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Assessment of Genetic Variability for Yield and Yield Related Traits in Safflower Core Subset Germplasm

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

One hundred and fifty safflower genotypes of Core subset germplasm provided by ICAR-IIOR, were evaluated to study genetic variability, correlation and principal component analysis (PCA). A wide range of phenotypic data with near normal distribution was observed for most of the traits analysed. High variability was observed for all the traits studied indicating diverse nature of the germplasm. Significant positive correlation was observed for seed yield with test weight and oil

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content. Genotype GMU 6869 has been identified as potential genotype surpassing the best check A1 for seed yield and earliness. Twenty three genotypes significantly superior to the 2nd best check PBNS-12 were identified. High heritability along with GAM was recorded for the traits number of effective capitula/plant, test weight and single plant yield indicating that these characters may be considered as selection criteria for genetic improvement in safflower. Principal component analysis revealed that first four principal components contributed 65.2% of total variance. PCA-variables plot and PCA Bi-plots revealed that two traits viz., LPB and HPB contributed maximum variations in PC1, while two traits viz., DAF & DAM contributed to the maximum variability in PC-2. Safflower accessions displaying highest performance for the traits studied were identified. These genotypes can be used as parental lines for improvement of specific traits in safflower breeding program.

Keywords: Augmented; core germplasm; correlation; genetic diversity; heritability; PCA; safflower; yield.

1. INTRODUCTION

Safflower (*Carthamus tinctorius* L.) is a member of the Compositae or Asteraceae family grown for its high-quality edible oil from seeds. The flowers are loaded with medicinal properties and are also used to extract dye for textiles. The crop is grown during rabi season under residual soil moisture conditions. Safflower remained an underutilized, minor crop despite its healthy oil composition. Safflower has greatest variability of fatty acid in its seed oil composition [1, 2]. The pharmacological and nutritional applications of safflower oil have extensively been reviewed [3]. Genetic diversity in safflower has been explored using agro-morphological, fatty acid composition and ISSR molecular markers [4].Characterization of the conserved germplasm is prerequisite to identify and utilize the accessions with desired agronomic traits. Germplasm evaluation, genetic divergence, heritability, correlation and path analysis among safflower genotypes were reported [5-7]. Germplasm characterization is a continuous activity to identify novel accessions with desirable traits [8,9]. However, extensive characterization of all the collections for each crop species is a herculean task as it requires more time and resources. Hence the concept of core germplasm/core set has been devised such that it captures the entire range of genetic variability of any crop [10-12]. Being smaller in size and diverse in nature, the core set can be efficiently characterized in short time with limited resources. A thorough understanding of existing genetic variability in a crop species is of utmost important to design an effective breeding program. Recently not only morphological characterization but NGS based techniques are also being used to study genetic diversity, population structure and tolerance to biotic stresses in pigeonpea minicore germplasm and landraces [13-16].

The efficiency of breeding program is based on selection criteria employed along with genotypic coefficient of variation and trait heritability [17-19]. Considerable diversity has been observed in safflower across the globe [20, 21]. Genetic diversity of safflower germplasm has been previously investigated based on the agro-morphological traits [22, 23]. Identification of yield and yield attributing traits are critical for genetic improvement in safflower [24-26]. In plant breeding programmes, yield being a quantitative trait is controlled by a number of contributing characters [27-29]. Hence it is essential to have information pertaining to different morphological traits that affect yield genetic improvement of safflower [30, 31]. Correlation coefficient analysis helps researchers to differentiate considerable association between characters and thus aids in selection of appropriate genotypes [32]. Based on multivariate analysis, the traits such as number of effective capitula/plant, seed yield and days to flowering have been identified as the most important attributes for grain yield in safflower [33, 25, 33, 34]. Considerable genetic variation exists for these characters and are affected by environmental conditions [30, 35]. The present study has been carried out to characterize and evaluate core subset of safflower germplasm for yield and yield related traits. The information generated will be useful to the breeders for selection of parental lines for varietal development in safflower.

2. MATERIALS AND METHODS

2.1 Plant Material

The safflower core subset of germplasm consisted of 150 genotypes along with two national checks (A1 and PBNS-12) provided by ICAR-IIOR, Hyderabad (Table 1). The experiment was conducted during Rabi 2014–15

at Agricultural Research Station, Tandur in augmented randomized complete block design (ARCBD). The crop was raised using standard agricultural practices and data was collected from five random plants. The traits include: rosette period, angle of 1st primary branch to main stem (APB), Days to 50% flowering (DTF), Days to Maturity (DTM), Diameter of main capitula at maturity (cm) (Dia-Cap), No. of effective capitula/plant (EC), Length of longest primary branch (cm) (LPB), height of the primary branch from ground level (HPB) (cm), Oil content (%), Plant height (cm) (PH), 100-seed weight (g) (TW) and Single plant Yield (g) (SPY).

