HETEROSIS AND COMBINING ABILITY STUDIES IN SWEET SORGHUM (*SORGHUM BICOLOR* L.) HYBRIDS FOR GREEN FODDER YIELD AND QUALITY TRAITS

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SUMMARY

An experiment was conducted to exploit heterosis in F_1 hybrids of sweet sorghum (*Sorghum bicolor* L.) and to identify parents with desirable genetic effects with respect to single-cut green fodder yield and quality traits. All the 48 F_1 hybrids produced by crossing four lines and twelve testers in line x tester mating design were evaluated to assess general and specific combining ability and gene action governing the green fodder yield and quality traits. Analysis of variance revealed the presence of sufficient variation in the experimental material. The SCA variance was greater in magnitude than GCA variance for most of the characters studied, indicating the preponderance of non additive gene action for several characters. Line 185A and testers RSSV138-1, RSSV466 and RSSV404 emerged as good general combiners for single-cut green fodder yield where as PMS71A, NSSV14, SSV84 were found to be good combiners for sugar brix, ADF and NDF. Based on *sca* effects, 185A x RSSV466, 185A x RSSV138-1, PMS71A x RSSV138-1 and PMS71A x RSSV404 were identified as good specific combiners for green fodder yield.185A x RSSV466 recorded maximum single-cut green fodder yield with 12.53 per cent heterosis over the best check CSV30F.

Key words : Standard heterosis, combining ability, sweet sorghum, green fodder yield

In India, Sorghum (*Sorghum bicolor* (L.) Moench) is one of the most important forage crop 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 soils, 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 (Anonymous, 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 green 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 and also to assess the possibility of commercial exploitation of heterosis for single-cut green fodder yield and quality through estimating of heterosis over better parent and standard check.

MATERIALS AND METHODS

In the present investigation, four lines, namely

185A, ICS38A, 24A, PMS71A twelve testers PMS130, KR135, SSV74, SSVV84, NSSV14, RSSV138-1, RSSV404, RSSV466, IS18542, 6NRL, BNM16, UK81 and forty eight F_1 hybrids along with the standard check CSV30F were sown in randomized block design with three replications at the research farm of AICRP on Forage Crops, Agricultural Research Institute, Rajendranagar, Hyderabad, Telangana 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. The soil was sandy loam in texture with pH of 8.13, low in available nitrogen and medium in available phosphorous and available K_2O. 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 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 quality 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 green fodder yield and quality traits indicated that general combining ability (GCA) and specific combining ability (SCA) mean squares were highly significant for all the characters.

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 green fodder yield and quality 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 estimates of heterosis over the best standard check revealed significant heterosis in desirable direction for green fodder yield and quality traits in many cross combinations. The range of standard heterosis of different characters along with number of significant crosses are presented in the Table 3. In the present study, well known variety CSV30F is used as standard check to get the information on superiority of the crosses. The results revealed that crosses, 185A x RSSV466 (days to 50 per cent flowering), PMS71A x SSV74 (sugar brix), 185A x RSSV466 (green fodder yield), PMS71A x RSSV404 (dry matter content), 185A x RSSV466 (dry fodder yield), ICS38A x SSV84 (ADF), 185A x NSSV14

TABLE 1

Analysis of variance for yield and quality traits in sweet sorghum

Source of variation	d. f.	Days to 50% flowering	Green fodder yield	Dry matter content	Dry fodder yield	Sugar brix	Acid detergent fibre	Neutral detergent fibre	Crude protein
Replications	2	1.764	4.876	1.992	0.084	0.122	0.148	0.018	0.005
Crosses	47	186.541**	262.145**	99.757**	18.958**	32.831**	56.263**	97.803**	7.676**
Lines	3	1316.206	733.290**	820.5260**	46.768**	272.447**	59.771	131.480	11.868
Testers	11	216.647	456.227**	65.495	37.360**	26.175	51.375	129.117	8.051
Line*Tester	33	73.809**	154.619**	45.677**	10.206**	13.266**	57.7554**	84.303**	7.170**
Error	94	16.255	7.155	3.335	0.882	0.424	1.026	0.937	0.093
Total	143	51.911	90.931	35.007	6.687	11.071	93.406	69.949	2.584

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

(NDF) and ICS38A x PMS130, ICS38A x RSSV466 (crude protein) exhibited highly significant heterosis in the desirable direction for fodder yield and quality. In the present study, hybrid 185A x RSSV466 exhibited highest significant positive heterosis of 12.53 per cent over the best check with highest green fodder yield of 62.47 t/ha. In addition, the hybrid also exhibited significant heterosis in desirable direction for days to 50 per cent flowering NDF and crude protein.

