

Original Research Article

Combining Ability Analysis for Forage Yield and Quality Traits in Forage Sorghum [*Sorghum bicolor* L.Moench]

ABSTRACT

The present study was conducted at GBPUAT Pantnagar to study/evaluate the combining ability for nine yield related and three quality traits in which consisted of seventy F1 crosses developed through line x tester mating design that involved ing ten female lines and seven pollinator (male) lines, during Kharif 2018 (now old).The Complete Randomization in random block design (C.R.B.D.) experiment was with three replications. Observations were recorded on plant height, stem girth, number of leaves per plant, leaf length, leaf width, leaf area, leaf:stem ratio, green fodder yield per plot, dry fodder yield per plot (yield related traits) total soluble solids, HCN content, green fodder yield per plot, dry fodder yield per plot, and protein percent (quality traits). The results indicated highly significant differences among treatments (Crosses) for all the characters. Among lines 11 A2, ICSA-467, ICSA-469, 993100 A, ICSA-271, and ICSA-276 exhibited good general combining ability for different yield related and quality traits whereas among testers CSV-15, PC-5, 04 K 693, 04 K 700 and 04 K 668 showed good general combining ability for most of the yield related and quality characters. Among seventy crosses, twenty four crosses for plant height, nine crosses for number of leaves, one cross for leaf length, fourteen crosses for leaf width, thirteen crosses for leaf area, five crosses for stem girth, thirteen crosses for total soluble solids, nine crosses for leaf:stem ratio, eight crosses for HCN content, sixteen crosses for green fodder yield, eight crosses for dry fodder yield and seven crosses for protein per cent exhibited good specific combining ability.

Keywords: Forage sorghum, GCA, SCA, Line x Tester, HCN, yield and quality traits.~~and Tester.~~

1. Introduction: Sorghum [*Sorghum bicolor* (L.) Moench], $2n=2x=20$, a C_4 plant of family *Poaceae*, is a major food, feed and fodder crop globally. It is the fifth most important crop after wheat, rice, maize and barley and is widely cultivated in the semi-arid regions of the world (Anglani, 1998old ref.). Sorghum is a species of tropical origin having moved or been moved from Ethiopia and surrounding areas of Northeast Africa. Sorghums is are remarkably drought-resistant and vitally important where the climate is too dry for maize, i.e., annual rainfall ranging from 350 to 750 mm (FAO and ICRISAT 1996). It also tolerates an shocking array of soils. These characteristic features make sorghum an ideal food crop in semi-arid areas of Africa, Asia (and elsewhere) where other crops, such as maize, would generally fail. It has extensive variability of usage such as grain sorghum, forage sorghum, and sweet sorghum, providing feed, food, fodder, fiber and fuel. viz: (grain sorghum, forage sorghum, and sweet sorghum). The crop is mainly grown in subtropical and tropical areas because of its quick growing habit, good palatability and drought tolerance capacity, where agro-climatic conditions such as temperature, rainfall, and soil are erratic. Much of the crop is grown in the marginal and stress-prone areas of the semi-arid tropics, mainly on small holdings. In Northern Western India, it is grown for meeting the major fodder requirement of *kharif* and *rabi* seasons. Nutritionally, among the *kharif* fodders, sorghum is a crop *par excellence* with starch (63-68%), high digestibility (50-60%), dry matter content (20-35%), sugars (8-17%), crude protein (7.5-10.0%), calcium (0.53%), phosphorus (0.24%), and crude fiber (30-32%) (Sheoran et al., 2000). Besides s the higher content of carbohydrates, it also has iron (Fe) and vitamin B₃ contents which are higher than rice and maize.

It is a (Some varieties are) short- season forage that attains its complete bloom in 52-60 days after sowing if harvested at 50% flowering or heading stage. It has the potential to give high forage yield (Iqbal, 2015). Forage sorghums include sudangrass, sorghum varieties ?, hybrids ?, and sorghum × sudangrass hybrids (Kalton, 1988). A major staple food of many countries in Asia and Africa, sorghum is now a major feed crop in the United States, Mexico, Australia, Argentina, and South Africa (Miller and Kebede, 1984). Globally, the sorghum is grown on an area of 41.14 million hectares with production of 58.72 million tons annually. In India, it is grown for food, feed and fodder purpose on an area of around 5.0 million hectares with 4.5 million tons of grain production per annum (USDA Foreign Agriculture Service, 2019old ref). Sorghum is known by different names in Africa, such -thatas *guinea-corn*, *durra* in the Sudan, *mshelia* in Ethiopia and Eritrea, *dawa* or *sorgho* in West Africa, *mtama* in East Africa, *kaffir corn* in South Africa and *amabele* or *mabele* in several countries in Southern Africa. In the Indian sub-continent, it is known as *jowar* (Hindi), *cholam* (Tamil Nadu), *jonna* (Andhra Pradesh) and *jola* (Karnataka). Five basic (land) races of cultivated sorghum are recognized as *Bicolor*, *Caudatum*, *Guinea*, *Kafir*, and *Durra* (Harlan and de Wet, 1972). Sorghum is an often cross-pollinated crop with 5-25% cross pollination depending on the cultivar and climatic conditions and therefore, has the unique opportunity of being exploited both for non-additive genetic component by

developing hybrids and for additive genetic component by developing varieties. Up to 50% cross-pollination has been reported in sorghum (Doggett, 1988). *However, from the breeding point of view, sorghum is considered a self-pollinated crop which normally follows classical breeding procedures such as hybridization, mass selection, and backcrossing, pedigree selection. Discovery of male sterility in sorghum due to interaction of milo cytoplasm with *kafir* genes (Stephen, 1954) opened avenues for utilization of male sterility for commercial exploitation of heterosis in sorghum through hybrid development. With the growing human population and increasing demands for meat and milk, there is need for more feed and fodder to feed increased population of livestock. Currently in India, on an average there is deficit of green and dry fodder to the extent of 40%, which may further increase in future because of increasing population, with the growing affluence and rising economies, are turning to non vegetarian diets and therefore, we need to increase the productivity of forage and fodder crops in a sustainable manner (Anonymous, 2001). Combining ability analysis proposed by Griffing (1956) is a milestone in the history of practical utility of plant breeding methods that helps in identifying the best combiners for hybridization programme and characterization of nature and magnitude of gene actions involved in controlling the inheritance of different yield related traits. It is an efficient technique to identify best and poor combiners and discriminate between them. This technique is very useful in selection of desirable parental material in early stages of breeding programme. The combining ability estimates together with *per se* performance of parents and hybrids and their heterotic response provide additional information regarding worth of parents and the specific crosses for hybrid breeding as well as transgressive breeding. The general combining ability (*gca*) and specific combining ability (*sca*) are equated with additive gene action and non-additive gene action, respectively (Sprague and Tatum; 1942 and Griffing 1956). The selection criteria of parents is usually based on *per se* performance and general combining ability. Crossing of two parents with high general combining ability in desired direction may result into best performing crosses due to increased frequency of desirable genes. General combining ability (*gca*) is defined as the average performance of parental lines in a series of cross combinations. The information pertaining to the *gca* effects of the parents is of great importance because proper parental lines identified based on their *gca* effects and mean performance in desirable direction will produce desirable end products in terms of good hybrids and/or transgressive segregants. Further, the parents with high *gca* effects also produce useful segregants in early generations. The diverse parents having combination of significant additive and additive x additive interactions are supposed to produce good recombinants out of their cross combinations in advance generations. The performance of a cross can deviate from the average general combining ability of two parents and this deviation is termed as specific combining ability (*sca*). The desirable recombinants in segregating generations will be achieved if good general combiners are crossed for the traits in which the improvement is desired. If any character which is under

unidirectional control by a set of favorable alleles with predominant additive effects, the selection of parents can be done only on the basis of *per se* performance. However, sometimes the phenotypically superior parents may give rise to poor recombinants in segregating generations, therefore it is necessary to select parental lines not only on the basis of *per se* performance but also on the basis of *gca* effects. Line x tester mating design is used routinely to generate material for estimation of combining ability effects which provide basic idea about the genetic potential of parents. The objective of this study was to determine the combining ability of 17 parents for fodder yield and its yield components. The study envisaged assessing general combining ability of parents and specific combining ability of crosses by following a line x tester (L x T) mating design.*