Table 1. List of safflower genotypes (Core subset germplasm)

S.No	Genotype	S.No	Genotype	S.No	Genotype
1	A-1	52	GMU 3256	103	GMU 5046
2	GMU 1047	53	GMU 3281	104	GMU 5075
3	GMU 1059	54	GMU 330	105	GMU 5081
4	GMU 1078	55	GMU 3386	106	GMU 5133
5	GMU 1137	56	GMU 3436	107	GMU 5163
6	GMU 1185	57	GMU 3491	108	GMU 5170
7	GMU 1250	58	GMU 3537	109	GMU 5239
8	GMU 1287	59	GMU 3607	110	GMU 5295
9	GMU 1315	60	GMU 3617	111	GMU 5335
10	GMU 1339	61	GMU 3629	112	GMU 5361
11	GMU 1354	62	GMU 3639	113	GMU 5663
12	GMU 1409	63	GMU 3703	114	GMU 5668
13	GMU 1485	64	GMU 3707	115	GMU 5701
14	GMU 1603	65	GMU 3740	116	GMU 5728
15	GMU 1626	66	GMU 3780	117	GMU 5825
16	GMU 1638	67	GMU 3822	118	GMU 5841
17	GMU 1695	68	GMU 3852	119	GMU 5848
18	GMU 1708	69	GMU 3929	120	GMU 5908
19	GMU 1748	70	GMU 3968	121	GMU 5923
20	GMU 1765	71	GMU 40	122	GMU 593
21	GMU 1812	72	GMU 4010	123	GMU 5935
22	GMU 1824	73	GMU 4038	124	GMU 599
23	GMU 1855	74	GMU 4066	125	GMU 6026
24	GMU 1871	75	GMU 4109	126	GMU 6057
25	GMU 1875	76	GMU 4201	127	GMU 6119
26	GMU 2016	77	GMU 4223	128	GMU 6192
27	GMU 2129	78	GMU 4234	129	GMU 6252
28	GMU 2136	79	GMU 4305	130	GMU 6306
29	GMU 216	80	GMU 4381	131	GMU 6312
30	GMU 2198	81	GMU 4400	132	GMU 638
31	GMU 224	82	GMU 4420	133	GMU 6424
32	GMU 2240	83	GMU 4429	134	GMU 6506
33	GMU 2413	84	GMU 4502	135	GMU 6548
34	GMU 2432	85	GMU 4507	136	GMU 6556
35	GMU 2437	86	GMU 4549	137	GMU 659
36	GMU 2472	87	GMU 4558	138	GMU 6663
37	GMU 2594	88	GMU 4623	139	GMU 671
38	GMU 2616	89	GMU 4627	140	GMU 6851
39	GMU 2718	90	GMU 4646	141	GMU 6869
40	GMU 2749	91	GMU 4688	142	GMU 707
41	GMU 2860	92	GMU 4693	143	GMU 7191
42	GMU 2944	93	GMU 4696	144	GMU 744
43	GMU 2969	94	GMU 473	145	GMU 765
44	GMU 2985	95	GMU 4773	146	GMU 774

S.No	Genotype	S.No	Genotype	S.No	Genotype
45	GMU 2987	96	GMU 4812	147	GMU 819
46	GMU 3047	97	GMU 4839	148	GMU 821
47	GMU 3084	98	GMU 4934	149	GMU 864
48	GMU 3095	99	GMU 4966	150	GMU 878
49	GMU 3177	100	GMU 4972	151	GMU 95
50	GMU 3189	101	GMU 5032	152	PBNS-12
51	GMU 3208	102	GMU 5044		

2.2 Statistical Analysis

The augmented analysis of variance (ANOVA) was carried out using 'augmented RCBD' R package in RStudio 1.3. (https://aravind-j.github.io/augmentedRCBD/https://cran.r-project.org/package=augmentedRCBD) [36]. The ANOVA and genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), broad sense heritability and genetic advance as per cent mean (GA), Principal Component Analysis (PCA) andCorrelation were obtained.

3. RESULTS AND DISCUSSION

3.1 ANOVA and Mean Performance of the Genotypes

Analysis of variance- treatment adjusted (ANOVA) revealed highly significant differences among the genotypes for the traits, days to 50% flowering, days to maturity, no. of effective capitula/plant, oil content, test weight and single plant yield. Analysis of variance- block adjusted (ANOVA) revealed highly significant differences among the genotypes for the traits days to 50% flowering, days to maturity, oil content and single plant yield. The mean sum of squares (MSS) for checks was the same under both cases of heterogeneity elimination (adjustment) and non-adjustment for all the traits (Table 2). The MSS of the test entries is comparable both under adjustment of blocks and treatment adjustment. Critical difference (CD) between test entries between the blocks is slightly higher compared to within the blocks for all the traits, indicating that environmental effect was insignificant.

The mean values for all the traits [rosette period, angle of 1st primary branch to main stem, Days to 50% flowering, Days to Maturity, Diameter of main capitula at maturity (cm), No. of effective capitula/plant (EC), Length of longest primary branch (cm), height of the primary branch (cm), Oil content (%), Plant height (cm), 100-seed weight (g) and Single plant Yield (g)] along with standard error, standard deviation, range and coefficient of variation are presented in Table 3.

