Leaf to stem ratio
Replications	2	1.764	1.515	0.226	47.738	0.016	0.122	0.094
Crosses	47	186.541**	2410.438**	5.038**	172.985**	1.022**	32.831**	15.002**
Lines	3	1316.206	11776.320**	4.326	796.594**	3.998**	272.447**	80.357**
Testers	11	216.647	3870.859**	14.313**	143.020	0.654	26.175	12.968
Line*Tester	33	73.809**	1072.188**	2.011**	126.281**	0.889**	13.266**	9.739**
Error	94	16.255	1.218	0.135	46.732	0.010	0.424	0.274
Total	143	51.911	793.064	1.748	88.242	0.343	11.071	5.112

Source of variation	d.f.	Green fodder yield	Dry matter content	Dry fodder yield	Acid detergent fibre	Neutral detergent fibre	Crude protein
Replications	2	4.876	1.992	0.084	0.148	0.018	0.005
Crosses	47	262.145**	99.757**	18.958**	56.263**	97.803**	7.676**
Lines	3	733.290**	820.5260**	46.768**	59.771	131.480	11.868
Tester	11	456.227**	65.495	37.360**	51.375	129.117	8.051
Line*Tester	33	154.619**	45.677**	10.206**	57.7554**	84.303**	7.170**
Error	94	7.155	3.335	0.882	1.026	0.937	0.093
Total	143	90.931	35.007	6.687	93.406	69.949	2.584

*significant at 5% level, **significant at 1% level

As the main objective of the present study is to obtain a single genotype with high yield per unit area and early in duration combined with superior quality, the hybrid 185A x RSSV466 was identified with high green fodder yield (62.47 t ha^{-1}) coupled with earliness (72 days for 50 per cent flowering) and high crude protein (10.06%). This hybrid had both parents as high combiners (High x High). High sca effect coupled with per se performance expressed by this hybrid might be due to combination of favourable genes from both the parents. It is recommended for further evaluation under All India trials before commercial cultivation.

Table 2 Estimation of general and specific combining ability variances for yield, yield components and quality traits in sweet sorghum

Source of variation	Days to 50% flowering	Plant height	No of leaves /plant	Leaf length	Leaf breadth	Sugar brix	Leaf to stem ratio	Green fodder yield	Dry matter content	Dry fodder yield	Acid detergent fibre	Acid detergent fibre	Crude protein
σ^2gca	31.302	325.591	0.383	18.115	0.0961	6.206	1.931	24.478	18.294	1.722	2.269	5.391	0.411
σ^2sca	19.544	354.258	0.625	30.408	0.289	4.303	3.141	49.114	13.949	3.108	18.825	27.796	2.362
σ^2gca / σ^2sca	1.60	0.919	0.612	0.602	0.331	1.476	0.614	0.498	1.311	0.55	0.12	0.194	0.174

Table 3 General combining ability effects of parents for yield, yield components and quality traits in sweet sorghum