The *per se* performance of parents was considered as the first important criterion for selection. As the parents with high mean values may not necessarily able to transmit their superior traits to their progenies. Persual of the *per se* performance of parents indicated that the parents RSSV404, RSSV466, 185A and 6NRL recorded significant high green fodder yield and PMS71A, ICS38A, RSSV404 and SSV84 recorded with high mean values for quality traits.The second criterion of selection is the general combining ability (*gca*) effects of parentsThe general combining ability effects of lines and testers are presented in the Table 3. Amomg the parents, 185A showed significant *gca* effects in desirable direction for days to 50 per cent flowering, green fodder yield and crude protein. RSSV138-1 was found good general combiner for green fodder yield, dry fodder yield, dry matter content, sugar brix and ADF. RSSV404 showed high significant desirable *gca* effects for 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, green fodder yield, dry fodder yield and crude protein. 185A, RSSV138-1, RSSV404 and RSSV466 were identified as the good general combiners for green fodder yield. PMS71A NSSV14 and SSV84 were identified as the good general combiners for quality traits. High GCA values of these parents for fodder yield and quality traits indicated that they had favourable genes, therefore could be better choices for improvement of fodder yield and quality traits through hybridization.

The specific combining ability effects of hybrids for forage yield and quality traits 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).

PMS71A x RSSV138-1 ICS38A x PMS130 and 185A x RSSV466 recorded significant positive

TABLE 2

Estimation of general and specific combining ability variances for yield and quality traits in sweet sorghum

Source of variation	Days to 50% flowering	Green fodder yield	Dry matter content	Dry fodder yield	Sugar brix	Acid detergent fibre	Acid detergent fibre	Crude protein
σ^2gca	31.302	24.478	18.294	1.722	6.206	2.269	5.391	0.411
σ^2sca	19.544	49.114	13.949	3.108	4.303	18.825	27.796	2.362
σ^2gca/σ^2sca	1.60	0.498	1.311	0.55	1.476	0.12	0.194	0.174

TABLE 3

The range of standard heterosis and number of crosses showing significant heterosis for various traits in sweet sorghum

Characters	Range of heterosis	Superior Crosses	Noumber of hybrids having significant heterotic effect	
			+ve	-ve
Days to 50% flowering	-14.23 to 15.81	185A x RSSV466	16	14
Green fodder yield (t/ha)	-67.53 to 12.53	185A x RSSV466	1	47
Dry matter content (%)	-50.32 to 12.06	PMS71A x SSV74	7	34
Dry fodder yield (t/ha)	-75.54 to -13.45	PMS71A x RSSV404	-	48
Sugar brix (%)	-62.69 to 42.73	PMS71A x SSV74	12	22
Acid detergent fibre	-18.08 to 35.60	ICS38A x SSV84	25	6
Neutral detergent fibre	-49.78 to 7.90	185A x NSSV14	2	41
Crude protein (%)	-40.74 to 23.59	185A x KR135	16	23

sca effects for green fodder yield. 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 sugar brix, 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 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.

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. 185A x SSV74 and 185A x NSSV14 exhibited highly significant SCA effects coupled with high *per se* performance for ADF, NDF and crude protein. 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.

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. The hybrid 185A x RSSV466 also recorded 10.7 per cent increased green fodder yield over the best check variety CSV30F. It is therefore recommended for further evaluation under All India trials before commercial cultivation.

TABLE 4
General combining ability (gca) effects of parents and sca effects of hybrids for yield and quality traits in sweet sorghum