All the studied traits displayed a wide range of phenotypic data with near normal distribution for most of the traits (Fig. 1). Near-normal distribution with non-significant right hand skewness was observed for Rosette. LPB & PH; while non-significant right-handed skewness was observed for APB. Near-normal distribution with significant right-handed skewness was observed for the traits DAF, DAM, HPB, EC, TW & SPY. Near-normal distribution with significant left-handed skewness was observed for Dia-Cap & OC. Skewness and kurtosis values indicated a highly significant deviation from a normal distribution for traits HPB, DAM, DAF and OC.

The core germplasm comprised of genotypes with seed yield/plant ranging from 1.43–17.53 g, and 100 seed weight of 1.92–6.55 g. GMU 6869 has been identified as best genotype in terms of seed yield/ plant and earliness while twelve genotypes were on par with best check A1. More than 10% coefficient of variation was recorded for all traits except angle of 1st primary branch to main stem (APB), no. of effective capitula/ plant (EC), height of the primary branch (cm) (HPB), and Single plant Yield (g) (SPY) (Table 2). Box plots (Fig.2) revealed outliers for all the traits except plant height.

3.2 Heritability Estimates

Higher values of phenotypic coefficient of variability (PCV) were recorded compared to genotypic coefficient of variability (GCV) indicating environmental influence. High GCV was observed for the traits HPB, EC and SYP. While higher PCV was recorded for the traits HPB, EC, TW and SYP. Earlier studies support these results [22]. Heritability estimates along with genetic advance is more reliable and effective for selection rather than heritability

Table 2 Analysis of variance (ANOVA) for 150 safflower genotypes (Core subset germplasm)

ANOVA, Treatment Adjusted																															
Source	**Df**	**Mean.Sq**																													
		Rosette		**DTF**		**DAM**		**LPB**		**PH**		**APB**		**HPB**		**Dia-cap**		**EC**		**TW**		**OC**		**SYP**	
Block (ignoring Treatments)	4	31.90	ns	106.90	*	75.05	*	114.76	ns	193.68	ns	243.99	*	178.20	ns	0.17	*	222.13	*	1.04	*	7.72	**	16.80	**
Treatment (eliminating Blocks)	151	5.04	ns	48.98	*	42.40	*	92.74	ns	70.54	ns	50.06	ns	112.98	ns	0.04	ns	95.95	ns	0.68	ns	4.00	*	10.70	**
Treatment: Check	1	10.00	ns	4.90	ns	0.40	ns	4.62	ns	13.46	ns	48.40	ns	31.33	ns	0.09	ns	13.00	ns	0.20	ns	7.78	**	77.99	**
Treatment: Test and Test vs. Check	150	5.00	ns	49.27	*	42.68	*	93.33	ns	70.92	ns	50.07	ns	113.52	ns	0.04	ns	96.51	ns	0.68	ns	3.98	*	10.25	**
Residuals	4	5.75		7.40		7.15		24.87		44.74		23.40		28.02		0.02		27.05		0.15		0.30		0.61	
ANOVA, Block Adjusted																															
Source	**Df**	**Mean.Sq**																													
		Rosette		**DTF**		**DAM**		**LPB**		**PH**		**APB**		**HPB**		**Dia-cap**		**EC**		**TW**		**OC**		**SYP**	
Treatment (ignoring Blocks)	151	5.68	ns	51.73	*	44.33	*	91.74	ns	72.61	ns	54.49	ns	115.27	ns	0.04	ns	100.38	ns	0.70	ns	4.19	**	11.07	**
Treatment: Check	1	10.00	ns	4.90	ns	0.40	ns	4.62	ns	13.46	ns	48.40	ns	31.33	ns	0.09	ns	13.00	ns	0.20	ns	7.78	**	77.99	**
reatment: Test	149	5.46	ns	52.38	*	44.91	*	91.01	ns	70.42	ns	53.73	ns	116.41	ns	0.04	ns	101.31	ns	0.68	ns	4.16	**	10.22	**
Treatment: Test vs. Check	1	33.13	ns	1.55	ns	1.55	ns	287.87	*	458.06	*	173.67	ns	28.75	ns	0.28	*	48.56	ns	5.29	**	5.85	*	71.65	**
Block (eliminating Treatments)	4	7.75	ns	3.00	ns	2.35	ns	152.57	ns	115.50	ns	76.60	ns	91.86	ns	0.12	ns	55.11	ns	0.07	ns	0.57	ns	2.60	ns
Residuals	4	5.75		7.40		7.15		24.87		44.74		23.40		28.02		0.02		27.05		0.15		0.30		0.61	

Critical Difference													
Comparison	**APB**	**DTF**	**DAM**	**Dia-cap**	**EC**	**HPB**	**LPB**	**OC**	**PH**	**Rosette**	**SYP**	**TW**
A Test Treatment and a Control Treatment	18.02	10.13	9.96	0.55	19.37	19.72	18.58	2.03	24.91	8.93	2.91	1.44
Control Treatment Means	8.49	4.78	4.70	0.26	9.13	9.30	8.76	0.96	11.74	4.21	1.37	0.68
Two Test Treatments (Different Blocks)	23.26	13.08	12.86	0.72	25.01	25.46	23.98	2.63	32.16	11.53	3.75	1.86
Two Test Treatments (Same Block)	18.99	10.68	10.50	0.58	20.42	20.79	19.58	2.14	6.26	9.42	3.06	1.52