2. Materials and Methods: The experimental materials ~~for the present study~~ consisted of seventy F₁ crosses developed through line x tester mating design involving ten diverse *Sorghum bicolor* type CMS lines (female) viz., ICSA-467, 11A₂, HB 94004 A, SPA₂ 94012, ICSA-469, ICSA-271, 993100 A, ICSA-276, ICSA-293, SP55609 A and seven *Sorghum sudanense/Sorghum bicolor* type forage sorghum pollinator (male) lines viz., CSV-15, PC-5, 04 K 693 (UPMC-512), 04 K 700 (SDSL 921001 x IS-3359), 01 K 733 (SDSL 92101 x SDSL 92111), UPMC-8, 04 K 668 (SDSL- 92134 x SDSL-92140). The experimental materials obtained through such crossings were planted in *Kharif* 2018~~(old so expung)~~. Resultant 70 hybrids along with 17 parents and four checks were planted during *Kharif*18. The field experiment with 91 treatments (70 F₁s + 17 parents + 4 checks- (CSH-20MF, CSH-24MF, SSG 59-3 and CSH 13) were planted in random block design (R.B.D.)? with three replications. Each treatment was accommodated in a plot size of 3 m² (4 rows of 3m length spaced at 25 cm). Observations were recorded on plant height, stem girth, number of leaves per plant, leaf length, leaf width, leaf area, leaf:stem ratio, total soluble solids, HCN content, green fodder yield per plot, dry fodder yield per plot, protein percent and in-vitro dry matter disappearance.? 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 (1974still old ref)**. This design is related to North Carolina Design II of **Comstock and Robinson (1952)**. The following model of **Kempthorne (1957)** was used for estimating the *gca* and *sca* effects in combining ability analysis.

$$X_{ijk} = \mu + g_i + g_j + S_{ij} + e_{ijk}$$

where,

$$X_{ijk} = \text{Performance of } i^{\text{th}} \text{ line crossed with } j^{\text{th}} \text{ tester in } k^{\text{th}} \text{ observation}$$

$$\mu = \text{General mean}$$

$$g_i = \text{gca effect of } i^{\text{th}} \text{ line} \quad (i = 1, 2, \dots, l_j)$$

- g_j = *gca* effect of j^{th} tester (j = 1, 2, t_j)
 S_{ij} = *sca* effect of the ij^{th} combination and
 e_{ijk} = Error associated with ijk^{th} observation (k=1, 2,r)

In the analysis of variance for combining ability, the components due to lines, testers and line × tester were calculated by splitting the cross sum of squares.

Estimation of GCA effects

(a) For lines

$$g_i = (X_{i..}/tr) - (X_{...}/ltr)$$

Where,

- g_i = General combining ability effect of i^{th} line
 $X_{...}$ = Grand total
 $X_{i..}$ = Performance of i^{th} line crossed with the testers

(b) For testers

$$g_t = (X_{.jt}/lr) - (X_{...}/ltr)$$

Where,

- g_j = General combining ability of j^{th} tester
 $X_{...}$ = Grand total
 $X_{.jt}$ = Performance of j^{th} tester crossed with the lines

Estimation of SCA effects

$$S_{ij} = (X_{ij}/r) - (X_{i..}/tr) - (X_{.jt}/lr) - (X_{...}/ltr)$$

Where,

- S_{ij} = Specific combining ability of the cross between i^{th} line and j^{th} tester
 X_{ij} = Total of $(ij)^{\text{th}}$ combination overall replication

[Include methods for determining HCN, total soluble solids and protein percent.](#)

3. Result and Discussion:

3.1 Analysis of variance for combining ability: The analysis of variance for combining ability analysis in line x tester including parents (lines and testers), with respect to various characters ~~are~~ were presented in **Table 1**. The results indicated highly significant differences among treatments (Crosses) and parents for all the characters under study. Partitioning of variance due to parents in to variance due to lines, testers and line vs. tester also indicated highly significant differences in line, tester and line vs. tester for most of the characters. Mean squares due to crosses were highly significant for all the characters. However, when partitioning variance due to crosses in to line, tester and line x tester it was found that variance due to lines was highly significant for number of leaves per plant, leaf width, leaf :stem ratio and significant for plant height and protein per cent. Variance due to testers was highly significant for leaf length and significant for leaf :stem ratio. Variance due to line x tester interaction was highly significant for plant height, number of leaves per plant, leaf length, leaf width, leaf area , stem girth, TSS per cent, leaf: stem ratio, HCN content, green fodder yield, dry fodder yield and protein per cent. The findings were supported by several other workers **Indhubala**

et al. (2010); Prakash et al. (2010); Ghazy et al. (2011) and Chaudhari et al. (2017); Wagaw et al. (2020); and Rachman et al. (2022).

3.2 General combining ability (GCA) effects of parents: To develop high yielding hybrids as well as to select superior and desirable segregates in the subsequent generation to F₁, selection of parents for hybridization with good genetic worth is an integral part of yield improvement programme. Selection of parents based on *per se* performance alone may not be always effective because many times two phenotypically superior lines may produce poor hybrids. In such conditions, general combining ability effect of parental lines which indicate the presence of additive and additive x additive type of gene action can help in selecting parents to develop hybrids having high potential for yield and other traits. Parental lines with highly significant *gca* effects in desirable direction, coupled with high *per se* performance for components traits and yield implied that these lines contribute to enhanced performance of hybrids above the grand mean value. The estimates of general combining ability effects (*gca*) for lines (females) and testers (males) for each characters are presented in the **Table 2**, summary of general combining ability is presented in **Table 3** and best general combiners for different characters have been listed in **Table 4**.

