Original Research Article

SOURCE-SINK RELATIONSIONSHIP STUDIES IN MULTICAPSULE GENOTYPES OF SESAME

Abstract

A study was conducted to determine the source and sink relationship in multicapsule genotypes of sesame. Thirty-six multicapsule genotypes along with two single capsule genotypes as checks were used in this study. Data on source characters such as number of leaf axils, leaf area, SPAD chlorophyll, photosynthetic rate, plant height, stem girth was recorded at capsule formation stage. Similarly, data on sink related characters such as number of flowers per axil, number of capsules per axil, capsule length, breadth, seed weight, seed yield per plant, and oil content were recorded. There were 1 to 3 capsules per axil, genotypes, SC-500-1, PI-154298, JCS-1020, exhibited 3 capsules at every axil. The results indicated the source characters such as number of leaf axils per plant was significantly positively correlated with seed yield per plant, leaf area was significantly positively correlated with number of flowers per main stem, total capsule number per main stem and seed weight of the right capsule in the bunch of the capsules. SPAD chlorophyll was positively associated with, number of flowers per axil, number of capsules per axil and seed yield per plant. Photosynthetic rate was significantly associated with total number of capsules per main stem of the plant, oil content and test weight. There were 7 principal components which explained 80 of the variation presents in the genotypes. Characters such as number of flowers per axil, number of leaf axils per plant, number of capsules per axil in the main stem and capsule length, weight, seed weight of left and right capsules contributed for the variation. Variation in these characters distributed the genotypes across the axis in the PCA biplot. Genotypes such as SC-500, PI-154298 exhibited high capsules number per plant, capsules per axil, capsule length and capsule seed weight. This study indicated that the genotypes showing more than 1 capsules per axil have high leaf area, stem girth. These genotypes are potential source for utilization in yield improvement programmes.

INTRODUCTION

Sesame (*Sesamum indicum* L., 2n=26) is a major oil seed crop worldwide, with more than 96% of seed production accounted for by Africa and Asia (FAOSTAT, 2020). Sesame also known as Til or Gingelly, is one of the most important oilseed crop of tropical and temperate regions. Sesame is being cultivated and consumed in India since time immemorial for its the seeds have high nutritional value, due to protein quality and oil, and are also an important source of anti-oxidants compounds, like sesamol and sesamolin, both with anti-hypertensive and anti-cancerous properties (Dar *et al*. 2015). At present, Myanmar is the largest producer of sesame seeds in the world followed by India, China, Turkey, and Pakistan in Asia. In India, during 2020-21, sesame has been cultivated in an area of 17.50 lakh ha with a production of 9.58 lakh tones annually and productivity of 478 kg/ha. Being the fourth most important oilseeds crop in Indian agriculture, it is widely cultivated in the states of Uttar Pradesh, Rajasthan, Orissa, Gujarat, Andhra Pradesh, Tamil Nadu, Karnataka,