Table 3. Descriptive Statistics for 150 safflower genotypes (Core subset germplasm)

Trait	Mean	Std. Error	Std. Deviation	Range	CV
Rosette (days)	30.14	0.20	2.51	25-37	7.93
DAF (days)	87.90	0.60	7.38	80-112	3.10
DAM (days)	120.80	0.55	6.79	113.4-142.9	2.21
PH (cm)	87.98	0.78	9.63	65.48-113.08	7.57
APB	39.65	0.69	8.50	10.40-61.40	12.27
HPB (cm)	22.22	1.02	12.61	0.00-64.17	23.94
Dia-cap (cm)	1.77	0.02	0.26	1.10-2.29	8.37
EC	31.89	0.89	10.91	12.24-69.84	16.25
TW (g)	3.92	0.07	0.81	1.92-6.55	9.77
OC (%)	27.37	0.17	2.13	19.22-32.52	2.00
SYP (g)	7.55	0.26	3.21	1.43-17.53	10.14
LPB (cm)	50.53	0.96	11.88	25.90-84.20	9.82

alone [37]. Heritability estimates (broad sense) were moderate for PH, APB, Dia-Cap and high for all the remaining traits studied. While Genetic advance (GAM) as percent of mean was low for DAM, PH, moderate for DAF, Dia-Cap, OC and high for LPB, APB, HPB, EC, TW, OC, SPY. The traits EC TW and SPY have high heritability along with GAM, hence these characters can be considered as selection criteria (Fig.3). Our results are in agreement with earlier findings [26, 38] for seed yield. However low heritability for seed yield (37.58%) and number of capitula/ plant (19.58 %) were also reported in recent studies [5].

3.3 Correlation Coefficients

Correlation coefficients are one of the key determinants to decipher the relationship between yield and yield components [39-41]. SYP was significantly and positively correlated with test weight and oil content. TW is positively correlated with Dia-Cap, PH with HPB & LPB,OC with SYP & Dia-Cap. High positive correlations were observed between DAM & DAF, LPB & HPB;EC with LPB & HPB (Fig.4).Recent studies in safflower reported similar significant and positive correlation of seed yield with 100 seed weight [5]. However, recent studies reported that SYP was positively correlated with EC and negatively correlated with TW [42]. Multiple statistical analyses revealed that selection based on traits oil content, seed weight, seed yield and number of capitula/plant are effective for genetic improvement of oil yield in spring safflower [31]. Positive correlation between seed yield and no. of capitula/plant, 1000 seed weight, oil content and SYP was reported in safflower genotypes under arid conditions in Egypt [43]. Recent studies also indicated significant positive correlation of SYP with EC, TW, DAM and harvest index (%) [44-46].

3.4 Principal Component Analysis

In Principal component analysis a total of 11 principal components were extracted. The first four PCs accounted for 65.2% of total variance (Fig. 5A). PCA-variables plot (Fig. 5B) and PCA Bi-plots (Fig. 5C), revealed that two traits viz., LPB and HPB contributed maximum variations in PC1, while two traits viz., DAF & DAM contributed to the maximum variability in PC-2. In previous study of PCA in 20 safflower cultivars (comprising of Iranian and exotic), it was reported that first three PCs, explained around 80% of the total variance with 34, 32 and 14%, respectively [47]. Safflower germplasm mapping panel was evaluated for major seed yield traits and oil content. Superior genotypes for seed and oil yield were identified for utilization in varietal improvement program. PCA revealed that 1st four PCs contributed to 75.3% of total variation. Seed yield was correlated to no. of capitula/plant and number of branches/plant [48]. Evaluation of 122 safflower genotypes revealed that first two principal components accounted for 29.5% and 15.9% of the total variation, respectively. The genotypes in the first group reported higher grain yield than others [49].