Genotype	Days to 50% flowering	Plant height (cm)	No. of leaves /plant	Leaf length (cm)	Leaf breadth (cm)	Sugar brix (%)	Leaf to stem ratio	Green fodder yield (t/ha)	Dry matter content (%)	Dry fodder yield (t/ha)	Acid detergent fibre	Neutral detergent fibre	Crude protein (%)
185A	-8.425**	-22.586**	-0.182**	-6.944**	0.440**	-3.344**	-0.071	6.120**	-5.683**	-0.431**	0.161	0.462**	0.335**
ICS38A	3.025	-1.753**	0.123*	3.361**	-0.030	0.609**	2.133**	-4.604**	-0.148	-1.109**	-0.259	-0.488**	0.518**
27A	-0.036	21.443**	0.423**	2.270*	-0.049*	-0.558**	-0.939**	0.052	-0.170	-0.035	1.611**	2.304**	-0.077
PMS71A	5.436**	2.896**	-0.365**	1.313	-0.362**	3.293**	-1.123**	-1.568**	6.001**	1.575**	-1.514**	-2.279**	-0.776**
SE (lines)	0.9182	0.7232	0.0873	1.3956	0.0328	0.1424	0.1325	0.63580266+	0.4612	0.2212	0.2468	0.2254	0.0682
PMS130	-4.525	-31.218**	1.265**	-2.940	-0.034	-2.374**	1.260**	-1.313	-2.916**	-1.275**	1.350**	3.121**	0.418**
KR135	-2.025	-25.385**	-0.487**	-0.374	-0.044	-0.448*	1.312**	-3.921**	-3.486**	-2.036**	1.134**	2.571**	0.631**
SSV74	1.933	2.345**	-0.078	0.598	-0.118**	1.927**	-1.005**	-5.134**	2.777**	-0.653*	0.975**	1.821**	-1.018**
SSV84	4.158**	-20.195**	-0.556**	-2.549	-0.224**	2.118**	-0.273	-7.210**	0.757	-1.646**	-3.550**	-3.904**	0.630**
NSSV14	1.775	5.460**	-0.739**	-4.365*	-.284**	0.034	-1.238**	-2.694*	0.059	-0.724**	-2.925**	-7.754**	0.071
RSSV138-1	7.317**	29.555**	2.550**	8.048**	0.147**	1.195**	-1.441**	4.586**	3.350**	2.663**	-0.600	1.521**	-1.123**
RSSV404	0.075	17.375**	0.736**	1.516	0.047	0.151	0.562**	8.023**	1.887**	3.014**	-1.958**	-1.554**	1.047**
RSSV466	-6.425**	6.689**	-0.002	-3.959*	0.474**	-1.832**	-0.039	11.874**	-3.035**	1.890**	3.950**	0.771**	0.269**
IS18542	4.658**	5.872**	1.545**	2.771	0.233**	-1.188	0.690**	-5.053**	0.826	-1.041**	1.338**	3.022**	-1.571**
6NRL	-4.842**	14.251**	-0.557**	1.706	0.171**	-0.253	-0.458**	-4.614**	1.912**	-0.806**	--0.316	2.221**	0.411**
BNM16	-3.008	-5.307**	-0.470**	0.991	-0.049	-0.980**	1.473**	6.430**	-0.571	1.514**	0.375	0.146	0.489**
UK81	0.908	0.560	-0.677**	-1.444	0.316**	1.648**	-0.844**	-0.973	-1.560**	-0.898**	-0.225	-1.979**	-0.254**
SE (testers)	1.5903	1.2526	0.1512	2.4172	0.0568	0.2467	0.2296	1.1012	0.7989	0.3831	0.4274	0.3904	0.1182

*significant at 5% level, **significant at 1% level

Table 4 Specific combiningability effects for yield, yield components and quality ttraits

Genotype	Days to 50% flowering	Plant height (cm)	No of leaves /plant	Leaf length (cm)	Leaf breadth (cm)	Sugar brix (%)	Leaf to stem ratio
185A x PMS130	1.125	16.305**	0.767**	1.283	0.061	1.463**	-3.349**
185A x KR135	3.292	-9.954**	-1.007**	-2.374	-0.982**	0.067	-1.494**
185A x SSV74	0.067	-42.158**	-1.479**	1.561	-0.438**	-2.995**	-0.177
185A x SSV84	-2.158	-20.241**	-0.968**	-3.205	-1.262**	1.938**	-0.566
185A x NSSV14	-3.308	-18.806**	0.182	-20.292**	0.848**	-0.931**	1.989**
185A x RSSV138-1	12.017**	22.756**	1.576**	10.698**	0.314**	2.674**	-0.181
185A x RSSV404	-3.742	-10.888**	0.140	2.926	0.300**	-1.659**	1.530**