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West Bengal, Bihar, and Assam. In Telangana state, the crop is grown to an extent of 3899.4 ha with a total production of 7.62 lakh tonnes and productivity of 4.16 kg ha^{-1}. It is mainly grown in Jagtial, Nirmal, Warangal and Nizamabad districts of Telangana state (agri.telangana.gov.in, 2021). In sesame, flowers are produced in the leaf axils and later develop into capsules. Maximum number of flowers found at the leaf axil is 3, but all 3 flower may or may not form into capsules at an axil. However, genotypes from China, Israel~~real~~, Turkey have 3 capsules per leaf axil at each leaf axil over the length of the main stem. These genotypes ~~are~~ mostly have single stem with any branches. Indian genotypes have large extant of variation for capsule number per axil. Maximum number of capsules per leaf axil is 3 but may not be uniform at all the leaf axil along the length of the plant due to environmental variation linked to nutrition of the plant. Theoretically, a greater number of capsules/leaf axils per plant would result in a higher seed yield. The character association studies in multicapsule genotypes of sesame are pivotal for understanding the genetic basis underlying this trait's variability. Such studies not only shed light on the complex interactions among different characteristics of the plant but also aid in the development of improved cultivars with superior capsule attributes. By identifying the correlations between capsule number and other source-sink significant traits, we can unravel the genetic factors responsible for enhanced seed production and formulate targeted breeding strategies. The correlation coefficient analysis indicated that plant height, number of branches, number of capsules per plant and 1000 seed weight had the significant positive effect on seed yield (Yol *et al*.2010). One of the approaches to increase the number of capsules is by promoting additional capsules at each axil. The number of capsules at each node (2 leaf axil in each node) may vary from two to six (Morris 2009). Genotypes bearing a greater number of capsules at each axil have a yield advantage compared to genotypes with single capsules. Cultivated varieties in China, Korea, and elsewhere are predominated by multi capsules at each leaf axils on single stem plants (Morris 2009). Genotypes with additional capsules per leaf axil are needed since theoretically, plants bearing more than one capsule at each axil will add a greater number of capsules per plant than one capsule in each leaf axil, which consequently would result in more seed yield. Yield is the end product of multiplicative interaction between various yield components and source characters such as leaf number, leaf area, SPAD chlorophyll content, photosynthetic rate and stem girth. This necessitates a thorough understanding of character association by each character on seed yield. This research paper aims to comprehensively investigate source characters of multicapsule genotypes of sesame, unraveling the character associations that can influence yield. The knowledge generated through this study will not only enhance our understanding of sesame genetics but also pave the way for the development of high-yielding, resilient cultivars that can meet the growing demands of the global sesame industry, ensuring food security and economic prosperity for regions dependent on this remarkable crop. With this background, the present study was taken up with the main objective to analyze the character association analysis for seed yield and its related traits in a collection of 36 genotypes through correlations, path coefficient analysis and principal component analysis.

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MATERIALS AND METHODS

Experimental site:

The experiment was carried out at ICAR-Indian Institute of Oilseeds Research, Narkhoda farm, Hyderabad during summer, 2023 which is situated at a scope of 17^{0} 15^{l} 30. 1608^{ll} N longitude, 78^{0} 19^{l} 11. 1324^{ll} E and altitude 569 meters above sea level.

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Experimental Materials and Design:

The experimental material consisted of 36 sesame genotypes including four checks that were collected from ICAR-Indian Institute of Oilseeds Research (IIOR). The trial was laid out in Randomized Block Design (RBD) with three replications. Seeds of each genotype was sown in rows by hand on a separate plot size of 6.75 m2 (2 rows x 5m row length x 45cm between rows and 15cm between plants within rows). Other cultural practices were followed as recommended for the area and fertilizers are applied at the rate of 30:30:20 NPK (kg/ha).

Data Collection:

The source characters which help in indirect estimation of photosynthates are number of leaf axils per plant, leaf area, SPAD chlorophyll, photosynthates assimilation rate, stem girth and plant height. Five plants per plot were randomly selected and labelled to record the values of the all the traits during capsule formation stage (approximately 50 days after sowing). Write the abbreviations and expansion used the paper

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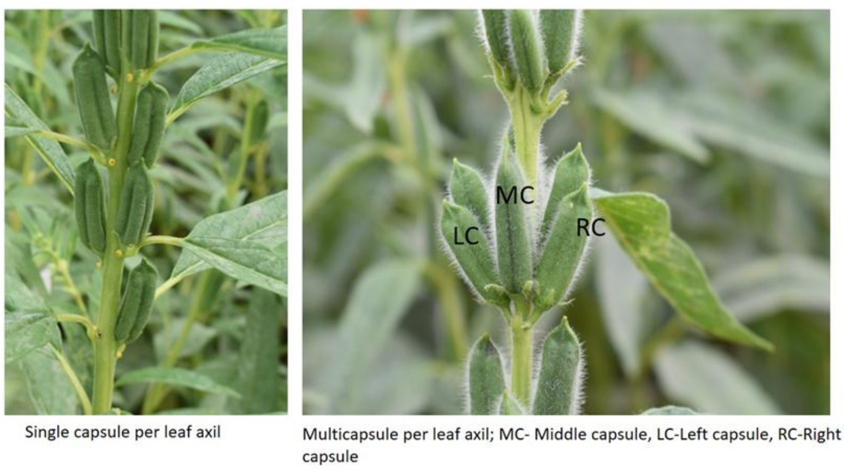
Sink characters such as number of flowers per axil, number of capsules per axil, total number of capsules per plant in the main stem, capsule length, breadth, and seed weight per capsule of middle capsule and adjacent capsules of multicapsule bunch at axil (Fig 1.) were recorded for main stem from the randomly selected plants. Seeds yield per plant was recorded by harvesting 5 selected plants and harvest index, oil content and test weight were estimated. Phenological traits such as days to flowering, days to maturity were recorded over the plot by observation.



