



RESEARCH ARTICLE

Multivariate analysis of diverse safflower germplasm for genetic improvement of yield and yield related traits

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Abstract

A set of 120 safflower germplasm obtained from ICAR-Indian Institute of Oilseeds Research, Hyderabad was evaluated in an augmented block design (ABD) for seed yield and identification of trait specific germplasm in deep black soils. Data on six agro-morphological traits was recorded. Analysis of variance treatment adjusted (ANOVA) revealed highly significant differences among the genotypes for all the traits studied except for number of effective capitula/plant (EC). Considerable genotypic and phenotypic coefficient of variation was observed among the germplasm with higher values for 100-seed weight, effective number of capitula/plant and seed yield per plant (SYP). Significant positive correlation was observed between seed yield per plant and number of effective capitula/plant. The first four principal components contributed nearly 80 % of total variance. Principal component analysis (PCA)-biplots revealed days to 50 % flowering (DAF), days to maturity (DAM) and 100-seed weight as major contributor for PC-1. The D² analysis was carried out and the genotypes were grouped into 9 clusters with 5th cluster being the largest with 27 genotypes. Early maturing genotypes were grouped into two clusters with 10 genotypes. GMU 1110 (26.27 g) and GMU 2232 (30.78 g) were superior in seed yield/plant over both the national checks A1 (19.46 g) and PBNS-12 (19.38 g). GMU 4128 is early maturing with duration of 115days and seed yield/plant of 23.11 g. While GMU 3773 and GMU 7351 were early maturing genotypes with seed yield on par with the national checks. Bold, seeded genotypes (GMU 3438 and GMU 4983) with test weight more than 6.0 g were identified. Superior genotypes for seed yield may be utilised as donors in safflower breeding program or subjected to multi-location testing to identify stable lines.

Keywords: correlation; D² analysis; genetic diversity; germplasm; principal component analysis; safflower

Introduction

Safflower (*Carthamus tinctorius* L.) is an important oil seed crop belonging to family Compositae or Asteraceae, grown for its high-quality edible oil. In addition to seed oil, the flowers are rich in medicinal properties and the extracted dyes are used in textile industries. It is hardy and drought tolerant crop grown on residual soil moisture during rabi season. However, the crop is sensitive to moisture stress during flowering and seed filling stages which hastens maturity resulting in lower seed yield and oil content (1). In spite of its healthy oil composition, safflower has remained a neglected and underutilised crop. The medicinal and nutritional benefits of safflower oil have been well studied and elucidated (2). The main thrust of safflower crop improvement is yield enhancement along with pest and disease resistance. Effective breeding program is largely dependent on genetic variability of the available germplasm, selection of parents and selection methodologies. Hence systematic characterisation of the germplasm is the prerequisite to identify trait specific accessions for utilisation in crop breeding. Safflower genetic diversity has been studied based on morphological, biochemical and molecular markers (3–5). Germplasm evaluation including advanced breeding lines for agro-morphological traits is a continuous activity aimed at

the identification of superior germplasm (6). Recently five superior safflower genotypes were identified based on multi-trait genotype-ideotype distance index (MGDI) (7). Studies have reported safflower germplasm evaluation along with genetic divergence, heritability, correlation and path analysis (8). Quantitative traits such as seed yield is governed by many traits/yield attributes; hence it is important to collect information pertaining to various agro-morphological traits affecting yield in safflower (9). The correlation coefficient quantifies the strength and direction of the correlation between different traits and thus aids in selection (10). Correlation has been used by plant breeders to identify traits that are useful as selection criteria to improve crop yields (8, 11). A thorough trait association analysis of 120 safflower germplasm accessions identified significant positive correlations between seed yield per plant (SYP) and many yield component traits, such number of primary and secondary branches, plant height, number of capitula per plant and 100-seed weight (12). Multivariate analysis indicated the traits such as number of effective capitula/plant (EC), seed yield and days to flowering as the most important attributes for seed yield in safflower (13–15). In this study 118 safflower genotypes were evaluated in augmented block design for agro-morphological traits. The focus is on characterisation and identification of trait specific germplasm along with potential safflower genotypes for seed yield.

The promising and trait specific genotypes will be utilised as parental lines for safflower crop improvement programs. Genetic variability existing in the germplasm will be analysed, which assists plant breeders in planning crosses for safflower crop improvement.

Materials and Methods

Plant material

The safflower germplasm consisted of 120 genotypes provided by ICAR- Indian Institute of Oilseeds Research (IIOR), Hyderabad (Supplementary Table 1).