Genotype						
185A x RSSV466	0.758	31.882**	1.078**	7.315*	0.170*	0.218	0.231
185A x IS18542	-7.992**	-2.752	-1.303**	-4.089	-0.086	-0.280	1.235**
185A x6NRL	2.842	27.236**	0.367	6.774	0.470**	0.752*	1.186**
185A x BNM16	0.008	7.894**	0.296	-2.849	0.266**	0.759*	-1.105**
185A x UK81	-2.908	-1.273	0.352	2.253	0.340**	-2.006**	0.702*
ICS38A x PMS130	-1.258	16.672**	-0.080	-2.121	-0.262**	-0.430	0.328
ICS38A x KR135	-2.425	-7.360**	-0.275	-2.288	-0.049	-0.212	0.622
ICS38A x SSV74	-5.617*	17.875**	0.963**	-8.110*	0.212**	-0.894*	0.180
ICS38A x SSV84	0.725	-5.950**	0.960**	4.571	0.531**	0.491	-0.483
ICS38A x NSSV14	4.108	4.761**	-0.066	9.537**	-0.149	1.020**	-1.881**
ICS38A x RSSV138-1	-6.133**	-32.944**	-1.005**	-6.056	0.107	-2.211**	0.909**
ICS38A x RSSV404	-2.192	-6.527**	-1.221**	-4.178	-0.030	0.865*	-0.247
ICS38A x RSSV466	3.975	-15.068**	-0.333	-3.269	-0.450**	-0.201	-0.263
ICS38A x IS18542	3.558	-1.518	1.490**	9.964**	0.560**	0.178	-1.282**
ICS38A x x6NRL	4.058	14.103**	0.015	2.999	-0.107	1.766**	-1.394**
ICS38A x BNM16	2.558	1.428	-0.092	-1.893	-0.314**	0.127	3.308**
ICS38A x UK81	-1.358	14.528**	-0.355	0.845	-0.050	0.482	0.202
27A x PMS130	-4.864*	-7.877**	-0.598**	4.213	1.058**	-3.00**	0.670*
27A x KR135	-4.031	12.651**	0.625**	0.903	0.65**	-1.899**	0.598
27A x SSV74	3.344	10.990**	0.139	5.868	-0.155	2.853**	1.192**
27A x SSV84	1.119	27.254**	0.527*	1.879	0.478**	0.982**	-0.517
27A x NSSV14	2.169	0.066	0.020	6.621	0.892**	2.300**	0.138
27A x RSSV138-1	1.294	7.537**	0.187	-3.879	-0.130	3.009**	-0.272
27A x RSSV404	8.869**	11.751**	1.002**	-3.221	-0.120	1.155**	-1.942**
27A x RSSV466	-2.297	-6.763**	-0.237	-3.758	0.139	-3.111**	2.216**
27A x IS18542	5.953**	-0.247	-0.474*	-2.124	-0.610**	1.051**	-3.537**
27A x 6NRL	-6.881**	-31.693**	-0.472*	-9.253**	-0.044	-2.00**	1.961**
27A x BNM16	-5.381*	-7.334**	-0.526*	-4.081	0.049	-2.206**	-0.453
27A x UK81	0.703	-16.334**	-0.103	-1.041	-0.424**	0.865*-	-0.052
PMS71A x PMS130	4.997*	-25.100**	-0.089	-3.374	-0.857**	1.966**	2.350**
PMS71A x KR135	3.164	4.664**	0.657**	3.759	0.380**	2.044**	0.275
PMS71A x SSV74	2.206	13.293**	0.377	0.681	0.381**	1.035**	-1.195**
PMS71A x SSV84	0.314	-1.063	-0.518*	-3.245	0.253**	-2.429**	1.566**
PMS71A x NSSV14	-2.969	13.979**	-0.135	4.134	0.193*	-2.388**	-0.245
PMS71A x RSSV138-1	-7.178**	2.651	-0.758**	-0.762	-0.291**	-3.472**	-0.455
PMS71A x RSSV404	-2.936	5.664**	0.080	4.473	-0.151	-0.362	0.659*
PMS71A x RSSV466	-2.436	-10.050**	-0.418	-0.288	0.142	3.095**	-2.184**
PMS71A x IS18542	-1.519	4.517*	0.287	-3.462	0.136	-0.950**	3.584**
PMS71A x x6NRL	-0.019	-9.646**	0.090	-0.520	-0.318**	-0.518	-1.752**
PMS71A x BNM16	2.814	-1.988	0.322	0.661	-0.002	1.320**	-1.750**
PMS71A x UK81	3.564	3.079	0.106	-2.057	0.135	0.658	-0.852*
SE (crosses)	3.1806	2.5051	0.3024	4.8344	0.1137	0.4934	0.4591

*significant at 5% level, ******significant at 1% level

Table 4 (cont.).

Genotype	Green fodder yield (t/ha)	Dry matter content (%)	Dry fodder yield (t/ha)	Acid detergent fibre	Neutral detergent fibre	Crude protein (%)
185A x PMS130	-9.080**	-0.502	-1.838**	2.189**	2.163**	-2.291**
185A x KR135	-2.915	2.585*	0.290	6.739**	3.013**	1.406**
185A x SSV74	0.645	-3.105**	-0.360	-0.836	8.563**	2.178**
185A x SSV84	0.987	1.402	1.067	0.689	-1.612**	1.410**
185A x NSSV14	6.198**	-1.010	1.131*	2.604**	-20.562	1.089**