Single capsule per leaf axil

Multicapsule per leaf axil; MC- Middle capsule, LC-Left capsule, RC-Right capsule

Figure 1: Pictorial representation of genotypes with single capsules per axil, genotypes with multicapsules per axil, middle caspsule at the node (MC), left capsule at the node (LC) and right capsule at the node (RC)

Data Analysis

Correlation Analysis

Estimation of the phenotypic and genotypic correlation coefficients were computed following the procedures suggested by Falconer (1981) from corresponding variance and covariance components. The significance of phenotypic correlation coefficients was tested by comparison of estimated values with the tables of correlation coefficients (Fisher and Yates, 1963) at 5 per cent and 1 per cent level of significance with n-2 degrees of freedom where ‘n’ is the number of genotypes used in the experiment.

Principal Component Analysis

The principal component analysis (PCA) was carried out according to Banfield's approach (1978). Principal component analysis (PCA) was used to find out the characters, which accounted more to the total variation. The eigen values and eigen vectors were computed from data matrix. Eigen values define the amount of total variation that is displayed on principal components. The proportion of variation accounted for each principal component (PC) is expressed as the eigen value divided by the sum of the eigen values.

RESULTS AND DISCUSSION:

Correlation Analysis

Correlation between the source- sink characters were studied using Pearson’s correlation coefficient (Table 1.). Number of leaf axils per plant (NLAMS) are the major source for production of photosynthates which gets accumulated in the capsules formed at that axil. A significant positive association was found between NLAMS and seed yield per plant. Higher the number of leaves per plant resulted in higher seed yield per plant. However, NLAMS was negatively but significantly associated with capsule length, breadth and capsule seed weight. Leaf area was significantly positively associated with number of flowers per axil, total number of capsules per plant, seed weight per capsule (right capsule) and test weight. SPAD chlorophyll was positively correlated with number of flowers per axil and number of capsules per axil. Higher the chlorophyll content, there is high probability of capsule formation form each flower at the axils without any flower drop. Chlorophyll content is positively associated capsule breadth and seed yield per plant (Sravanthi *et al*. 2021). Photosynthates assimilation rate is positively associated total number of capsules per plant, test weight and oil content (Gopika *et al*. 2022). The results significantly indicated that more than one capsules at axil resulted in higher seed yield per plant (Figure 2.). Reasoning of the observations are insufficient to substantiate it.

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Seed yield per plant was significantly positively correlated with number of leaf axils per plant and photosynthetic rate. ~~Number of leaf axils per plant was significantly positively correlated with seed yield per plant~~ and negatively correlated with leaf area which indicates that genotypes with more number of leaves have smaller leaves and low seed yield per plant. Capsule length positively correlated with capsule breadth of left and right capsusle only but there was no significant relation in the middle capsule. Capsule weight was significantly positively correlated with capsule length in the middle capsules, however in adjacent capsules, both length and breadth are positively correlated with higher seed weight of the capsule. Similar observations were made by OZCINAR *et al.* (2017), Teklu *et al.* (2014), Ogbonna *et al.* (2012), Pandey *et al.* (2021), Fang *et al.* (2023). Seed yield per plant was positively and significantly associated with capsule seed weight of middle capsule only and

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Comment [AUT6]: LIMIT THE NO. OF REFERENCES ON THE SAME ASPECT negatively but non significant association was found between capsule seed weight of adjacent capsules.

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Principal Component Analysis

The principal component analysis (Table 2) revealed that seven principal components, have accounted for 80.50% of the total variation. The first two principal components PC1 and PC2 contributed more to 50 % of the total variation. Therefore, in this study, differentiation of the genotypes into different cluster was because of a cumulative effect of a number of characters rather than the contribution of specific few characters (Figure 3).