Perusal of the results of *gca* effects of parents with respect to plant height revealed that amongst lines 993100A was best combiner for plant height, showing highly significant positive *gca* effects. Among testers 04 K700 was best combiner showing significant positive *gca* effects. Among lines ICSA 293, ICSA 276, ICSA 467 and among testers 04 K 693 and 04 K 668 were also good general combiners. For number of leaves, ICSA 276 and SP55609 A among lines and 04K 700 and 04 K 693 among testers were good combiners having highly significant *gca* effect values. The genotypes *viz.* 11 A2 and 993100 A amongst lines and PC 5 and UPMC 8 amongst testers were found to be good combiners for leaf length. For leaf width ICSA 271, 993100 A, ICSA 276 and ICSA 293 among lines and 04 K 693 among testers showed positive significant *gca* effects. For leaf area, the line 993100 A was best general combiner with positive significant *gca* effects followed by ICSA 271, ICSA 276 and SP 55609 A and among testers, PC 5 showed positive significant *gca* effect, were identified as good general combiners. The results indicated that for stem girth, line ICSA 276 was found best general combiner for stem girth followed by lines 993100 A, SP 55609 A, ICSA 271 and among testers PC 5 was found best general combiner followed by 04 K 700 and 04 K 693 which had significant positive *gca* values, were identified as good general combiners for stemgirth. For TSS, the line SPA2 94012 among lines and PC 5 among tester were found best general combiners with positive significant *gca* effects. The lines ICSA 467, ICSA 469, SP 55609 A and the tester 04 K 700 also showed positive significant *gca* effects for TSS. For leaf : stem ratio, lines 11 A2, SP 55609 A and ICSA 467 and testers CSV 15 and PC 5 among testers exhibited significant positive *gca* effects. The lines HB 94004 A and ICSA 469 also showed

positive significant *gca* effect. For HCN content, the negative estimates are desirable. The lines HB 94004 A, ICSA 469 and ICSA 467 showed negative significant *gca* effect while the testers 01 K 733 and CSV 15 had negative significant *gca* effect. These parental lines and testers were identified as good general combiner for low HCN content. For green fodder yield positive estimates are desirable and lines ICSA 293, ICSA 271, 11 A₂, SP 55609A and testers 04 K 700 and 04 K 668 exhibited positive significant *gca* effects. For dry fodder yield also positive estimates are desirable like green fodder yield. Among lines SP 55609 A and ICSA 293 and among testers 04 K 700 and 04 K 668 showed positive significant *gca* effects for dry fodder yield. Positive estimates are desirable for *gca* effects for protein content. The lines 11 A₂, ICSA 467 and ICSA 469 exhibited positive significant *gca* effects while among testers 04 K 700 and CSV 15 exhibited positive significant *gca* effects which indicated their worth as good combiner for higher protein per cent in the fodder. High general combining ability of these parents for fodder yield and yield contributing traits as well as quality characters indicated that they had favorable genes; therefore these parents could be better choices for improvement for fodder yield and yield contributing traits as well as quality characters. Combining ability is a powerful tool to select good combiners and thus selecting the appropriate parental lines for hybridization programme. In addition, the information on nature of gene action will be helpful to develop efficient crop improvement programme. General combining ability is due to additive and additive × additive gene action and is fixable in nature (Sprague and Tatum, 1942). These results are uniform with findings of Kadam *et al.* (2007); Sharma *et al.* (2007) and Kumar and Chand (2015); Kumari *et al.* (2018); Rocha *et al.* (2018); Rathod *et al.* (2019); Veldandi *et al.* (2021).

3.3 Specific combining ability (SCA) effects of parents

The estimates of general combining ability effects (*sca*) for lines (females) and testers (males) for each character are presented in the **Table 5**. Twenty four crosses had highly significant positive *sca* effects for plant height *viz.* ICSA 467 X 04 K 693, ICSA 467 X 04 K 700, ICSA 467 X 01 K 733, 11 A₂ X 01 K 733, 11 A₂ X UPMC 8, 11 A₂ X 04 K668, HB 94004 A X 04 K 693, HB 94004 A X 04 K 700, HB 94004 A X 01 K 733, SPA₂ 94012 X 04 K 693, SPA₂ 94012 X 01 K 733, SPA₂ 94012 X UPMC 8, L SPA₂ 94012 X 04 K 668, ICSA 469 X 04 K 693, ICSA 469 X UPMC 8, ICSA 271 X PC 5, ICSA 271X 04 K 693,993100 A X 04 K 700, ICSA 276 X CSV 15, ICSA 276 X 04 K 700, ICSA 293 X CSV 15, ICSA 293 X PC 5, SP 55609 A X CSV 15 and SP 55609 A X 04 K668. This indicated presence of additive and non-additive gene actions are involved in good *sca* effect.

Nine crosses exhibited highly significant positive *sca* effects for number of leaves per plant *viz.*, HB 94004 A X 04 K 693, SPA₂ 94012 X UPMC 8, ICSA 469 X UPMC 8, ICSA 271X 04 K 668,993100AXCSV15, ICSA

276 X 04 K 700 and ICSA 293 X 01 K 733 while four crosses had significant positive *sca* effects viz., ICSA 467 X PC 5, 11 A₂ X PC 5, ICSA 469 X PC 5 and ICSA 276 X CSV 15. This indicated presence of additive and non-additive gene actions are involved in good *sca* effect.

Only single cross ICSA 271 X 04 K 668 had significant positive *sca* effects for leaf length.

For leaf width seven crosses were marked with highly significant positive *sca* effects viz., ICSA 467 X PC 5, 11 A₂ X PC 5, SPA₂ 94012 X UPMC 8, ICSA 469 X 04 K 693, ICSA 469 X UPMC 8, ICSA 271 X 04 K 668 and SP 55609 A X 04 K while eight crosses had highly significant positive *sca* effects viz., 11 A₂ X 01 K 733, HB 94004 A X 01 K 733, ICSA 271 X 04 K 693, 993100 A X 04 K 700, 993100 A X 01 K 733, ICSA 276 X CSV 15, ICSA 276 X 04 K 700 and ICSA 293 X 04 K 693. Three crosses ICSA 467 X 04 K 693, 993100 A X UPMC 8 and ICSA 276 X PC 5 had significant positive *sca* effects. This indicated presence of additive and non-additive gene actions are involved in good *sca* effect.

Thirteen crosses exhibited highly significant positive *sca* effects for leaf area viz., ICSA 467 X CSV 15, ICSA 467 X PC 5, 11 A₂ X PC 5, HB 94004 A X 01 K 733, SPA₂ 94012 X CSV 15, SPA₂ 94012 X UPMC 8, SPA₂ 94012 X 04 K 668, ICSA 469 X 04 K 693, ICSA 271 X 04 K 668, 993100 A X 01 K 733, ICSA 276 X 04 K 700, ICSA 293 X 01 K 733 and SP 55609 A X 04 K 668 while four crosses had significant positive *sca* effects viz., 993100 A X CSV 15, 993100 A X 04 K 700, ICSA 276 X CSV 15 and SP 55609 A X 04 K 700. The crosses ICSA 469 X UPMC 8, ICSA 271 X 04 K 693 and SP 55609 A X 04 K 693 were also marked with significant positive *sca* effects. This indicated presence of additive and non-additive gene actions are involved in good *sca* effect.

Five crosses had highly significant positive *sca* effects for stem girth viz., 11 A₂ X PC 5, SPA₂ 94012 X UPMC 8, SPA₂ 94012 X 04 K 668, 993100 A X 04 K 700 and ICSA 293 X 01 K 733. Other eight crosses also had highly significant positive *sca* for stem girth viz. ICSA 467 X PC 5, ICSA 469 X 04 K 700, ICSA 469 X UPMC 8, ICSA 271 X 04 K 693, ICSA 271 X 04 K 668, ICSA 276 X CSV 15, ICSA 276 X 04 K 700 and SP 55609 A X 04 K 668. Three crosses ICSA 467 X CSV 15, ICSA 467 X 04 K 700, HB 94004 A X 04 K 693 also exhibited significant positive *sca* effects for stem girth. This indicated presence of additive and non-additive gene actions are involved in good *sca* effect.