185A x RSSV138-1	-10.809**	7.146**	-0.586	3.939**	6.763**	-2.527**
185A x RSSV404	-0.480	-2.228	-1.546**	-4.303**	-0.062	-0.757**
185A x RSSV466	12.473**	2.711 *	3.074**	-4.811**	2.613**	0.819**
185A x IS18542	-3.640*	-5.073**	-1.988**	-4.399**	-3.238**	-2.079**
185A x6NRL	3.958*	-0.436	1.257*	-4.345**	0.563	-0.984**
185A x BNM16	-5.986**	0.663	-1.346*	3.164**	1.838**	0.671**
185A x UK81	8.650**	-2.154	0.845	-0.086	-0.037	0.994**
ICS38A x PMS130	15.547**	-0.106	3.841**	1.909**	-1.587**	1.448**
ICS38A x KR135	-4.605**	1.204	-0.608	-0.474	1.263*	-2.701**
ICS38A x SSV74	3.308*	-4.616**	-0.248	6.884**	-3.587**	0.254
ICS38A x SSV84	-2.163	2.557*	-0.191	-4.791**	1.238*	-0.953**
ICS38A x NSSV14	-2.505	-3.715**	-1.413*	-4.316**	5.988**	0.475**
ICS38A x RSSV138-1	-2.855	-5.105**	-2.667**	-5.841**	1.213*	0.356*
ICS38A x RSSV404	0.651	-1.136	-0.391	2.118**	0.088	-0.071
ICS38A x RSSV466	-7.387**	0.480	-1.468**	3.043**	-0.937	1.598**
ICS38A x IS18542	2.623	1.122	0.901	-5.828**	-3.888**	1.238**
ICS38A x x6NRL	0.102	5.576**	1.379*	2.276**	-0.087	-0.304
ICS38A x BNM16	0.837	3.279**	1.376*	6.684**	-2.012**	-0.809**
ICS38A x UK81	-3.553*	0461	-0.513	-1.666**	2.313**	0.530**
27A x PMS130	1.157	-3.871**	-0.736	-0.561	-0.579	2.034**
27A x KR135	11.432**	-2.500*	1.859**	-2.945**	-1.329*	0.071
27A x SSV74	-2.222	5.426**	0.939	-5.186**	-6.279**	-0.911**
27A x SSV84	-1.972	-0.027	-0.391	2.239**	1.046	0.529**
27A x NSSV14	-1.618	2.921*	0.619	-2.786**	6.896**	-2.003**
27A x RSSV138-1	-1.942	4.894**	1.099*	0.289	-6.679**	0.074
27A x RSSV404	-8.879**	3.620**	-1.321*	0.714	-0.804	-0.886**
27A x RSSV466	-3.703*	-5.721**	-3.005**	2.805**	-1.129*	-1.757**
27A x IS18542	1.427	2.541*	1.234*	7.561**	4.423**	0.503**
27A x 6NRL	3.058	-2.445*	0.439	0.405	0.221	2.048**
27A x BNM16	7.318**	-4.369**	0.089	-5.686**	2.796**	0.666**
27A x UK81	-4.056*	-0.523	-0.823	3.064**	1.421*	-0.368*
PMS71A x PMS130	-7.623**	4.4205**	-1.266*	-3.536**	0.004	-1.191**
PMS71A x KR135	-3.911*	-1.288	-1.541**	-3.320**	-2.946**	1.224**
PMS71A x SSV74	-1.731	2.295*	-0.331	-0.861	1.304*	1.521**
PMS71A x SSV84	3.148*	-3.392**	-0.485	1.864**	-0.671	-0.986**
PMS71A x NSSV14	-2.075	1.803	-0.337	5.039**	7.679**	0.439**
PMS71A x RSSV138-1	15.605**	-6.934**	2.153**	1.614**	-1.296*	2.097**
PMS71A x RSSV404	8.708**	-0.255	3.259**	1.472**	0.779	1.714**
PMS71A x RSSV466	-1.383	2.531*	1.399*	-1.036	-0.546	-0.731**
PMS71A x IS18542	-0.410	1.410	-0.146	2.576**	2.703**	0.339*
PMS71A x 6NRL	-7.118**	-2.696*	-3.075**	1.664**	-0.696	-0.760**
PMS71A x BNM16	-2.169	0.427	-0.188	-4.161**	-2.621**	-0.528**
PMS71A x UK81	-1.042	2.216	0.490	-1.311*	-3.696**	-0.096
SE (crosses)	2.2024	1.5977	0.7662	0.8549	0.7807	0.2363

*significant at 5% level, **significant at 1% level

Table 5 Top ranking desirable crosses for *sca* effects with their *per se* performance