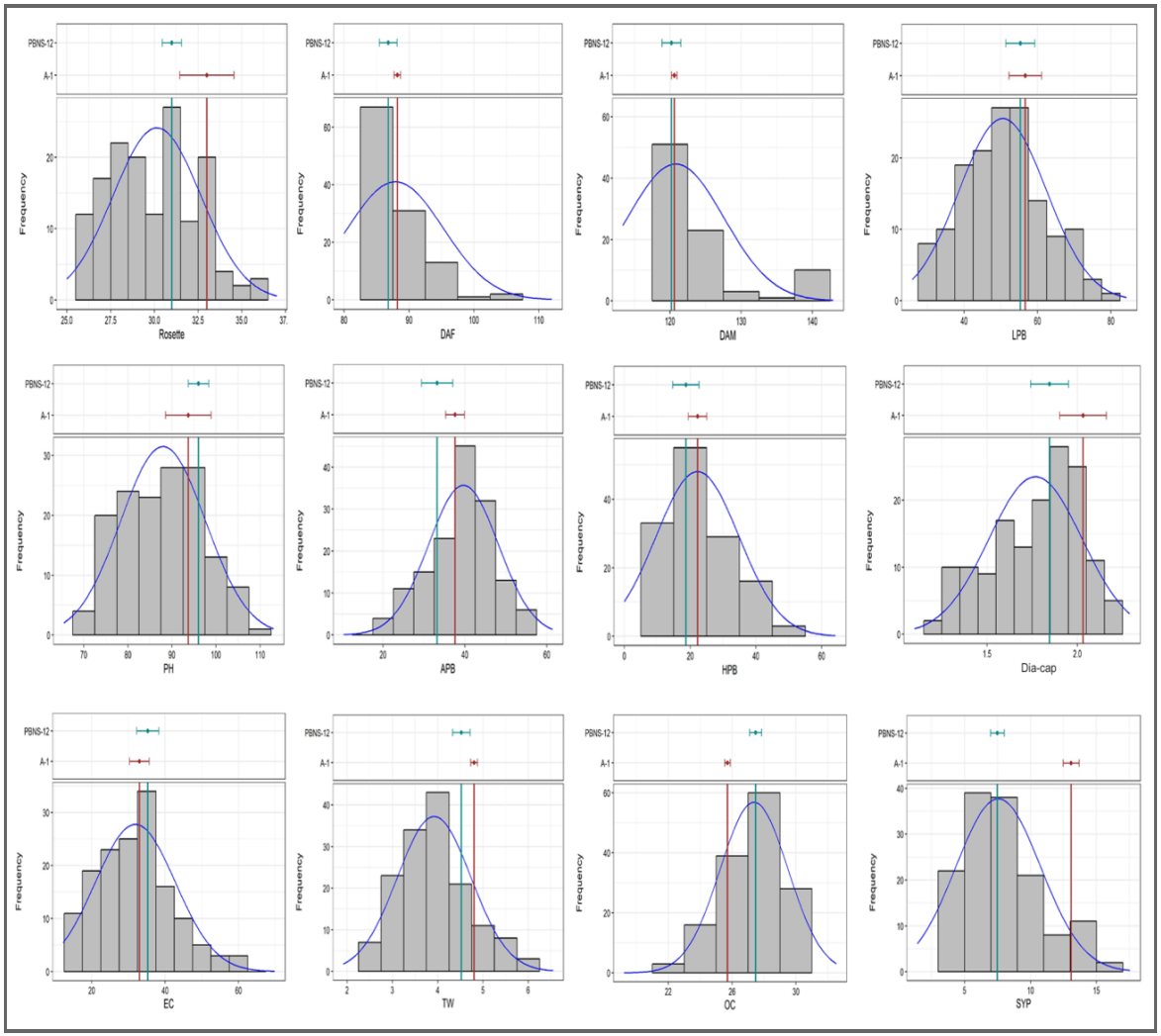

Fig. 1. Mean phenotypic distribution for 12 traits in 150 safflower genotypes (Core subset germplasm)