Genotype	Days to 50% flowering	Green fodder yield (t/ha)	Dry matter content (%)	Dry fodder yield (t/ha)	Sugar brix (%)	Acid detergent fibre	Neutral detergent fibre	Crude protein (%)
The gca efffects of parents								
185A	-8.425**	6.120**	-5.683**	-0.431**	-3.344**	0.161	0.462**	0.335**
ICS38A	3.025	-4.604**	-0.148	-1.109**	0.609**	-0.259	-0.488**	0.518**
27A	-0.036	0.052	-0.170	-0.035	-0.558**	1.611**	2.304**	-0.077
PMS71A	5.436**	-1.568**	6.001**	1.575**	3.293**	-1.514**	-2.279**	-0.776**
SE (lines)	0.9182	0.6358	0.4612	0.2212	0.1424	0.2468	0.2254	0.0682
PMS130	-4.525	-1.313	-2.916**	-1.275**	-2.374**	1.350**	3.121**	0.418**
KR135	-2.025	-3.921**	-3.486**	-2.036**	-0.448*	1.134**	2.571**	0.631**
SSV74	1.933	-5.134**	2.777**	-0.653*	1.927**	0.975**	1.821**	-1.018**
SSV84	4.158**	-7.210**	0.757	-1.646**	2.118**	-3.550**	-3.904**	0.630**
NSSV14	1.775	-2.694*	0.059	-0.724**	0.034	-2.925**	-7.754**	0.071
RSSV138-1	7.317**	4.586**	3.350**	2.663**	1.195**	-0.600	1.521**	-1.123**
RSSV404	0.075	8.023**	1.887**	3.014**	0.151	-1.958**	-1.554**	1.047**
RSSV466	-6.425**	11.874**	-3.035**	1.890**	-1.832**	3.950**	0.771**	0.269**
IS18542	4.658**	-5.053**	0.826	-1.041**	-1.188	1.338**	3.022**	-1.571**
6NRL	-4.842**	-4.614**	1.912**	-0.806**	-0.253	--0.316	2.221**	0.411**
BNM16	-3.008	6.430**	-0.571	1.514**	-0.980**	0.375	0.146	0.489**
UK81	0.908	-0.973	-1.560**	-0.898**	1.648**	-0.225	-1.979**	-0.254**
SE (testers)	1.5903	1.1012	0.7989	0.3831	0.2467	0.4274	0.3904	0.1182
The sca effects of hybrids								
185A x PMS130	1.125	-9.080**	-0.502	-1.838**	1.463**	2.189**	2.163**	-2.291**
185A x KR135	3.292	-2.915	2.585*	0.290	0.067	6.739**	3.013**	1.406**
185A x SSV74	0.067	0.645	-3.105**	-0.360	-2.995**	-0.836	8.563**	2.178**
185A x SSV84	-2.158	0.987	1.402	1.067	1.938**	0.689	-1.612**	1.410**
185A x NSSV14	-3.308	6.198**	-1.010	1.131*	-0.931**	2.604**	-20.562	1.089**
185A x RSSV138-1	12.017**	-10.809**	7.146**	-0.586	2.674**	3.939**	6.763**	-2.527**
185A x RSSV404	-3.742	-0.480	-2.228	-1.546**	-1.659**	-4.303**	-0.062	-0.757**
185A x RSSV466	0.758	12.473**	2.711 *	3.074**	0.218	-4.811**	2.613**	0.819**
185A x IS18542	-7.992**	-3.640	-5.073**	-1.988**	-0.280	-4.399**	-3.238**	-2.079**
185A x6NRL	2.842	3.958*	-0.436	1.257*	0.752*	-4.345**	0.563	-0.984**
185A x BNM16	0.008	-5.986**	0.663	-1.346*	0.759*	3.164**	1.838**	0.671**
185A x UK81	-2.908	8.650**	-2.154	0.845	-2.006**	-0.086	-0.037	0.994**
ICS38A x PMS130	-1.258	15.547**	-0.106	3.841**	-0.430	1.909**	-1.587**	1.448**
ICS38A x KR135	-2.425	-4.605**	1.204	-0.608	-0.212	-0.474	1.263*	-2.701**
ICS38A x SSV74	-5.617*	3.308*	-4.616**	-0.248	-0.894*	6.884**	-3.587**	0.254
ICS38A x SSV84	0.725	-2.163	2.557*	-0.191	0.491	-4.791**	1.238*	-0.953**
ICS38A x NSSV14	4.108	-2.505	-3.715**	-1.413*	1.020**	-4.316**	5.988**	0.475**
ICS38A x RSSV138-1	-6.133**	-2.855	-5.105**	-2.667**	-2.211**	-5.841**	1.213**	0.356*
ICS38A x RSSV404	-2.192	0.651	-1.136	-0.391	0.865*	2.118**	0.088	-0.071
ICS38A x RSSV466	3.975	-7.387**	0.480	-1.468**	-0.201	3.043**	-0.937	1.598**