Experimental details

The experiment was conducted during rabi at Agricultural Research Station, Tandur in deep black soils. The geographic coordinates for the Agricultural Research Station (ARS) in Tandur, Vikarabad district, Telangana, are 17.227110° N latitude and 77.586360° E longitude. The experiment was laid out in augmented block design (ABD) with five blocks along with A1 and PBNS-12 which are national checks used in ICAR-All India Coordinated Research Project on Safflower (AICRP on Safflower) [ABD: unreplicated genotypes alongside replicated checks]. Each germplasm was grown in a plot size of 2.25 m². Standard spacing of 45 × 20 cm was followed and the crop was raised using standard agricultural practices. The observations were recorded on five randomly selected plants from each accession on six traits i.e. days to 50 % flowering (DAF), days to maturity (DAM), EC, no. of seeds/capitula (SPC), 100-seed weight (g) and SYP (g). Effective capitula containing one or more fully developed mature seeds.

Statistical analysis

The augmented analysis of variance (ANOVA) was carried out using 'augmented RCBD' R package (16). in RStudio 1.3. (<https://aravind-j.github.io/augmentedRCBD/https://cran.r-project.org/package=augmentedRCBD>). 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) and correlation were obtained (17). The multivariate analysis of genetic divergence using D² statistic was carried out (18). The data was analysed by INDOSTAT services Ltd (version 8.5), Hyderabad, India.

Results

Analysis of variance and mean performance of the genotypes

A set of diverse safflower germplasm maintained by ICAR-IIOR were evaluated to identify promising lines for utilisation as donors in hybridisation program. Analysis of variance- treatment adjusted (ANOVA) revealed highly significant differences among the genotypes for all the traits, except for no. of effective capitula/plant. The block-adjusted ANOVA revealed highly significant differences for the traits days to maturity and 100-seed weight. 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 indicating some fixed effect stabilising the performance of checks. The MSS of the test entries is almost comparable both under adjustment of blocks and treatment adjustment. It was observed that critical difference (CD) between two test entries between the blocks was slightly higher compared to that within the blocks for all the traits recorded which indicted that environmental effect was insignificant (Table 1).

The mean values for all the traits (DAF, DAM, EC, SPC, 100-seed weight (g) and SYP) along with standard error, standard deviation, range, skewness and kurtosis and coefficient of variation are presented in Table 1. The traits displayed a wide range of phenotypic data with near normal distribution for most of them (Supplementary Fig. 1). Near-normal distribution with non-significant left-hand skewness was observed for DAF; while non-significant right-handed skewness was observed for SYP. Near-normal distribution with significant right-handed skewness was observed for the traits EC and SPC, while left-handed skewness was observed for DAM and seed weight.

Coefficient of variation and heritability estimates

Low to high coefficient of variation was observed for the all the traits studied (Fig. 1a). Higher values of phenotypic coefficient of variability (PCV) were recorded compared to genotypic coefficient of variability (GCV) indicating environmental influence. Low GCV and PCV was observed for the traits DAF, medium for DAM and SPC while traits 100-seed weight, EC and SYP displayed high GCV and PCV. The broad sense heritability estimates were classified as low (< 30 %), moderate (30–60 %) and high > 60 %) (19). High heritability was recorded for all the traits studied (Fig. 1 b and c). Heritability estimates along with genetic advance (GA) is more reliable for effective selection (20). However recent reports indicated low heritability for seed yield (37.58 %) and number of capitula/plant in safflower (19.58 %) (21).

Correlation coefficients

Correlation coefficient has been one of the key determinants to investigate the relationship between yield and yield components (22). The SYP has significant correlation with EC, positive correlation with DAF and DAM, while nonsignificant positive correlation with SPC and 100-seed weight. The SPC has significant negative correlation with 100 seed weight (Fig. 2). Several studies also indicated significant positive correlation of SYP with EC (4, 9, 23, 24).

Principal component analysis

A total of 6 principal components were identified. The first four PCs explained nearly 80 % of total variance (Fig. 3a). Evaluation of 120 safflower genotypes revealed that first two principal components accounted for 24.6 % and 20.8 % of the total variation, respectively. The PCA-variables plot and PCA Bi-plots are presented in Fig. 3 b and c. PCA-variables plot revealed seed weight as the major contributor of PC1 and has the strongest positive loading, around +0.6. The traits SYP, DAM and DAF have strong negative loadings and DAM and DAF have high positive correlation (small angle) with each other. While SPC is the major contributor for PC2 and has a strong positive loading (~+0.5), SYP, EC and seed weight are negative. Yield contributing traits SPC versus seed weight also points in substantially different directions, suggesting that higher SPC is present in accessions with lower seed weight. The PCA biplot suggests that the accessions can be differentiated broadly into SPC-rich, DAM/DAF-associated, SYP-associated and seed-weight-associated groups.