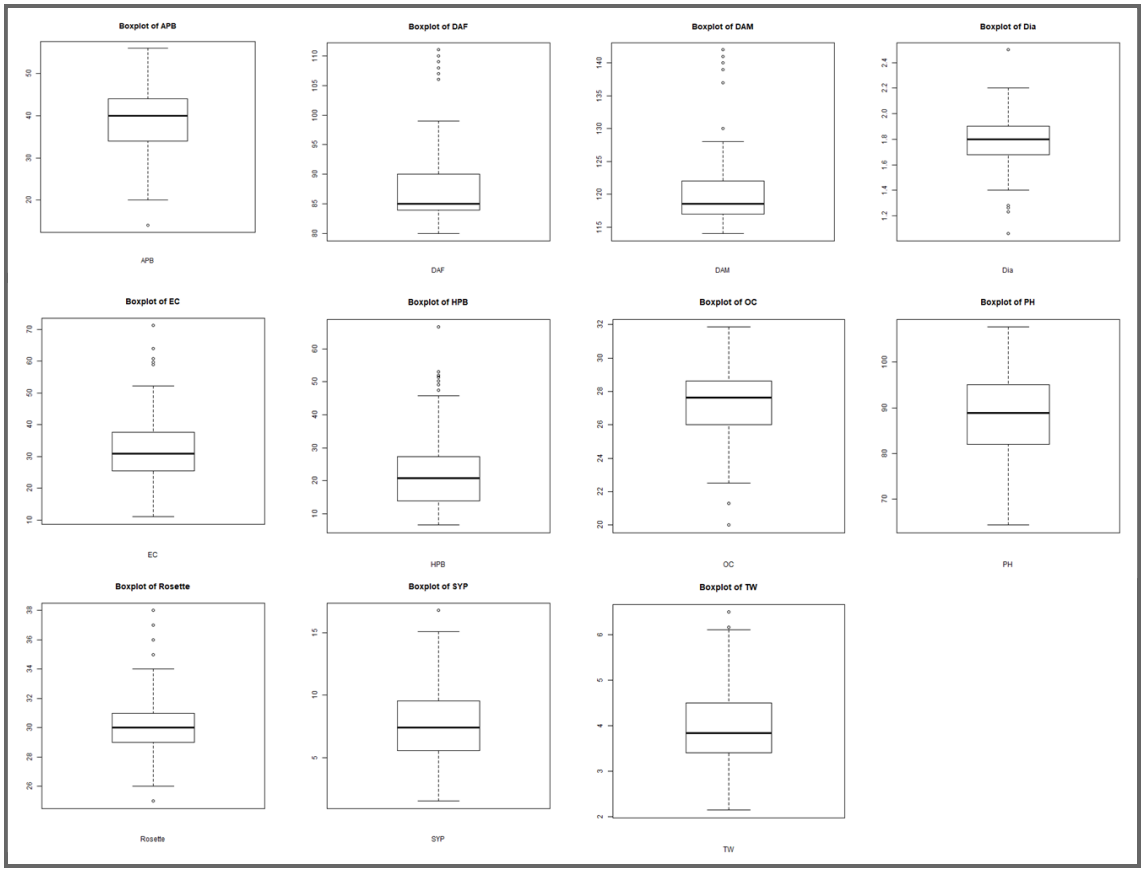

Fig. 2. Box-plots depicting variation in the data of 12 traits studied in safflower germplasm. The vertical lines represent the variation and dots represent the outliers

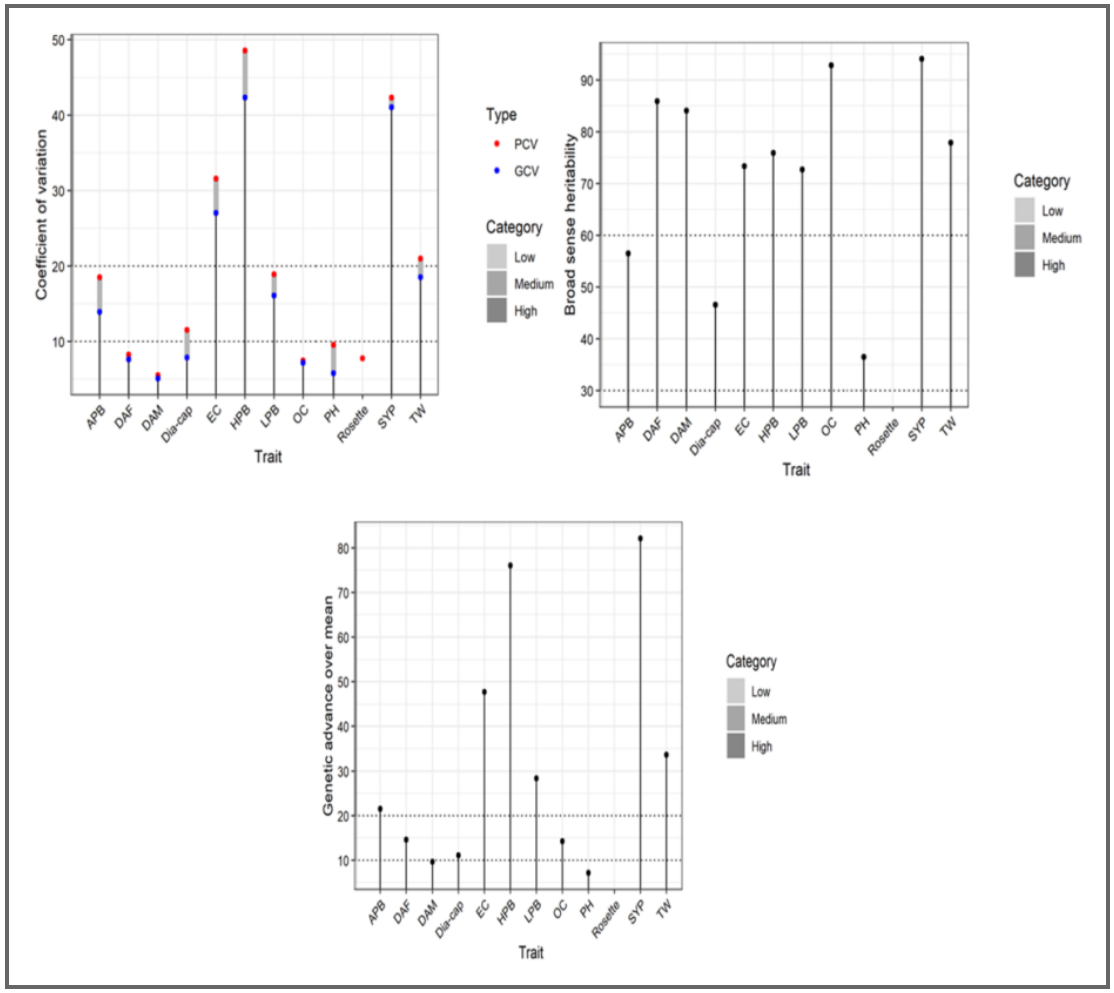

Fig. 3. Coefficient of variation, heritability in broad sense and genetic advance as per cent of mean for 12 traits in 150 safflower genotypes (Core subset germplasm)