For total soluble solids thirteen crosses had highly significant positive *sca* effects viz., ICSA 467 X CSV 15, ICSA 467 X 04 K 700, 11 A₂ X PC 5, 11 A₂ X 04 K 668, HB 94004 A X CSV 15, HB 94004 A X 04 K 693, ICSA 469 X 04 K 693, ICSA 469 X 04 K 668, ICSA 271 X 01 K 733, ICSA 276 X 01 K 733, ICSA 276 X UPMC 8, ICSA 293 X 04 K 700 and ICSA 293 X 01 K 733 while two crosses 993100 A X 04 K 733 and SP 55609 A X 04 K 668 exhibited significant positive *sca* effects. This indicated presence of additive and non-

additive gene actions are involved in good *sca* effect. This indicated presence of additive and non-additive gene actions are involved in good *sca* effect.

For leaf:stem ratio nine crosses exhibited highly significant positive *sca* effects viz., ICSA 467 X PC 5, 11A2XCSV15,11A2X04K693,HB 94004 A X PC 5,SPA2 94012XPC5,SPA2 94012 X 04 K 668,ICSA 271 X UPMC 8,ICSA 276 X 01 K 733andICSA 293 X 04 K 700 while other three crosses ICSA 276 X 04 K 668, ICSA 293 X 04 K 700 and SP 55609 A X 01 K 733 also hadhighlysignificantpositivescaeffects. This indicated presence of additive and non-additive gene actions are involved in good *sca* effect.

Eightcrosseshadhighlysignificantnegativescaeffects for hydrocyanic acid content viz.,11A2X04K668,SPA2 94012 XPC5,ICSA 271 X UPMC 8,ICSA 271X 04 K 668,ICSA 276 X 01 K 733, ICSA 293 X UPMC 8, SP 55609 A X CSV 15 and SP 55609 A X 04 K 693 whereas five crosses had significant negative *sca* effects viz. ICSA 467 X 04 K 700, HB 94004 A X 01 K 733, SPA₂ 94012 X 04 K 693, ICSA 271 X 01 K 733 and 993100 A X CSV 15. Crosses HB 94004 A X PC 5 and ICSA 469 X PC 5had also significant negative *sca* effects. This indicated presence of additive and non-additive gene actions are involved in good *sca* effect.

For green fodder yield sixteen crosses had highly significant positive *sca* effects viz., ICSA 467 X CSV 15, ICSA467X04K700,HB 94004 A X 04 K 700,SPA₂ 94012 X 04 K 693,SPA₂ 94012 X 04 K 700,ICSA 469 X 04 K 668,ICSA 271 X PC 5,993100 A X 04 K 700, 993100 A X 04 K 668, ICSA 276 X CSV 15,ICSA 276 X PC 5, ICSA 276 X UPMC 8, ICSA 293 X CSV 15, ICSA 293 X 01 K 733, SP 55609 A X 01 K 733 and SP 55609 A X UPMC 8 had significant positive *sca*. This indicated presence of additive and non-additive gene actions are involved in good *sca* effect.

For dry fodder yield eight crosses had highly significant positive *sca* effects viz., 11 A₂ X 04 K 693, SPA₂ 94012 X 04 K 700,ICSA 271 X PC 5,993100AX04K668,ICSA 276 X CSV 15, ICSA 293 X CSV 15, ICSA 293 X 04 K 700 and SP 55609 A X 04 K 693 whereas three crosses ICSA 467 X CSV 15, ICSA 467 X 04 K 700 and ICSA 469 X 01 K 733 had significant positive *sca* effects. The crosses ICSA 469 X 04 K 668, ICSA 276 X UPMC 8 and ICSA 293 X 01 K 733 also had significantpositivesca.This indicated presence of additive and non-additive gene actions are involved in good *sca* effect.

Sevencrosseshadhighlysignificantpositivescaeffects for protein per cent viz.,ICSA467X04K668,11A2XUPMC8,HB 94004 A X PC 5,HB 94004 A X 04 K 700,ICSA 469 X PC 5,ICSA 271 X 01 K 733andICSA 293 X UPMC 8 whereas six crosses viz. ICSA 467 X 01 K 733,ICSA467XUPMC8,ICSA 469 X CSV 15,993100AX04K693 and ICSA 293 X CSV 15, and HB 94004 A X CSV 15 had significant positive *sca* effect. This indicated presence of additive and non-additive gene

actions are involved in good *sca* effect.

The above results on *sca* effects indicated that presence of additive and non-additive gene actions are involved in good *sca* effect. The good x good, good x low, low x good, average x good, good x average and low x low general combining parents suggested various types of gene interaction such that additive x additive, additive x dominant, dominant x additive and dominant x dominant in the inheritance. Further, good specific cross combination hybrids for forage yield and component traits involving low x low general combiners parents revealed over dominance and epistasis types of gene action. These findings of the present investigation are in perfect agreement with the earlier reports of Premalatha *et al.*, (2006), Paliwal (2012) and Prabhakar *et al.*, (2013). In general, the cross involving both the parents with good *gca* values or at least parent with good *gca*, could be used both for exploitation of heterosis in F1 as well as for selection of good segregants in the later generations provided that additive genetic variance present in the good combiner and complementary epistatic effects present in the other parent/combiner act in the same direction to maximize the estimates of desirable plant attributes. Further an association between good heterotic response of the cross combinations and its corresponding high *sca* effects, indicate that the beneficial *sca* effect because of dominance while heterosis is because of epistatic variance. Specific combining ability as most important factor in determining heterosis as well as per se performance of hybrids has been reported earlier by several workers Dabholkar *et al.*, (1989), Bhadourija and Saxena (1997), Kenga *et al.*, (2004), Yadav and Pahuja (2007), Han *et al.*, (2012), Paliwal (2012), Kumar and Shrotria (2016), Chaudhari *et al.* (2017), Vekariya *et al.* (2017), Rocha *et al.* (2018), Muturi *et al.* (2019) and Rathod *et al.* (2019).

4. Summary and Conclusion

The analysis of variance for combining ability indicated highly significant differences among treatments (Crosses) and parents for all the characters under study. Variance due to testers was highly significant for leaf length and significant for leaf stem ratio. Variance due to line x tester interaction was highly significant for plant height, number of leaves per plant, leaf length, leaf width, leaf area, stem girth, TSS per cent, leaf: stem ratio, HCN content, green fodder yield, dry fodder yield and protein per cent. Among lines, the line 993100 A was good general combiner for plant height, number of leaves, leaf width, leaf area and stem girth. The line ICSA 467 was good general combiner for plant height, total soluble solids, leaf: stem ratio, hydrocyanic acid content and protein percent. The line 11 A₂ was observed good combiner for leaf length, leaf: stem ratio, green fodder yield per plot and protein percent. ICSA 469 was good general combiner for total soluble solids, hydrocyanic acid content and protein percent. The line ICSA 271 was good general combiner for leaf width, leaf area, stem girth and green fodder yield. The line ICSA 276 was good general combiner for plant height, number of leaves, leaf width, and leaf area and stem girth. The line ICSA 293 was good general combiner for

plant height, leaf width, green fodder yield, and dry fodder yield. The line SP 55609 A was good general combiner for number of leaves, leaf area, stems girth, total soluble solids, leaf: stem ratio, green fodder yield, and dry fodder yield. Among tester, the tester CSV 15 was found good general combiner for leaf: stem ratio, hydrocyanic acid content and protein percent. The tester PC-5 exhibited good general combining ability for leaf area, stem girth, total soluble solids and leaf: stem ratio. The tester 04 K 693 was found good general combiner for plant height, stem girth and number of leaves. The tester 04 K 700 was found good general combiner for plant height, stem girth and number of leaves, total soluble solids, dry fodder yield and protein percent. The tester 04 K 668 was found good general combiner for plant height, green fodder yield, and dry fodder yield. The results of present study clearly states that parents are having good general combining ability for different yield related and quality traits and crosses also exhibited good specific combining ability for different yield related and quality traits. From present study we can conclude that parents having good general combining ability and crosses having good specific combining ability can be used in our crop improvement programme.