For breeding GMU 3423, GMU 3420, GMU 1217 may be preferred for SPC trait, GMU 3446, GMU 6037, GMU 5081 for DAM/DAF, GMU 3438, GMU 2985, GMU 3716, GMU 4128 for seed weight. Two distinct genotypes GMU 2687, GMU 2232 are identified, of which GMU 2232 is identified as promising genotype for seed yield.

Table 1. Analysis of variance (ANOVA), descriptive statistics and estimates of variance for safflower germplasm

Source	d. f	DAF	DAM	EC	SPC	Seed wt	SYP
ANOVA, Treatment Adjusted							
Block (ignoring Treatments)	4	126.11*	175.49**	19.10 ^{ns}	116.90*	1.51**	122.52*
Treatment (eliminating Blocks)	119	35.74 ^{ns}	278.41**	70.23 ^{ns}	30.68 ^{ns}	0.68*	30.35 ^{ns}
Treatment: Check	1	0.90 ^{ns}	0.90 ^{ns}	0.40 ^{ns}	2.68 ^{ns}	0.55*	0.02 ^{ns}
Treatment: Test and Test vs. Check	118	36.04 ^{ns}	280.76**	70.82 ^{ns}	30.92 ^{ns}	0.68*	30.61 ^{ns}
Residuals	4	9.15	9.15	13.26	7.33	0.06	10.52
^{ns} $p > 0.05$; * $p \leq 0.05$; ** $p \leq 0.01$							
ANOVA Block Adjusted							
Treatment (ignoring Blocks)	119	39.77 ^{ns}	284.10**	70.42 ^{ns}	34.22 ^{ns}	0.72*	34.24 ^{ns}
Treatment: Check	1	0.90 ^{ns}	0.90 ^{ns}	0.40 ^{ns}	2.68 ^{ns}	0.55*	0.02 ^{ns}
Treatment: Test vs. Check	117	40.33 ^{ns}	288.06**	69.64 ^{ns}	34.62 ^{ns}	0.64*	33.25 ^{ns}
Treatment: Test	1	13.01 ^{ns}	103.41*	232.21*	19.32 ^{ns}	9.36**	184.03*
Block (eliminating Treatments)	4	6.35 ^{ns}	6.35 ^{ns}	13.16 ^{ns}	11.64 ^{ns}	0.37 ^{ns}	6.79 ^{ns}
Residuals	4	9.15	9.15	13.26	7.33	0.06	10.52
^{ns} $P > 0.05$; * $P \leq 0.05$; ** $P \leq 0.01$							
Standard Errors							
CD between a Test Treatment and a Control Treatment		4.06	4.06	4.89	0.33	3.63	4.35
CD between check Treatment Means		1.91	1.91	2.30	0.15	1.71	2.05
CD between Two Test Treatments (Different Blocks)		5.24	5.24	6.31	0.42	4.69	5.62
CD between Two Test Treatments (Same Block)		4.28	4.28	5.15	0.35	3.83	4.59
Mean±SE		81.72±0.57	119.61±1.53	29.54±0.79	24.65±0.55	4.19±0.08	15±0.51
SD		6.30	16.75	8.69	5.98	0.87	5.61
Range		67.40-93.40	117.4-133.40	9.54-58.84	13.29-45.14	0.62-6.52	2.73-30.78
Skewness		-0.34 ^{ns}	-6.0**	0.55*	1.00**	-0.52*	0.07 ^{ns}
Kurtosis		2.02**	43.06**	3.72 ^{ns}	4.71**	4.60**	2.53 ^{ns}
CV (%)		3.7	2.52	12.44	11.01	5.75	21.20

d.f.: degrees of freedom; DAF: days after flowering; DAM: days after maturity; EC: effective capitula per plant; SPC: seeds per capitula; Seed wt: seed weight; SYP: seed yield per plant; ANOVA: analysis of variance; ^{ns}: $p > 0.05$; * $p \leq 0.05$; ** $p \leq 0.01$; CD: critical difference; SE: standard error; SD: standard deviation; CV: coefficient of variation.