ICS38A x IS18542	3.558	2.623	1.122	0.901	0.178	-5.828**	-3.888**	1.238**
ICS38A x x6NRL	4.058	0.102	5.576**	1.379*	1.766**	2.276**	-0.087	-0.304
ICS38A x BNM16	2.558	0.837	3.279**	1.376*	0.127	6.684**	-2.012**	-0.809**
ICS38A x UK81	-1.358	-3.553*	0461	-0.513	0.482	-1.666**	2.313**	0.530**
27A x PMS130	-4.864*	1.157	-3.871**	-0.736	-3.00**	-0.561	-0.579	2.034**
27A x KR135	-4.031	11.432**	-2.500*	1.859**	-1.899**	-2.945**	-1.329*	0.071
27A x SSV74	3.344	-2.222	5.426**	0.939	2.853**	-5.186**	-6.279**	-0.911**
27A x SSV84	1.119	-1.972	-0.027	-0.391	0.982**	2.239**	1.046	0.529**
27A x NSSV14	2.169	-1.618	2.921*	0.619	2.300**	-2.786**	6.896**	-2.003**
27A x RSSV138-1	1.294	-1.942	4.894**	1.099*	3.009**	0.289	-6.679**	0.074
27A x RSSV404	8.869**	-8.879**	3.620**	-1.321*	1.155**	0.714	-0.804	-0.886**
27A x RSSV466	-2.297	-3.703*	-5.721**	-3.005**	-3.111**	2.805**	-1.129*	-1.757**
27A x IS18542	5.953**	1.427	2.541*	1.234*	1.051**	7.561**	4.423**	0.503**
27A x 6NRL	-6.881**	3.058	-2.445*	0.439	-2.00**	0.405	0.221	2.048**
27A x BNM16	-5.381*	7.318**	-4.369**	0.089	-2.206**	-5.686**	2.796**	0.666**
27A x UK81	0.703	-4.056*	-0.523	-0.823	0.865*-	3.064**	1.421*	-0.368*
PMS71A x PMS130	4.997*	-7.623**	4.4205**	-1.266*	1.966**	-3.536**	0.004	-1.191**
PMS71A x KR135	3.164	-3.911*	-1.288	-1.541**	2.044**	-3.320**	-2.946**	1.224**
PMS71A x SSV74	2.206	-1.731	2.295*	-0.331	1.035**	-0.861	1.304*	1.521**
PMS71A x SSV84	0.314	3.148*	-3.392**	-0.485	-2.429**	1.864**	-0.671	-0.986**
PMS71A x NSSV14	-2.969	-2.075	1.803	-0.337	-2.388**	5.039**	7.679**	0.439**
PMS71A x RSSV138-1	-7.178**	15.605**	-6.934**	2.153**	-3.472**	1.614**	-1.296*	2.097**
PMS71A x RSSV404	-2.936	8.708**	-0.255	3.259**	-0.362	1.472**	0.779	1.714**
PMS71A x RSSV466	-2.436	-1.383	2.531*	1.399*	3.095**	-1.036	-0.546	-0.731**
PMS71A x IS18542	-1.519	-0.410	1.410	-0.146	-0.950**	2.576**	2.703**	0.339*
PMS71A x 6NRL	-0.019	-7.118**	-2.696*	-3.075**	-0.518	1.664**	-0.696	-0.760**
PMS71A x BNM16	2.814	-2.169	0.427	-0.188	1.320**	-4.161**	-2.621**	-0.528**
PMS71A x UK81	3.564	-1.042	2.216	0.490	0.658	-1.311*	-3.696**	-0.096
SE (crosses)	3.1806	2.2024	1.5977	0.7662	0.4934	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*	*gca* status of parents	Values of gca effects of		*Per se* performance
				P-1	P-2	
Days to 50% flowering	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	92.00
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
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	34.00
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	31.20
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	34.20
27A x NSSV14		-5.186	L x H	1.611	-2.925	38.50
Neutral detergent fibre	Non additive					
185A x NSSV14		-20.562	L x H	0.462	-7.754	33.70
27A x RSSV138-1		-6.679	L x L	2.304	1.521	58.70
27A x SSV84		-6.279	L x H	2.304	-3.904	61.00
ICS38A x 6NRL		-3.888	H x L	-0.488	2.221	63.20
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
27A x 6NRL		2.048	L x H	-0.077	0.411	10.94

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

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