5. References

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7. Tables: In next page

Table 1: Analysis of variance for combining ability analysis in line x tester for yield related and quality traits.

Source of Variation	df	Plant Height (cm)	Number of Leaves	Leaf Length (cm)	Leaf Width (cm)	Leaf Area (cm ²)	Stem Girth (cm)
Replicates	2.00	18.16	0.06	45.98	0.02	15.05	0.01
Crosses	69.00	2950.27* *	2.72**	87.32**	1.11**	5409.38**	0.06* *
Line Effect	9.00	5702.24*	8.10**	110.22*	3.11**	7767.67	0.09
Tester Effect	6.00	3823.67	3.40	359.26**	0.81	8156.67	0.05
Line X Tester Effect	54.00	2394.57* *	1.75**	53.29**	0.81**	4711.07**	0.05* *
Error	138.00	18.78	0.25	27.71	0.05	378.48	0.00
Total	209.00	986.59	1.06	47.56	0.40	2035.92	0.02

Continued..

Source of Variation	df	TSS (%)	Leaf:stem Ratio	HCN (ppm)	Green Fodder Yield (Kg)	Dry Fodder Yield (Kg)	Protein
Replicates	2.00	0.20	0.01	23.59	0.35	0.04	0.29
Crosses	69.00	7.98**	0.01**	560.50**	6.81**	0.30**	1.47**
Line Effect	9.00	6.78	0.02**	972.40	4.92	0.32	3.01*
Tester Effect	6.00	8.12	0.01*	420.09	4.27	0.22	0.89
Line X Tester Effect	54.00	8.17**	0.01**	507.45**	7.40**	0.31**	1.28**
Error	138.00	0.49	0.02	60.45	0.46	0.03	0.13
Total	209.00	2.96	0.01	225.19	2.56	0.12	0.58

* Significant at 5% level of probability, ** Significant at 1% level of probability

Table 2: General combining ability effects of lines and testers for yield related and quality traits.

	Plant Height (cm)	No. of Leaves	Leaf Length (cm)	Leaf Width (cm)	Leaf Area (cm ²)	Stem Girth (cm)
Lines						
ICSA 467	4.92**	0.17	1.05	-0.29**	-5.34	-0.04*
11A2	-20.51**	-0.61**	4.78**	-0.63**	-14.85**	-0.08**
HB94004 A	-16.21**	0.14	-0.47**	-0.23**	-33.48**	-0.09**
SPA2 94012	-14.60**	-1.01**	0.18	-0.48**	-23.82**	-0.05**
ICSA469	-12.58**	-0.66**	0.58	0.18**	4.97	-0.02
ICSA271	7.40**	0.17	-3.60**	0.52**	17.36**	0.04*
993100A	27.27**	0.49**	1.10	0.42**	22.75**	0.07**
ICSA276	8.86**	1.50**	-0.07	0.26**	16.75**	0.10**
ICSA293	21.30**	-0.18	-2.84*	0.15**	-0.77	0.02
SP 55609A	-5.17**	0.52**	-0.71	0.09	16.40**	0.06**
SE (gi)	0.966	0.107	1.361	0.054	4.252	0.014
SE (gi-gj)	1.366	0.151	1.925	0.077	6.013	0.020
CD 95% GCA(Line)	1.91	0.21	2.69	0.11	8.41	0.03
Testers						
CSV15	-16.42**	-0.13	-0.38	-0.14**	-2.27	-0.05**
PC5	-4.18**	-0.48**	7.21**	-0.07	34.17**	0.04**
04K693	12.00**	0.59**	-3.59**	0.35**	6.95	0.03**
04K700	16.01**	0.69**	-1.76	-0.04	-12.09**	0.04**
01K733	-3.50**	-0.49**	-1.69	0.02	-4.78	-0.07**
UPMC8	-6.34**	0.16	0.74	0.00	-10.80**	-0.01
04K668	3.02**	-0.01	-0.53	-0.11*	-11.18**	0.01
SE (gt)	0.808	0.089	1.139	0.045	3.557	0.011
SE (gi-gj)	1.143	0.127	1.610	0.065	5.031	0.016
CD 95% GCA(Tester)	1.60	0.18	2.25	0.09	7.04	0.02

Continued..

	TSS (%)	Leaf:stem Ratio	HCN (ppm)	Green Fodder Yield (kg)	Dry Fodder Yield (kg)	Protein %
Lines						
ICSA 467	0.52**	0.03**	-6.22**	-0.40**	-0.13**	0.42**
11A2	-1.22**	0.04**	3.23	0.36*	0.00	0.65**
HB94004 A	-0.40*	0.01*	-10.71**	-0.84**	-0.18**	-0.15
SPA2 94012	0.57**	-0.01*	3.88	-0.33*	-0.09*	-0.18
ICSA469	0.43**	0.01*	-10.63**	0.01	-0.01	0.25**
ICSA271	-0.52**	-0.01	-0.06	0.54**	0.03	0.02
993100A	0.07	-0.05**	8.84**	-0.39**	-0.03	-0.18*
ICSA276	0.05	-0.04**	4.49*	0.08	0.01	-0.13
ICSA293	0.05	-0.02**	4.25*	0.67**	0.19**	0.02
SP 55609A	0.45**	0.03**	3.74*	0.32*	0.21**	-0.72**
SE (gi)	0.161	0.004	1.890	0.144	0.037	0.090
SE (gi-gj)	0.022	0.006	2.672	0.203	0.052	0.127
CD 95% GCA(Line)	0.32	0.01	3.74	0.29	0.07	0.18
Testers						
CSV15	-0.10	0.03**	-4.51**	-0.36**	-0.08**	0.16*
PC5	0.61**	0.03**	5.81**	0.18	0.01	-0.03
04K693	0.26	-0.01**	0.46	-0.49**	-0.08**	-0.18*
04K700	0.51**	-0.01**	1.39	0.56**	0.15**	0.26**
01K733	-0.29*	-0.01*	-5.00**	-0.09	-0.05	0.01
UPMC8	-0.09	0.01	0.23	-0.14	-0.01	0.01
04K668	-0.91**	-0.02**	1.64	0.34**	0.06*	-0.23**
SE (gt)	0.135	0.003	1.581	0.120	0.031	0.075
SE (gi-gj)	0.141	0.005	2.236	0.107	0.043	0.106
CD 95% GCA(Tester)	0.27	0.01	3.13	0.24	0.06	0.15

* Significant at 5% level of probability, ** Significant at 1% level of probability

Table 3: Summary of table for general combining ability of parents for different characters in different years.