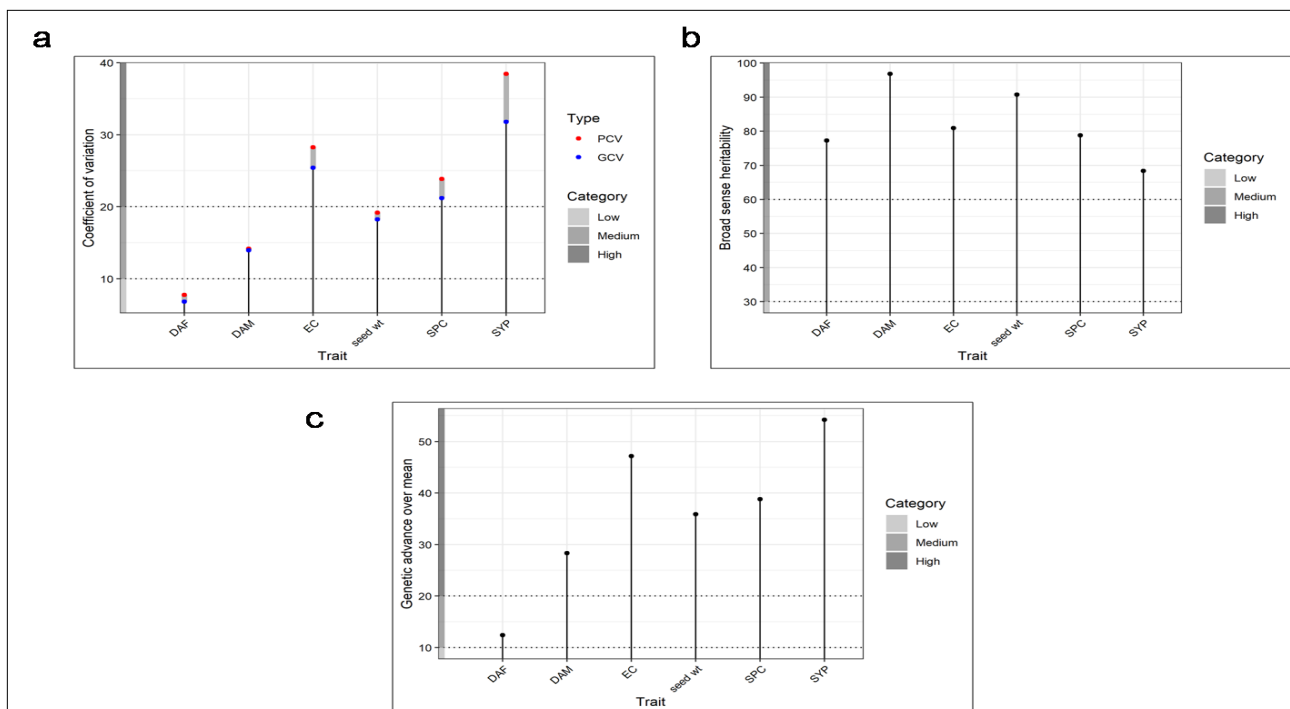


Fig. 1. Graphical representation of genetic parameters for six yield-related traits in safflower germplasm. a: Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV); b: broad-sense heritability; c: genetic advance as a percentage of mean (GAM). DAF: days to 50% flowering; DAM: days to maturity; EC: effective capitula per plant; Seed wt: 100-seed weight; SPC: seeds per capitula; SYP: seed yield per plant.