The characters having relatively higher value in the first principal component (PC1) were NFAMS, NCAMS, MSLCB, MSLCL, MSRCB and MSRCL had more contribution to the total variation and they were responsible for the differentiation of the genotypes. Second principal component was dominated by NCAB, SYP, and HI (Table 2). A biplot (Fig.4) representing the ordination of genotypes and the morphological traits with PC1 in the abscissa and PC2 in the ordinate depicted a clear pattern of grouping of genotypes in the factor plane. All the genotypes were widely scattered across different quarters (Fig.4).

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Genotypes with monostem and multicapsule per axil were grouped together. These genotypes can be selected for higher TCMS, MSMCL, OC and PAR. Most promising genotypes for these traits are PI-154298, SC-500-1, PI-158040, PI-158056 along with a multicapsule variety of Telangana JCS-1020 (check). Characters such as TW, MSLCL, MSLCB, MSLCW showed low variation across the genotypes. Two checks genotypes GT-10 and Swetha Til were grouped together and were outliers since they were the only genotypes with single capsules per axil (Pandey *et al* 2021). In multicapsule genotypes, IC-500811, G-44, IC-500779, variation for number of capsules per axil over the length of the main stem was found, and hence they must be rejected since they are unstable for production of muticapsules at every axil. The prominent characters identified in a particular principal component are prime contributors to total variability and have the tendency to hang together and can be used effectively for selection in crop breeding programmes. Such biplots based on PCA analysis were used by Furat and Uzan, (2010).

Conclusion--------------------

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Table 1: Correlation coeeficient (r) between source and sink characters in multicapsular sesame.

Source-Sink characters	NLAMS	LA	SPAD Chlorophyll	PAR	SG
NFAMS	0.048	0.269**	0.231*	0.009	-0.204
NCAMS	0.119	0.210	0.213*	-0.014	-0.178
NCAB	0.173	-0.198	-0.110	-0.029	0.266**
TCMS	0.073	0.339**	-0.183	0.370**	-0.080
MSMCB	-0.084	0.145	-0.152	0.032	0.032
MSMCL	-0.035	0.049	0.002	0.076	-0.224*
MSMCSW	-0.012	0.015	0.065	-0.072	0.030
MSRCB	-0.136	0.167	0.221*	0.045	-0.209
MSRCL	-0.094	0.202	0.197	0.088	-0.222*
MSRCSW	-0.137	0.363**	0.143	-0.023	-0.157
MSLCB	-0.030	0.112	0.157	0.039	-0.301**
MSLCL	-0.035	0.146	0.188	0.105	-0.277**
MSLCSW	-0.014	0.087	0.022	0.103	-0.290**
SYP	0.226**	-0.034	0.378**	0.061	0.021
TW	-0.068	-0.362**	0.042	0.236*	0.232*
HI	-0.084	-0.156	-0.017	-0.117	0.311**
OC	0.000	0.120	0.202	0.327**	0.014

**** Significant at 0.01: *Significant at 0.05**

NLAMS =Number of leaf axils/main stem, NLAB= Number of leaf axils/branches, NFAMS= Number of flowers/axil in main stem, NFAB= Number of flowers/axil in branches, NCAMS= Number of capsules/axil in main stem, NCAB= Number of capsules/axil in branches, TCMS= Total number of capsule/main stem, TCPB= Total number of capsule/branches, MSMCL(mm) = Capsule character length /middle capsule, MSRCL(mm) = Capsule character length /right capsule, MSLCL(mm) = Capsule characters length /left capsule, MSMCW(mm) = Capsule characters width /middle capsule, MSRCW(mm) = Capsule characters width / right capsule (main stem), MSLCW(mm) = Capsule characters width / left capsule , MSMCSW(mg) = Capsule seed weight / middle capsule, MSRCSW(mg) = Capsule seed weight /right Capsule, MSLCSW(mg) = Capsule seed weight /left Capsule, SG= Stem girth (cm), SPAD= SPAD chlorophyll, PAR= Photosynthetic assimilation rate, LA= Leaf area, TW= Test weight (g), HI= Harvest index(%), SYP= Seed yield/plant (g).