Parents	PH	NL	LL	LW	LA	SG	TSS	L:S	HCN	GFY	DFY	PP
ICSA 467	G	A	A	L	L	L	G	G	G	L	L	G
11A2	L	L	G	L	L	L	L	G	L	G	L	G
HB94004 A	L	A	L	L	L	L	L	G	G	L	L	L
SPA2 94012	L	L	A	L	L	L	G	L	L	L	L	L
ICSA469	L	L	A	G	A	L	G	A	G	A	L	G
ICSA271	G	A	L	G	G	G	L	L	A	G	L	L
993100A	G	G	A	G	G	G	A	L	L	L	L	L
ICSA276	G	G	L	G	G	G	A	L	L	A	L	L
ICSA293	G	L	L	G	L	A	A	L	L	G	G	L
SP 55609A	L	G	L	A	G	G	G	G	L	G	G	L
CSV15	L	L	L	L	L	L	L	G	G	L	L	G
PC5	L	L	G	L	G	G	G	G	L	A	L	L
04K693	G	G	L	G	A	G	A	L	L	L	L	L
04K700	G	G	L	L	L	G	G	L	L	G	G	G
01K733	L	L	L	L	L	L	L	L	G	L	L	L
UPMC8	L	A	L	L	L	L	L	L	L	L	L	L
04K668	G	L	L	L	L	L	L	L	L	G	G	L

*PH= Plant Height, NL= Number of Leaves, LL= Leaf Length, LW= Leaf Width, LA= Leaf Area, SG= Stem Girth, TSS= Total Soluble Solids, L:S= Leaf: Stem Ratio, HCN= Hydrocyanic Acid Content, GFY= Green Fodder Yield, DFY= Dry Fodder Yield, PP= Protein %

Table 4: Best general combiners among parental lines for 12 characters in 2017-18 (Y₁), 2018-19 (Y₂) and pooled over year (P).

Characters		
	Genotype	<i>gca</i> value
Plant height (cm)	993100A,	27.27**
	ICSA293	21.30**
	ICSA276	8.86**
No. of leaves	ICSA 276	1.05**
	SP55609A	0.52**
Leaf length (cm)	11A2	4.78**
Leaf width (cm)	ICSA271	0.52**
	993100 A	0.42**
Leaf area (cm ²)	993100A	22.75**
	ICSA271	17.36**
Stem girth(cm)	ICSA276	0.10**
	993100A	0.07**
TSS (%)	SPA2 94012	0.57**
	ICSA 467	0.52**
Leaf:Stem Ratio	11A2	0.04**
	ICSA 467	0.03**
HCN (ppm)	ICSA 469	-10.63**
	HB 94004 A	-10.71**

Green Fodder Yield (Kg)	ICSA293	0.67**
	ICSA271	0.54**
Dry Fodder Yield (Kg)	SP 55609 A	0.21**
	ICSA 293	0.19**
Protein per cent	11 A2	0.65**
	ICSA 467	0.42**

Table 5: Specific combining ability for different yield related and quality traits.

SI. No.	Cross	PH	NL	LL	LW	LA	SG
L ₁ X T ₁	ICSA 467 XCSV15	-13.23**	0.57 *	0.33	0.39 **	32.64 **	0.08 *
L ₁ X T ₂	ICSA 467 XPC5	1.93	0.91 **	1.70	0.65 **	84.29 **	0.13 **
L ₁ X T ₃	ICSA 467 X04K693	26.41 **	-0.42	0.37	0.29 *	5.60	-0.04
L ₁ X T ₄	ICSA 467 X04K700	14.61 **	-0.29	-0.29	-0.12	-21.36	0.08 *
L ₁ X T ₅	ICSA 467 X01K733	35.11 **	0.10	0.54	0.05	-11.72	0.05
L ₁ X T ₆	ICSA 467 XUPMC8	-62.71**	-0.56	-3.73	-0.69**	-50.97**	-0.12**
L ₁ X T ₇	ICSA 467 X04K668	-2.14	-0.32	1.08	-0.58**	-38.49**	-0.18**
L ₂ X T ₁	11A2 XCSV15	-47.34**	-0.81**	5.97	-0.37*	-25.14*	-0.08*
L ₂ X T ₂	11A2 XPC5	-6.10*	0.73 *	1.27	0.79 **	51.14 **	0.26 **
L ₂ X T ₃	11A2 X04K693	-15.89**	0.00	-0.89	-0.37*	-31.47**	-0.09*
L ₂ X T ₄	11A2 X04K700	-5.69*	-0.64 *	-7.72*	-0.14	-34.97**	-0.13**
L ₂ X T ₅	11A2 X01K733	37.14 **	-0.01	-1.83	0.56 **	12.35	-0.04
L ₂ X T ₆	11A2 XUPMC8	30.66 **	0.22	2.94	-0.11	12.91	0.02
L ₂ X T ₇	11A2 X04K668	7.22 **	0.53	0.25	-0.34*	15.17	0.07
L ₃ X T ₁	HB94004 A XCSV15	-18.24**	-0.06	-3.19	0.10	-15.58	-0.03
L ₃ X T ₂	HB94004 A XPC5	-18.94**	-0.09	4.28	-0.81**	-21.47	0.03
L ₃ X T ₃	HB94004 A X04K693	13.61 **	1.55 **	2.59	-0.26	2.55	0.08 *