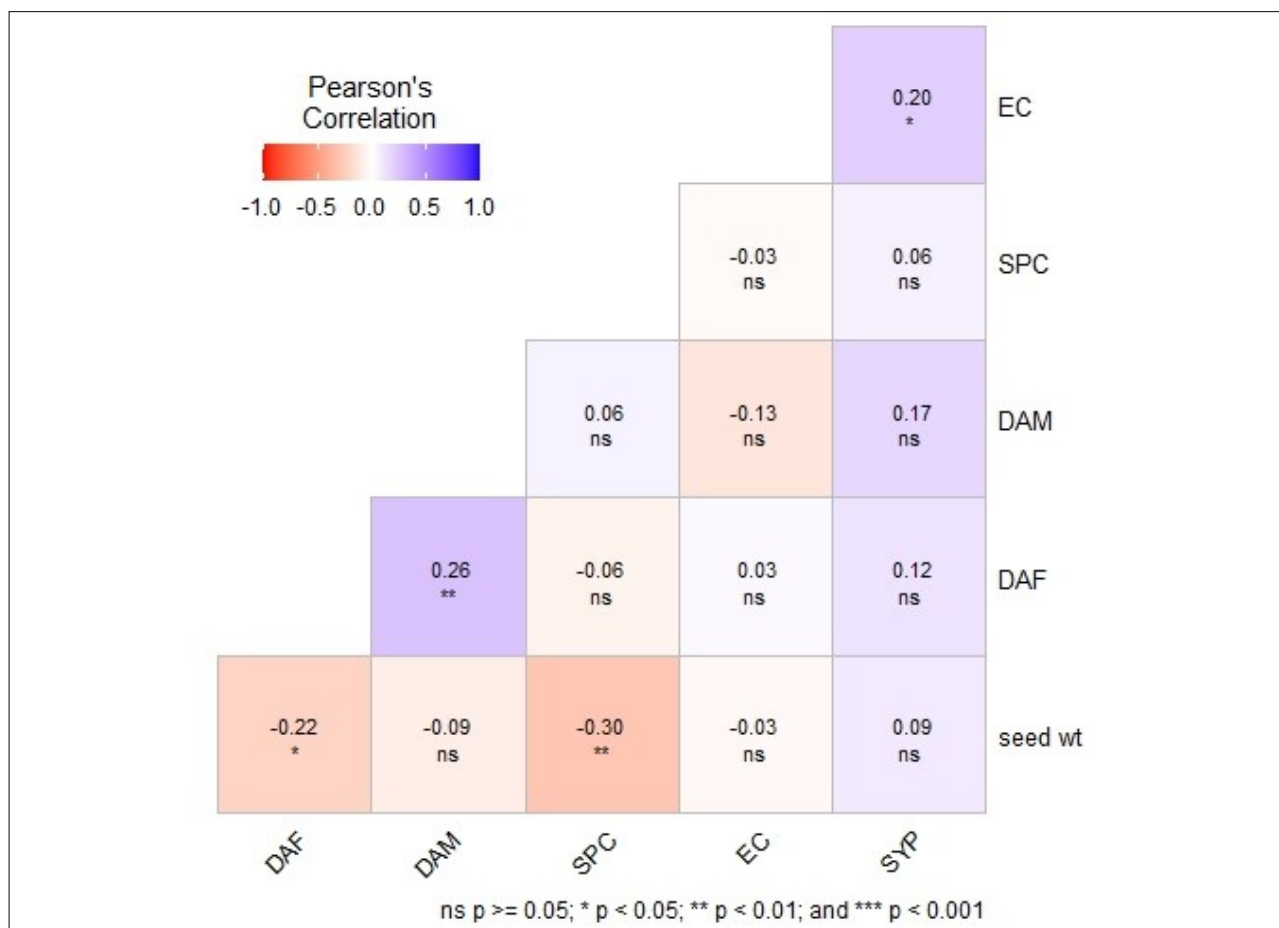


Fig. 2. Correlation coefficients among component yield and yield related traits among 120 safflower germplasm.