Table 2. Eigen values and factor lodgings of the principal components analysis

PC	Eigen value (%)	% Variance	Cummulative % variance
1	6.54	29.75	40.66
2	2.40	10.91	49.07
3	1.85	8.40	57.00
4	1.74	7.93	63.94
5	1.52	6.94	70.60
6	1.46	6.66	76.25
7	1.24	5.64	80.51

PC Loadings

CHARACTERS	PC1	PC2	PC3	PC4	PC5	PC6	PC7
NLAMS	-0.016	0.129	0.149	0.118	-0.564	-0.052	0.402
LA	0.114	-0.145	0.350	-0.203	0.452	-0.053	0.083
SPAD45	0.102	-0.019	0.454	-0.011	-0.206	0.053	0.147
PAR	0.020	-0.123	-0.034	0.285	0.318	0.357	-0.019
SG	-0.129	0.217	0.304	0.089	0.350	0.002	0.048
NFAMS	0.370	0.129	0.061	0.028	0.016	0.019	0.032
NCAMS	0.343	0.169	0.092	0.084	-0.015	0.040	0.044
NCAB	-0.059	0.533	-0.027	0.100	0.085	-0.044	0.183
TCMS	0.164	-0.288	0.415	-0.092	-0.191	0.073	-0.017
MSMCB	-0.028	-0.284	-0.139	0.011	0.261	0.019	0.599
MSMCL	0.047	-0.286	-0.173	0.200	0.118	-0.490	0.308
MSMCSW	0.129	-0.021	0.131	0.463	-0.042	-0.369	-0.246
MSLCB	0.346	0.098	-0.139	0.009	-0.027	0.150	0.116
MSLCL	0.348	0.002	-0.136	0.064	-0.005	0.094	0.131
MSLCSW	0.224	-0.012	-0.171	-0.032	-0.095	0.396	0.135
MSRCB	0.346	0.105	-0.091	-0.026	0.083	-0.027	-0.046
MSRCL	0.350	0.069	-0.115	0.045	0.115	-0.084	0.018
MSRCSW	0.284	0.095	0.161	-0.112	0.135	-0.227	-0.271
SYP	-0.120	0.343	0.180	0.367	0.109	-0.090	0.248
TW	-0.056	-0.064	-0.189	0.524	-0.032	0.222	-0.260
HI	-0.154	0.332	0.054	-0.173	0.143	0.251	0.036
OC	-0.004	-0.243	0.343	0.339	0.039	0.333	0.020

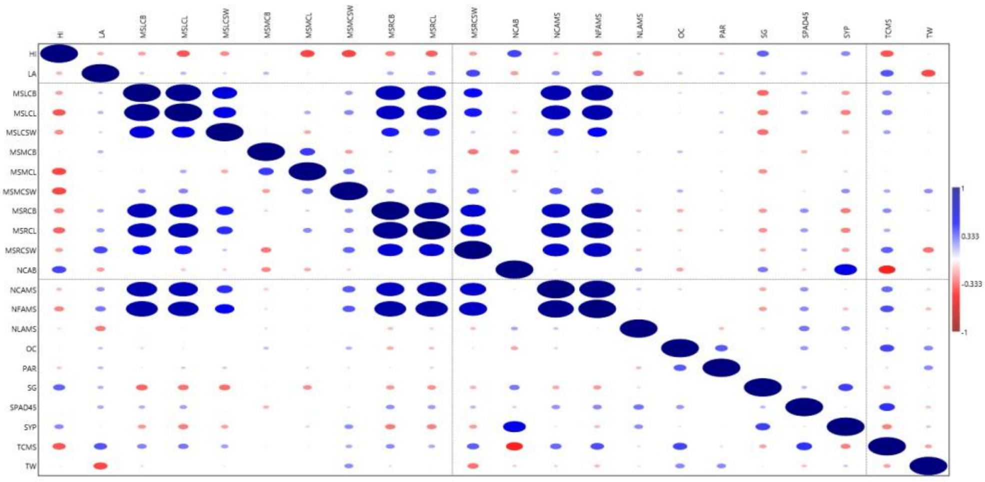

Figure 2: Heatmap of correlation coefficient of the between the yield and yield components comprising of source and sink characters