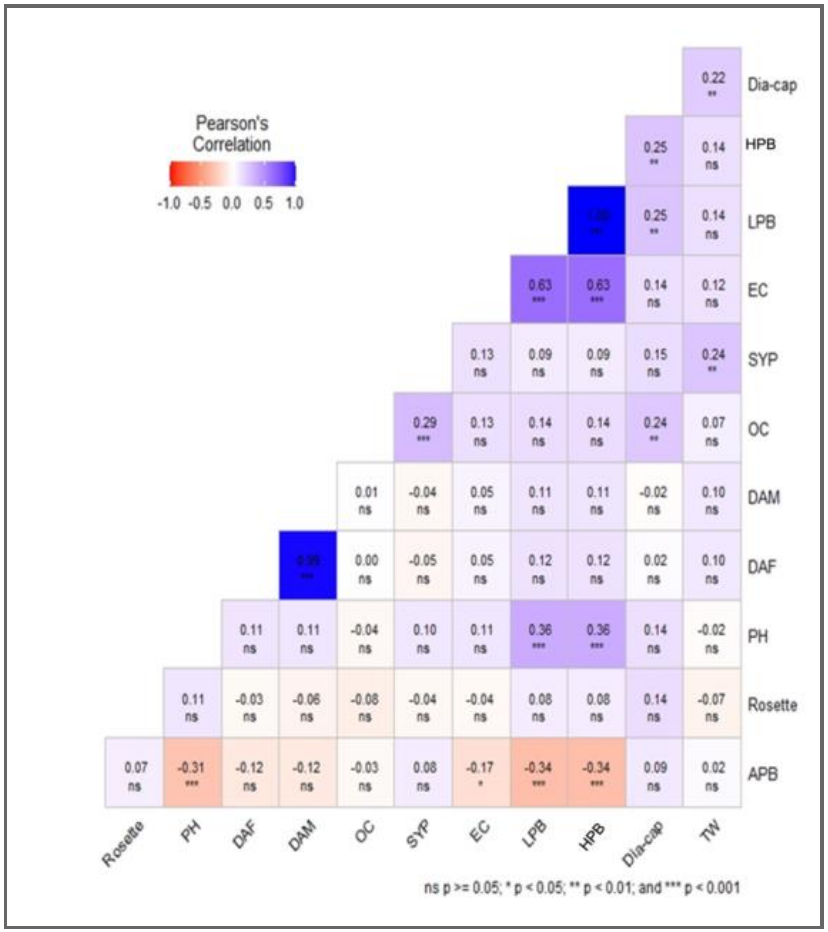

Fig. 4. Correlation coefficients among component yield, and yield related attributes among 150 safflower genotypes (Core subset germplasm)

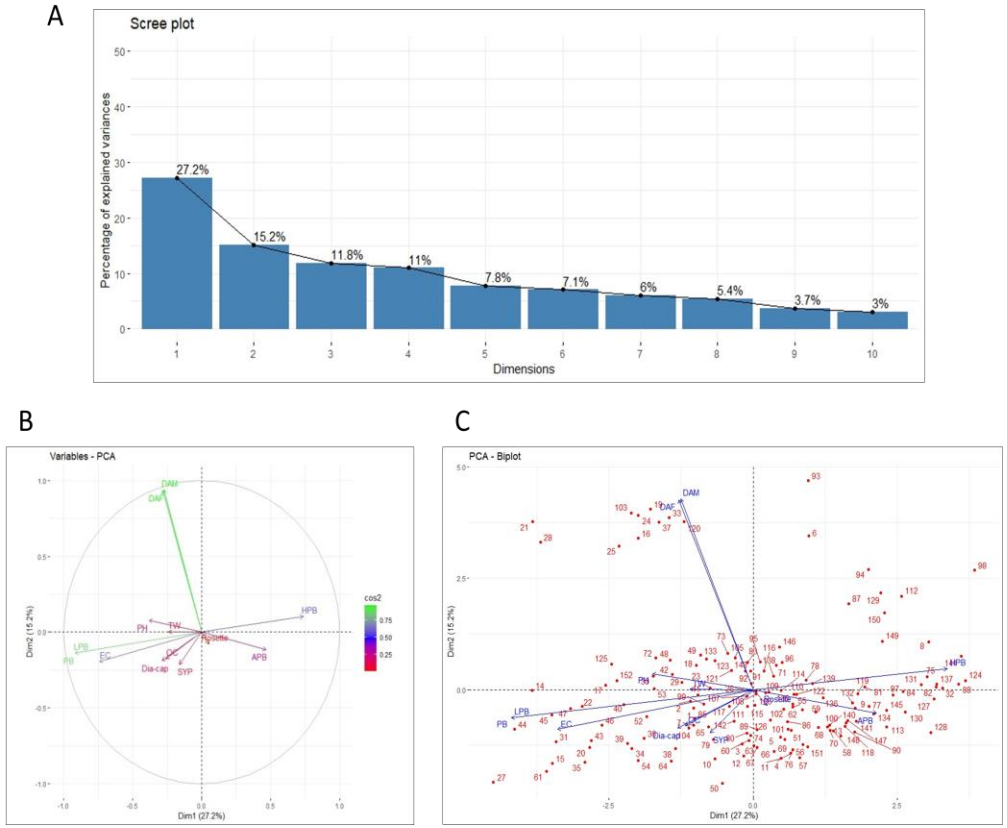

Fig. 5. (A) Scree Plot explaining the contribution of various principal components, (B) PCA-Variables Plot, (C) PCA-Biplots explaining the contribution of 12 traits to the total variation in 150 safflower genotypes (Core subset germplasm)