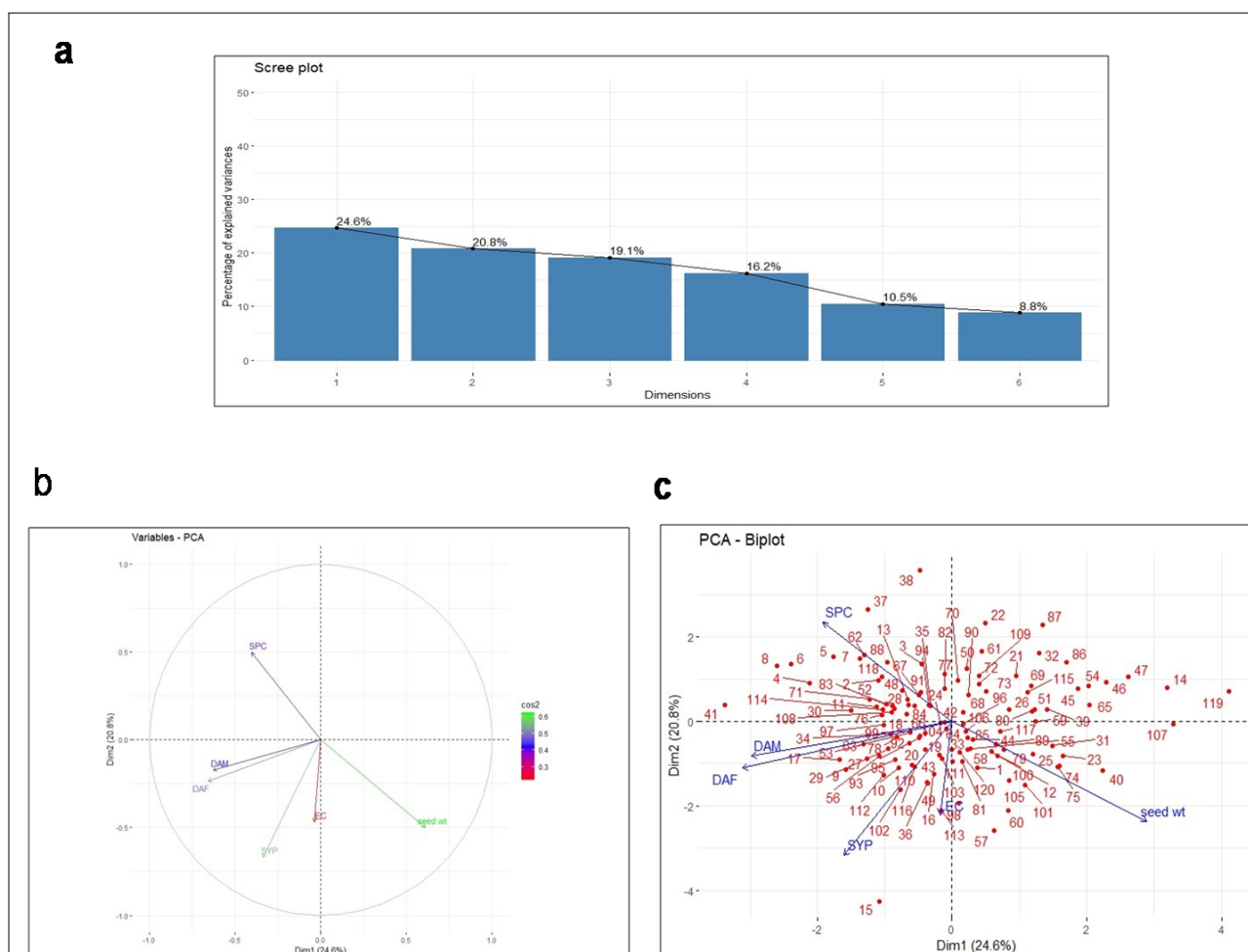


Fig. 3. Principal component analysis of safflower germplasm. a: Scree Plot depicting the contribution of 6 principal components; b: PCA-Variables Plot; c: PCA-Biplots explaining the contribution of 6 traits to the total variation in safflower germplasm.

Genetic diversity based on D² analysis

Based on Mahalanobis D² analysis 120 safflower genotypes were grouped into 9 clusters (Supplementary Fig. 2). Cluster V is the largest cluster with 27 genotypes followed by cluster I with 22 genotypes. Cluster VIII is the smallest cluster with only two genotypes (Table 2). Early maturing genotypes were present in cluster II and VIII with 118 days to maturity. Genotypes in cluster VIII had early flowering genotypes with highest number of effective capitula/plant, more SPC, 100-seed weight and highest SYP (Table 3). The average inter and intra cluster distances are presented in Table 4. Inter cluster distances ranged from 9372.65 to 1024955.00. Minimum inter cluster distance was observed between clusters II and III, while maximum inter cluster distance was between VII and VIII. Minimum intra cluster distance of 239.37 was observed for cluster VIII while maximum intra cluster distance was for 4742.58 for cluster V (Table 4). Hybridisation between genetically distant genotypes has been suggested by several researchers to generate promising breeding material (25). Germplasm belonging to clusters IX, VIII, VI and II have higher cluster means for EC, SPC and SPY and hence can be selected as parental

lines for hybridisation program involving seed yield improvement of safflower. Hybridisation between genotypes belonging to diverse clusters along with high cluster means is preferred for crop improvement. Hence crosses may be attempted between genotypes belonging to cluster IX with cluster I, VI and VII. Similarly crosses between genotypes of clusters VIII with V, VI and VII may result in better segregants and genotypes with high yield.

Trait wise performance of safflower genotypes

The safflower germplasm comprised of genotypes with seed yield/plant ranging from 2.73–30.78 g. Genotypes GMU 1110 (26.27 g) and GMU 2232 (30.78 g) exhibited significant superiority in seed yield over both the checks A1 (19.46 g) and PBNS-12 (19.38 g), while 17 genotypes were on par with best check for SYP. Around 20 genotypes were identified with early maturity (115 days) and five genotypes with bold seed. Thirteen genotypes possess more than 40 capitula/plant and genotypes with more than 35 seeds/capitula were also identified in this study (Table 5). Identification of trait specific germplasm is highly useful for breeders in planning crosses for safflower crop improvement (26).

Table 2. Grouping of 120 safflower germplasm into nine clusters based on D² analysis