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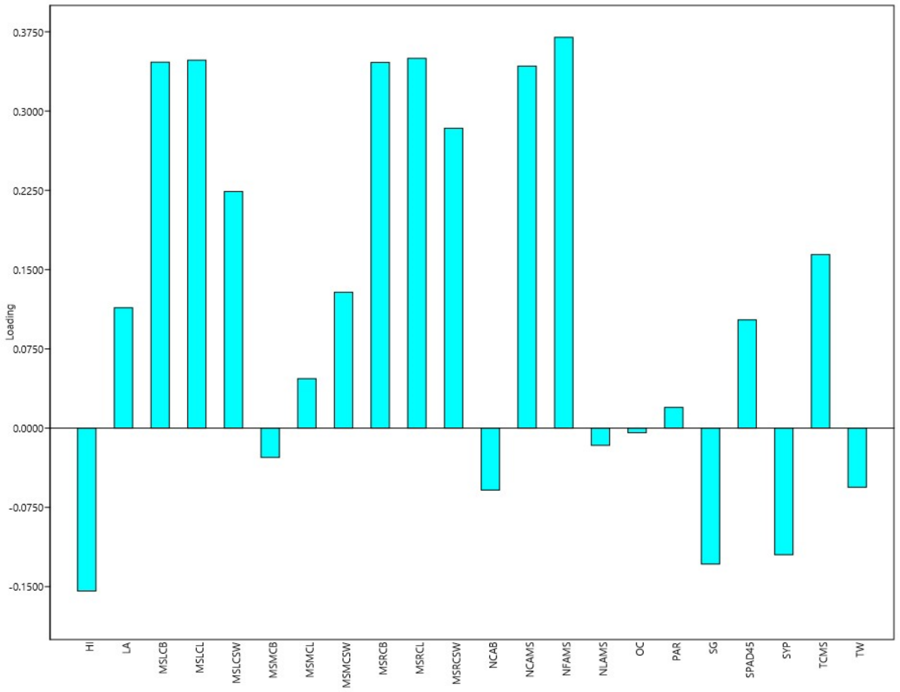

Figure 3. Characters contribution for the PCA loading values

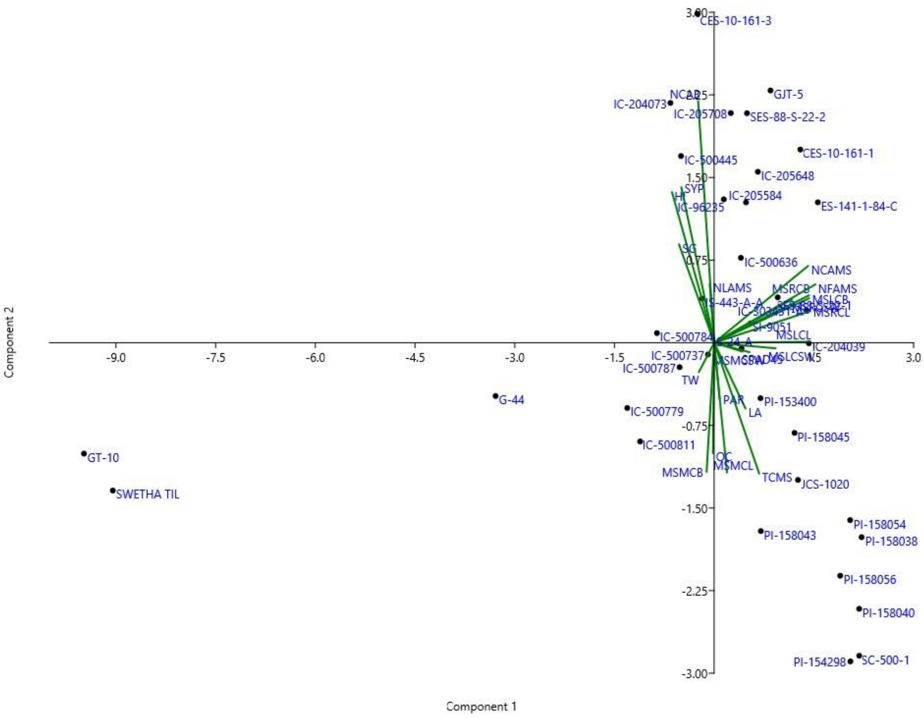

Figure 4: Biplot of PC 1 and PC 2 indicating the distribution of genotypes and yield and yield contributing characters