Table 4. Performance wise list of safflower core subset accessions under each trait

S. No.	Trait	Highest Performance accessions
1.	Rosette period	> 35days: GMU 765, GMU 5908, GMU 821, GMU 864, GMU 6424, GMU 1250
2.	Days to 50% flowering	> 100days: GMU 1137, GMU 1871, GMU 1855, GMU 2472, GMU 1626, GMU 2240, GMU 4693, GMU 2129, GMU 5044, GMU 1765, GMU 5848, GMU 1708
3.	Days to maturity	>135days: GMU 1137, GMU 1871, GMU 1626, GMU 1855, GMU 2129, GMU 4693, GMU 2240, GMU 2472, GMU 5044, GMU 1765, GMU 5848, GMU 1708
4.	Plant height (cm)	> 100cm: GMU 707, GMU 1485, GMU 2718, GMU 2432, GMU 2016, GMU 2198, GMU 1871, GMU 4839, GMU 2985, GMU 2136, GMU 2860, GMU 1875, GMU 1812, GMU 1824
5.	Length of the longest primary branch (cm)	> 70cm: GMU 216, GMU 3047, GMU 1185, GMU 2985, GMU 1765, GMU 2432, GMU 2944, GMU 1812, GMU 2016, GMU 2969, GMU 3617
6.	Angle of 1st primary branch to main stem	$>50^0$: GMU 3386, GMU 3780, GMU 1339, GMU 4109, GMU 4502, GMU 1287, GMU 5170, GMU 6057, GMU 40, GMU 6026, GMU 3177, GMU 3084, GMU 6119
7.	Height from ground level to 1st primary branch (cm)	>70cm: GMU 216, GMU 3047, GMU 1185, GMU 2985, GMU 1765, GMU 2432, GMU 2944, GMU 1812, GMU 2016, GMU 2969, GMU 3617
8.	Diameter of main capitula (cm)	> 2cm: GMU 2136, GMU 2432, GMU 3084, GMU 3208, GMU 330, GMU 774, A-1, GMU 2985, GMU 659, GMU 765, GMU 3047, GMU 1287, GMU 638, GMU 4109, GMU 1078, GMU 1485, GMU 2198, GMU 2413, GMU 5923, GMU 3436, GMU 2016, GMU 3491, GMU 819, GMU 1748, GMU 3929, GMU 3968, GMU 2987, GMU 1871
9.	No. of effective capitula/ plant	> 45: GMU 5044, GMU 1748, GMU 599, GMU 5170, GMU 2616, GMU 2718, GMU 5163, GMU 3208, GMU 3617, GMU 2944, GMU 2016, GMU 1485, GMU 95, GMU 3177, GMU 3047, GMU 40, GMU 2987
10.	100-seed weight (TW) (g)	>5.4g: GMU 2969, GMU 659, GMU 2198, GMU 1638, GMU 1287, GMU 5044, GMU 5133, GMU 1603, GMU 6548
11.	Oil content (%)	>30%: GMU 2594, GMU 1603, GMU 2413, GMU 2437, GMU 3780, GMU 2472, GMU 3852, GMU 3281, GMU 3740
12.	Seed Yield/plant(g)	> 13g: GMU 5663, GMU 5046, GMU 6506, GMU 5081, GMU 5825, GMU 5728, GMU 1603, GMU 3281, GMU 2987, GMU 6026, GMU 6119, GMU 2198, GMU 6869

3.5 Performance of Safflower Genotypes

The safflower genotypes were grouped based on performance wise for each of the traits to identify the best genotypes (Table 4). Based on yield contributing traits, seventeen genotypes with more than 45 effective capitula/plant, nine genotypes with TW of >5.4 g, nine genotypes with oil content of >30%, thirteen genotypes with SYP of >13 g were identified. The genotype GMU 6869 (17.53 g) has been identified to be significantly superior to the best check A1 (13.08 g), while thirteen genotypes were on par with A1. Twenty three genotypes were significantly superior to the 2nd best check PBNS-12 (7.49 g). In an effort to identify trait specific accessions for utilization in safflower breeding, 30 safflower germplasm accessions were evaluated. Genotypes will high SYP (4), OC (8) and bold capitula with high seed number (5) were identified [50, 51].

4. CONCLUSION

GMU 6869 was identified as superior genotype compared to best check A1. High heritability along with GAM was observed for the traits EC, TW and SPY and can be used for selection. Seventeen genotypes with > 45 capitula/plant and 9 with > 5.4 g of test weight were identified. The promising genotypes can be used as parental lines in safflower varietal breeding

program or evaluated in multi-locations to identify stable and high seed yielding lines for varietal release.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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