Cluster No.	No. of genotypes	Names of the genotypes
I	22	GMU 3731, GMU 5163, GMU 3730, GMU 6037, GMU 4038, GMU 3488, GMU 4093, GMU 3395, GMU 3661, GMU 5081, GMU 4201, EC-755687, GMU 2757, GMU 3400, GMU 3703, GMU 2987, GMU 3690, GMU 4101, GMU 3451, GMU 3992, GMU 3293, GMU 3480
II	8	GMU 2985, GMU 3332, GMU 3325, GMU 3494, GMU 4129, GMU 3778, GMU 5663, GMU 5728
III	19	GMU 3226, GMU 3640, GMU 3206, GMU 3383, A1, GMU 4502, GMU 7351, GMU 3773, GMU 3739, GMU 3590, GMU 3438, GMU 3266, GMU 3526, GMU 3624, GMU 3968, GMU 5908, GMU 4128, PBNS-12, GMU 1118
IV	14	GMU 3716, GMU 3781, GMU 244, GMU 6026, GMU 3490, GMU 3313, GMU 3493, GMU 3776, GMU 3449, GMU 3840, GMU 4009, GMU 3477, GMU 1157, GMU 3482
V	27	GMU 4035, GMU 4223, GMU 3465, EC-523367, GMU 2802, GMU 3675, GMU 6915, GMU 3446, GMU 2822, GMU 4814, GMU 3523, GMU 2720, GMU 6114, EC-523373, GMU 3704, GMU 3671, EC-755684, GMU 1217, GMU 3678, GMU 3702, EC-755675, GMU 3676, EC-755673, GMU 1110, GMU 3679, GMU 3420, GMU 3423
VI	8	GMU 3962, GMU 3996, GMU 3939, GMU 3683, GMU 3966, GMU 3654, GMU 1078, GMU 7390
VII	10	GMU 3858, GMU 3877, GMU 3663, GMU 2718, GMU 3649, GMU 4983, GMU 2687, GMU 3901, GMU 3891, EC-523368-2
VIII	2	GMU 3638, GMU 3645
IX	10	GMU 3384, GMU 3602, GMU 3355, GMU 394, GMU 2232, GMU 1339, GMU 3431, GMU 4082, GMU 2928, GMU 3635

Table 3. Cluster means of 120 safflower germplasm for six yield related traits of safflower

Cluster	Days to 50 % flowering	Days to maturity	No. of effective capitula/plant	No. of seeds/capitula	100-seed weight	Seed yield/plant
I	83.31	123.31	28.74	32.33	3.89	24.56
II	78.51	118.51	30.80	38.80	4.52	25.00
III	81.02	121.02	30.13	36.18	4.65	23.62
IV	79.77	119.77	26.85	33.26	4.56	24.15
V	82.68	122.68	28.17	28.31	3.88	25.64
VI	86.20	126.20	27.19	27.21	3.78	25.87
VII	81.40	121.40	28.25	20.16	4.20	21.67
VIII	78.20	118.20	42.84	50.65	5.34	28.66
IX	79.60	119.60	37.17	39.74	4.55	25.83

Table 4. Average intra and inter-cluster D² values for nine clusters of safflower germplasm

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	1815.98	87081.97	43196.54	11253.39	20848.19	58119.96	128110.60	432411.70	198038.20
II		1213.63	9372.65	39802.68	184038.40	282138.10	421154.30	133280.20	24618.01
III			1875.53	13222.07	116457.00	196024.20	314028.60	206491.20	59533.82
IV				2062.42	56146.89	113595.80	206405.80	314603.40	121840.70
V					4742.58	14230.68	52790.59	626227.80	334724.20
VI						2613.61	16409.34	799924.30	463828.90
VII							2741.68	1024955.00	638108.80
VIII								239.37	47980.02
IX									3866.92

Table 5. Trait wise performance of safflower genotypes

Sl. No.	Trait	Highest performance accessions
1.	Days to 50 % flowering	< 75days: GMU 2928, GMU 2985, GMU 3355, GMU 3423, GMU 3431, GMU 3438, GMU 3477, GMU 3480, GMU 3494, GMU 3590, GMU 3649, GMU 3679, GMU 3703, GMU 3704, GMU 3773, GMU 3781, GMU 4983, GMU 5163, GMU 6114, GMU 7351
2.	Days to maturity	< 115days: GMU 2928, GMU 2985, GMU 3355, GMU 3423, GMU 3431, GMU 3438, GMU 3477, GMU 3480, GMU 3494, GMU 3590, GMU 3649, GMU 3679, GMU 3703, GMU 3704, GMU 3773, GMU 3781, GMU 4983, GMU 5163, GMU 6114, GMU 7351
3.	No. of effective capitula / plant	> 40: EC-523373, GMU 1078, GMU 2718, GMU 3438, GMU 3624, GMU 3635, GMU 3638, GMU 3645, GMU 3663, GMU 3675, GMU 3704, GMU 3730, GMU 5908
4.	No. of seeds/capitula	>35: EC-523373, EC-755675, GMU 2928, GMU 3423, GMU 3638
5.	100-seed weight (g)	>5.4g: A1, GMU 3645, GMU 3716, GMU 3941, GMU 4983
6.	Seed yield/plant(g)	> 20g: GMU 1078, GMU 1110, GMU 2232, GMU 3266, GMU 3293, GMU 3313, GMU 3325, GMU 3449, GMU 3602, GMU 3645, GMU 3941, GMU 3992, GMU 4082, GMU 4128, GMU 4129, GMU 5728, GMU 5908, GMU 6026, GMU 7351