L ₃ X T ₄	HB94004 A X04K700	15.40 **	0.28	-3.67	0.19	6.84	-0.14**
L ₃ X T ₅	HB94004 A X01K733	32.91 **	-0.16	-2.02	0.60 **	40.99 **	0.17 **
L ₃ X T ₆	HB94004 A XUPMC8	-7.31**	-1.16**	1.75	0.02	20.08	-0.10**
L ₃ X T ₇	HB94004 A X04K668	-17.41**	-0.36	0.26	0.16	-33.40**	-0.01
L ₄ X T ₁	SPA2 94012 XCSV15	-34.38**	-0.79**	-2.07	0.11	44.83 **	-0.15**
L ₄ X T ₂	SPA2 94012 XPC5	-33.28**	-0.51	3.74	-0.20	-18.70	0.03
L ₄ X T ₃	SPA2 94012 X04K693	18.13 **	-0.74**	-0.86	-0.45**	-25.58*	-0.09*
L ₄ X T ₄	SPA2 94012 X04K700	-15.87**	0.39	-0.95	-0.33*	-41.32**	-0.11**
L ₄ X T ₅	SPA2 94012 X01K733	12.63 **	0.18	-4.23	-0.29*	-44.72**	-0.13**
L ₄ X T ₆	SPA2 94012 XUPMC8	46.01 **	1.62 **	1.51	0.87 **	54.96 **	0.23 **
L ₄ X T ₇	SPA2 94012 X04K668	6.78 **	-0.15	2.85	0.27	30.54 **	0.21 **
L ₅ X T ₁	ICSA469 XCSV15	-15.54**	-0.47	1.66	-0.05	10.06	0.06
L ₅ X T ₂	ICSA469 XPC5	-7.97**	0.81 **	-0.50	0.01	13.70	-0.01
L ₅ X T ₃	ICSA469 X04K693	25.84 **	-0.36	2.94	0.66 **	54.93 **	0.00
L ₅ X T ₄	ICSA469 X04K700	1.97	0.07	0.78	0.11	1.79	0.17 **
L ₅ X T ₅	ICSA469 X01K733	-23.86**	-0.70*	-0.20	-1.15**	-67.95**	-0.12**
L ₅ X T ₆	ICSA469 XUPMC8	14.86 **	1.20 **	0.71	0.68 **	22.18	0.12 **
L ₅ X T ₇	ICSA469 X04K668	4.69	-0.56	-5.39	-0.25	-34.70**	-0.21 **
L ₆ X T ₁	ICSA271 XCSV15	0.42	-0.17	0.21	-0.52**	-40.23**	-0.08*
L ₆ X T ₂	ICSA271 XPC5	42.78 **	-1.06**	2.48	0.01	12.07	0.02
L ₆ X T ₃	ICSA271 X04K693	5.93 *	-0.16	1.22	0.49 **	28.88 *	0.15 **
L ₆ X T ₄	ICSA271 X04K700	-18.87**	-0.13	1.16	0.01	2.76	-0.04
L ₆ X T ₅	ICSA271 X01K733	-8.57**	-0.03	-3.22	0.18	-13.76	-0.14**
L ₆ X T ₆	ICSA271 XUPMC8	-25.86**	0.17	-9.68**	-0.96**	-70.88**	-0.04
L ₆ X T ₇	ICSA271 X04K668	4.18	1.37 **	7.83 *	0.78 **	81.16 **	0.13 **
L ₇ X T ₁	993100A XCSV15	-0.38	1.32 **	2.01	0.18	25.58 *	0.02
L ₇ X T ₂	993100A XPC5	2.18	-0.20	-0.15	-0.60**	-47.97**	-0.21**
L ₇ X T ₃	993100A X04K693	-10.00**	-1.13**	4.39	-0.48**	-8.91	-0.03
L ₇ X T ₄	993100A X04K700	32.19 **	-0.47	-5.11	0.57 **	25.79 *	0.26 **
L ₇ X T ₅	993100A X01K733	-18.84**	0.32	3.25	0.44 **	51.81 **	0.03
L ₇ X T ₆	993100A XUPMC8	-0.06	-0.21	2.09	0.34 *	-7.31	-0.07
L ₇ X T ₇	993100A X04K668	-5.09*	0.36	-6.47	-0.46**	-38.98**	-0.01
L ₈ X T ₁	ICSA276 XCSV15	64.89 **	0.76 **	-2.26	0.57 **	24.12 *	0.17 **
L ₈ X T ₂	ICSA276 XPC5	-9.67**	0.04	-4.15	0.30 *	-14.55	-0.14**
L ₈ X T ₃	ICSA276 X04K693	-0.99	0.44	-5.61	-0.59**	-65.59**	0.00
L ₈ X T ₄	ICSA276 X04K700	20.67 **	1.07 **	4.06	0.50 **	52.43 **	0.12 **
L ₈ X T ₅	ICSA276 X01K733	-40.09**	-0.91**	5.25	-0.43**	7.74	-0.10**
L ₈ X T ₆	ICSA276 XUPMC8	1.35	-1.10**	0.09	0.20	18.20	0.07
L ₈ X T ₇	ICSA276 X04K668	-36.15**	-0.30	2.63	-0.56**	-22.36*	-0.11 **
L ₉ X T ₁	ICSA293 XCSV15	52.12 **	-1.18**	-6.92	0.15	-15.04	0.00
L ₉ X T ₂	ICSA293 XPC5	33.09 **	-0.53	-7.48*	-0.16	-54.72**	-0.11 **
L ₉ X T ₃	ICSA293 X04K693	-47.17**	0.57 *	-3.71	0.49 **	21.07	0.04
L ₉ X T ₄	ICSA293 X04K700	-45.04**	0.36	7.10	-0.75**	-16.23	-0.15**
L ₉ X T ₅	ICSA293 X01K733	-2.33	1.39 **	6.65	0.18	46.85 **	0.27 **
L ₉ X T ₆	ICSA293 XUPMC8	4.85	-0.27	3.52	-0.16	9.91	-0.03
L ₉ X T ₇	ICSA293 X04K668	4.48	-0.34	0.83	0.25	8.16	-0.02
L ₁₀ X T ₁	SP 55609A XCSV15	11.69 **	0.82 **	4.26	-0.56**	-41.24**	0.01
L ₁₀ X T ₂	SP 55609A XPC5	-4.01	-0.10	-1.20	0.00	-3.80	0.00
L ₁₀ X T ₃	SP 55609A X04K693	-15.87**	0.26	-0.43	0.22	18.53	-0.02

L₁₀ X T₄	SP 55609A X04K700	0.63	-0.64*	4.64	-0.06	24.27 *	-0.05
L₁₀ X T₅	SP 55609A X01K733	-24.10**	-0.18	-4.20	-0.16	-21.58	0.02
L₁₀ X T₆	SP 55609A XUPMC8	-1.79	0.09	0.80	-0.20	-9.08	-0.09*
L₁₀ X T₇	SP 55609A X04K668	33.45 **	-0.24	-3.86	0.74 **	32.89 **	0.12 **
	CD 95% SCA	5.06	0.56	7.12	0.29	22.25	0.07

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SI. No.	Cross	TSS	L:S	HCN	GFY	DFY	PP
L₁ X T₁	ICSA 467 XCSV15	2.00**	-0.02	15.66 **	1.07 **	0.20 *	-1.12**
L₁ X T₂	ICSA 467 XPC5	0.29	0.07**	-3.62	-1.30 **	-0.21*	-0.88**
L₁ X T₃	ICSA 467 X04K693	0.81	-0.02	2.07	-0.71	-0.08	0.45
L₁ X T₄	ICSA 467 X04K700	2.39**	-0.03**	-11.87*	1.07 **	0.20 *	-0.18
L₁ X T₅	ICSA 467 X01K733	-3.31**	-0.02	0.22	-0.36	-0.04	0.49 *
L₁ X T₆	ICSA 467 XUPMC8	-0.01	0.01	-8.93	-0.25	-0.10	0.60 *
L₁ X T₇	ICSA 467 X04K668	-2.19**	0.02	6.46	0.48	0.04	0.65 **
L₂ X T₁	11A2 XCSV15	-0.26	0.11**	-3.00	-1.86 **	-0.33**	-0.18
L₂ X T₂	11A2 XPC5	2.03**	-0.07**	-6.13	-1.40 **	-0.20*	-0.88**
L₂ X T₃	11A2 X04K693	-3.12**	0.03*	6.17	2.52 **	0.45 **	0.28
L₂ X T₄	11A2 X04K700	-0.37	-0.01	16.26 **	0.39	0.11	0.05
L₂ X T₅	11A2 X01K733	-0.07	-0.04**	-2.25	-0.63	-0.09	0.03
L₂ X T₆	11A2 XUPMC8	-0.27	0.01	9.14	0.19	-0.05	0.73 **
L₂ X T₇	11A2 X04K668	2.05 **	-0.03*	-20.21**	0.78 *	0.11	-0.04