Character and Cross	Predominant gene action	Values of *sca* effects	*gca* status of parents	Values of *gca* effects of parents		*Per se* performance
				P -1	P - 2	
Days to 50 % flowering	Non additive					
185A x IS18542		-7.992	H x L	-8.425	4.658	74.67
PMS71A x RSSV138-1		-7.178	L x L	5.436,	7.317	92
27A x 6NRL		-6.881	L x H	-0.036	-4.84	74.67
ICS38A x RSSV138-1		-6.133	L x L	3.025	7.317	90.67
Plant height (cm)	Non additive					
185A x RSSV466		31.882	L x H	-22.586	6.689	246.78
27A x SSV84		27.254	H x L	21.443	-20.195	259.30
185A x 6NRL		27.236	L x H	-22.586	14.251	249.70
185A x RSSV138-1		22.756	L x H	-22.586	29.55	260.52
Number of leaves /plant	Non additive					
185A x RSSV138-1		1.576	L x H	-0.182	2.550	13.38
ICS38A x IS18542		1.490	H x H	0.123	1.545	12.60
185A x RSSV466		1.078	L x L	-0.182	-0.002	10.33
Leaf length (cm)	Non additive					
185A x RSSV138-1		10.698	L x H	-6.994	8.048	88.80
ICS38A x IS18542		9.964	H x L	3.361	2.771	93.10

ICS38A x NSSV14		9.537	H x L	3.361	-4.365	85.53
185A x RSSV466		7.315	L x L	-6.994	-3.959	73.41
Leaf breadth (cm)	Non additive					
27A x PMS130		1.058	L x L	-0.049	-0.034	7.95
27A x NSSV14		0.892	L x L	-0.049	-0.284	5.75
185A x NSSV14		0.848	H x L	0.440	-0.284	7.98
Leaf to stem ratio	Non additive					
PMS71A x IS18542		3.584	L x H	-1.123	0.690	0.204
ICS38A x BNM16		0.653	H x H	2.133	1.473	0.241
PMS71A x PMS130		2.350	L x H	-1.123	1.260	0.197
27A x RSSV466		2.216	L x L	-0.939	-0.039	0.184
Sugar brix (%)	Additive					
PMS71A x RSSV466		3.095	H x L	3.293	-1.832	14.80
27A x RSSV138-1		3.009	L x H	-0.558	1.195	14.60
27A x SSV74		2.853	L x H	-0.558	1.927	14.47
185A x RSSV138-1		2.674	L x H	-3.344	1.195	10.77
Green fodder yield	Non additive					
PMS71A x RSSV138-1		15.605	L x H	-1.568	4.586	50.63
ICS38A x PMS130		15.547	L x L	-4.604	-1.313	41.63
185A x RSSV466		12.473	H x H	6.120	11.874	62.47
Dry matter content (%)	additive					
185A x RSSV138-1		7.146	L x H	-5.683	3.350	31.47
ICS38A x 6NRL		5.576	L x H	-0.148	1.912	34
Dry fodder yield	Non additive					
ICS38A x PMS130		3.841	L x L	-1.109	-1.275	9.78
PMS71A x RSSV404		3.259	H x H	1.575	3.014	16.17
185 A x RSSV466		3.074	L x H	-0.431	1.890	12.92
PMS71A x RSSV138-1		2.153	H x H	1.575	2.663	14.71
Acid detergent fibre	Non additive					
ICS38A x RSSV138-1		-5.841	L x L	-0.259	-0.600	31.2
ICS38A x IS18542		-5.828	L x L	-0.259	1.338	33.15
27A x BNM16		-5.686	L x L	1.611	0.375	34.2
27A x NSSV14		-5.186	L x H	1.611	-2.925	38.5
Neutral detergent fibre	Non additive					
185A x NSSV14		-20.562	L x H	0.462	-7.754	33.7
27A x RSSV138-1		-6.679	L x L	2.304	1.521	58.7
27A x SSV84		-6.279	L x H	2.304	-3.904	61
ICS38A x 6NRL		-3.888	H x L	-0.488	2.221	63.2
Crude protein (%)	Non additive					
185A x SSV74		2.178	H x L	0.335	-1.018	10.06
PMS71A x RSSV138-1		2.097	L x L	-0.776	-1.123	8.76 1
27A x 6NRL		2.048	L x H	-0.077	0.411	0.94

P-1: Parent-1
P-2: Parent-2

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