Nineteen promising genotypes which are either on par or superior to national checks A1 and PBNS-12 based on seed yield/plant were identified. Early maturing genotypes can be utilised as parental lines in the breeding program. The IIOR safflower germplasm is distinct from the general National Bureau of Plant Genetic Resources (NBPGR) collection. The IIOR manages the active, specialised working collection (GMU) for immediate breeding, while NBPGR manages the national, long-term conservation gene bank, although they work together. In India Mediterranean germplasm comprising of high oil content and high oleic acid are being used as parental lines in safflower breeding programme. These genotypes are low seed yielders and hence cannot be released as varieties.

Discussion

One major challenge for plant breeders is to develop climate resilient crop cultivars in response to rapid shifts in cultivation conditions and resources. The integration of crop genetic resources, breeding tools and approaches to incorporate genetic diversity into commercialised cultivars is highly needed. Genetic variability in the crop is the fundamental requirement for any plant-breeding program to deliver superior and highly adaptable cultivars. The germplasm comprised of genotypes with SYP ranging from 2.73–30.78 g and EC of 9.54–58.84. Genotypes GMU 1110 and GMU 2232 were identified for superior SYP compared to both the national checks A1 and PBNS-12. The similar variability was reported in recent study conducted (26). In contrast to the present studies narrow range variation was observed for DAF and DAM (21, 26). Higher variability (both genotypic and phenotypic) was observed for the traits 100-seed weight, EC and SYP in the safflower genotypes analysed, giving opportunity for genetic improvement of these yield related traits (4). The results agree with recent studies for EC and SPY but contradicted for SPC (24). The existence of sufficient coefficient of variation does not indicate heritable portion of the trait and only shows the extent of variability present for those traits. Hence heritability is studied which is a good indicator for transfer of characters to offspring (27). Higher heritability was recorded for all the traits studied which coincided with recent report for only EC, 100-seed weight and SYP (28). Strong positive correlation between SYP and EC corresponds well with several earlier studies in safflower (29–31). However few studies reported significant positive correlation of SYP with test weight (29, 32–34). The PCA is a statistical technique used to simplify large, complex datasets by reducing the number of variables while retaining as much important information and data variation as possible (35). The safflower germplasm revealed that first two principal components accounted for 45 % of

the total variation, while recent study reported 69.86 per cent of cumulative variance (7), while earlier study observed that the first and second principal components accounted for 29.5 % and 15.9 % of the total variation, respectively (36). The biplot provides valuable information on the association among traits and the clustering pattern of genotypes. A smaller angle between two trait vectors indicates a positive correlation between the corresponding traits, whereas an angle close to 90° suggests weak or no correlation. Hundred-seed weight was the major contributor to PC1, indicating a significant role in explaining the variation represented by the first principal component. The genotypes analysed were grouped into nine clusters depicting their diverse nature and substantial variability present within the germplasm. Earlier reports have shown the grouping of 45 safflower accessions into four major clusters based on different physiological traits (37). Around 31 safflower genotypes were classified into three groups with Cluster I being the largest, consisting of 14 genotypes. Five superior genotypes (IIOR Saff-667-19, IIOR Saff-652-19, IIOR Saff-625-19, IIOR Saff-675-19 and IIOR Saff-636-19) were identified based on the MGIDI selection index (7). The present study identified a set of 19 promising genotypes which are either on par or superior to national checks A1 and PBNS-12 and can be utilised for effectively for safflower crop improvement.

Conclusion

The 120 safflower germplasm accessions were characterised and grouped into 9 clusters based agro-morphological traits indicating the diverse nature of the entries analysed. Genotypes belonging to cluster VIII are highly useful for improving safflower yield owing to high cluster means for effective capitula per plant (EC), seeds per capitula (SPC) and seed yield per plant (SYP). Trait specific safflower germplasm was identified for early duration, EC, SPC and 100-seed weight. Plant breeders can select diverse and trait specific germplasm for utilisation as parental lines in hybridisation program. Promising germplasm GMU 1110 and GMU 2232 may be tested in replicated trials and multi-location trials for varietal release. Early maturing entries GMU 3773 and GMU 7351 are promising donors for varietal development.

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Authors' contributions

SNCVLP contributed to conceptualisation, investigation, formal analysis and writing original draft. AG contributed to data analysis. PS contributed to investigation, review and editing. All authors have read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

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