L ₃ X T ₁	HB94004 A XCSV15	1.99 **	0.02	-2.08	0.44	0.08	0.48 *
L ₃ X T ₂	HB94004 A XPC5	0.88 *	0.05 **	-13.02*	0.14	0.01	0.81 **
L ₃ X T ₃	HB94004 A X04K693	1.56 **	0.00	9.99 *	0.14	-0.01	-0.42
L ₃ X T ₄	HB94004 A X04K700	-0.52	-0.01	-7.67	1.09 **	0.15	1.52 **
L ₃ X T ₅	HB94004 A X01K733	-1.89**	-0.04**	-11.13*	-0.51	-0.19	-1.11**
L ₃ X T ₆	HB94004 A XUPMC8	-1.09*	-0.01	21.59 **	-0.37	0.17	-1.30**
L ₃ X T ₇	HB94004 A X04K668	-0.94*	-0.01	2.32	-0.93 *	-0.21*	0.01
L ₄ X T ₁	SPA2 94012 XCSV15	1.96 **	-0.02	-0.55	-0.17	-0.04	0.05
L ₄ X T ₂	SPA2 94012 XPC5	-1.75**	0.05 **	-15.64**	-2.54 **	-0.47**	-0.02
L ₄ X T ₃	SPA2 94012 X04K693	0.43	-0.01	-10.31*	1.13 **	0.07	-0.79**
L ₄ X T ₄	SPA2 94012 X04K700	-0.49	0.01	-0.37	1.50 **	0.34 **	-0.25
L ₄ X T ₅	SPA2 94012 X01K733	0.15	0.01	-6.26	0.07	0.05	0.36
L ₄ X T ₆	SPA2 94012 XUPMC8	-0.05	-0.08**	5.65	-0.05	0.11	0.24
L ₄ X T ₇	SPA2 94012 X04K668	-0.24	0.04 **	27.49 **	0.06	-0.05	0.42
L ₅ X T ₁	ICSA469 XCSV15	-0.73	0.01	-0.93	-0.12	0.02	0.54 *
L ₅ X T ₂	ICSA469 XPC5	0.22	0.00	-12.07*	-1.08 **	-0.16	1.28 **
L ₅ X T ₃	ICSA469 X04K693	1.41 **	-0.03*	-6.01	-0.44	-0.08	-0.27
L ₅ X T ₄	ICSA469 X04K700	-3.34**	0.02	3.95	-0.59	-0.19	0.14
L ₅ X T ₅	ICSA469 X01K733	-0.71	0.01	7.98	0.73	0.20 *	0.08
L ₅ X T ₆	ICSA469 XUPMC8	0.26	0.00	13.48 **	-0.22	-0.04	-0.80**
L ₅ X T ₇	ICSA469 X04K668	2.91 **	-0.01	-6.39	1.72 **	0.25 *	-0.97**
L ₆ X T ₁	ICSA271 XCSV15	-1.95**	0.01	6.50	-1.03 **	-0.15	-0.07
L ₆ X T ₂	ICSA271 XPC5	-1.83**	0.01	20.25 **	5.18 **	1.02 **	-0.42
L ₆ X T ₃	ICSA271 X04K693	0.69	-0.04**	24.76 **	0.10	0.07	-0.27
L ₆ X T ₄	ICSA271 X04K700	0.44	-0.02	-5.95	-0.87 *	-0.31**	-0.55*
L ₆ X T ₅	ICSA271 X01K733	2.74 **	-0.03*	-11.95*	-1.72 **	-0.36**	1.05 **
L ₆ X T ₆	ICSA271 XUPMC8	0.04	0.08 **	-14.75**	-0.75	-0.10	0.15
L ₆ X T ₇	ICSA271 X04K668	-0.14	-0.01	-18.87**	-0.90 *	-0.17	0.11
L ₇ X T ₁	993100A XCSV15	-0.71	0.01	-11.05*	-2.27 **	-0.48**	0.12
L ₇ X T ₂	993100A XPC5	-0.25	-0.01	11.95 *	0.35	0.11	0.19
L ₇ X T ₃	993100A X04K693	0.76	0.00	-6.07	-1.64 **	-0.35**	0.58 *
L ₇ X T ₄	993100A X04K700	0.85 *	-0.01	-4.84	1.31 **	0.14	0.17
L ₇ X T ₅	993100A X01K733	-0.35	0.01	22.61 **	-0.21	0.00	-0.75**
L ₇ X T ₆	993100A XUPMC8	0.45	0.00	-5.37	-0.24	-0.12	-0.50*
L ₇ X T ₇	993100A X04K668	-0.74	0.00	-7.24	2.70 **	0.70 **	0.18
L ₈ X T ₁	ICSA276 XCSV15	-1.52**	-0.08**	17.08 **	3.67 **	0.68 **	-0.50*
L ₈ X T ₂	ICSA276 XPC5	-0.73	-0.04**	2.33	1.21 **	0.26 **	0.20
L ₈ X T ₃	ICSA276 X04K693	-0.88*	0.02	-1.53	-1.79 **	-0.37**	0.25
L ₈ X T ₄	ICSA276 X04K700	0.37	-0.01	10.08 *	-3.50 **	-0.71 **	-0.39
L ₈ X T ₅	ICSA276 X01K733	2.00 **	0.06 **	-16.74**	0.15	0.09	0.10
L ₈ X T ₆	ICSA276 XUPMC8	1.47 **	0.01	-9.19	1.12 **	0.21 *	0.18
L ₈ X T ₇	ICSA276 X04K668	-0.71	0.04 **	-2.03	-0.86 *	-0.16	0.17
L ₉ X T ₁	ICSA293 XCSV15	-0.85*	-0.04**	-5.47	1.33 **	0.31 **	0.55 *
L ₉ X T ₂	ICSA293 XPC5	0.77	-0.05**	15.73 **	-0.21	-0.06	-0.40
L ₉ X T ₃	ICSA293 X04K693	-2.38**	0.04 **	0.37	-0.29	-0.13	0.27
L ₉ X T ₄	ICSA293 X04K700	1.87 **	0.08 **	-2.44	0.00	0.33 **	-0.62*
L ₉ X T ₅	ICSA293 X01K733	3.17 **	0.01	6.42	1.40 **	0.22 *	-0.57*
L ₉ X T ₆	ICSA293 XUPMC8	-1.53**	-0.02	-13.36**	-0.88 *	-0.27**	1.33 **
L ₉ X T ₇	ICSA293 X04K668	-1.05*	-0.02	-1.26	-1.36 **	-0.38**	-0.56*
L ₁₀ X T ₁	SP 55609A XCSV15	0.08	0.00	-16.17**	-1.07 **	-0.29**	0.13

L₁₀ X T₂	SP 55609A XPC5	0.37	-0.02	0.21	-0.36	-0.28**	0.11
L₁₀ X T₃	SP 55609A X04K693	0.72	0.01	-19.44**	0.98 *	0.43 **	-0.07
L₁₀ X T₄	SP 55609A X04K700	-1.20**	-0.02	2.87	-0.41	-0.04	0.11
L₁₀ X T₅	SP 55609A X01K733	-1.73**	0.04 **	11.08 *	1.08 **	0.13	0.31
L₁₀ X T₆	SP 55609A XUPMC8	0.73	0.00	1.72	1.46 **	0.18	-0.63**
L₁₀ X T₇	SP 55609A X04K668	1.05 *	-0.02	19.74 **	-1.68 **	-0.13	0.03
	CD 95% SCA	0.84	0.02	9.89	0.75	0.19	0.47

* Significant at 5% level of probability, ** Significant at 1% level of probability

***PH**= Plant Height, **NL**= Number of Leaves, **LL**= Leaf Length, **LW**= Leaf Width, **LA**= Leaf Area, **SG**= Stem Girth, **TSS**= Total Soluble Solids, **L:S**= Leaf: Stem Ratio, **HCN**= Hydrocyanic Acid Content, **GFY**= Green Fodder Yield, **DFY**= Dry Fodder Yield, **PP**= Protein %