Research Article

Estimation of Different Genetic Parameters in Various Safflower (*Carthamus tinctorius* L.) Genotypes under Field Condition

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Abstract | The study was carried out to investigate the genetic estimates regarding various economic traits i.e. days to flowering, plant height, days to maturity, no. of primary branches per plant, no. of secondary branches per plant, pods per plant, 1000-seed weight and yield per plant of 200 safflower accessions. Analysis of variance and principal component analysis were carried out to estimate the extent of variability for studied parameters and to partition the germplasm into various cluster groups on basis of their mean performance. A value of 74% was indicated by the first three PCs, which showed the highest variability between studied parameters. Eigen values >1 contributed variability between the genotypes under field condition. Minimum and maximum heritability estimates ranged between 77.4% - 99.0% for days to flowering and pods per plant, respectively. Genetic advance estimates ranged between 11.99-27.21% for number of primary branches per plant and yield per plant, respectively. However, coefficient of variance ranged between 2.67-19.31% for days to maturity and number of primary branches per plant. High broad sense heritability magnitudes predicted that studied parameters were under influence of additive genetic effects and less affected by environment. Thus, direct selection of accessions on basis of studied parameters could lead to genetic improvement of the material and these traits could also be helpful for potential improvement of yield in safflower (*Carthamus tinctorius*).

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Introduction

Safflower is famous oil seed crop of ancient world and belongs to compositae or Asteraceae family. It is a good source of high-quality oil mostly used for industrial, ornamental, biofuel and food purposes (Sehgal *et al*., 2009; Canavar *et al*., 2014). It is a multipurpose crop, mostly cultivated as cut flower, medicinal plant, vegetable crop, fodder crop, dye and oil extracting source for paint industry (Emongor, 2010; Emongor *et al*., 2015).

Safflower oil is rich source of vitamin 'E', polyunsaturated (linoleic acid) and monounsaturated (oleic acid) fatty acids, which are helpful in lowering blood cholesterol level (Baydar and Turgot, 1999; Arslan *et al*., 2003). Percent concentration of linoleum acid (70-87%) and oleic acid (11-87%) is much high as compared to olive oil, peanut, soybean, cotton seed and corn oil (Reza *et al*., 2013). Oil is also used in preparation of soft margarines and salad oil (Conge *et al*., 2007). Safflower seeds are rich in vitamins, minerals and tocopherols (Velasco *et al*., 2005). Petals of flower are used in manufacturing of dyes, food color and medicines (Istanbulluoglu, 2009; Emongor, 2010).

The crop was mainly cultivated in arid and semi-arid regions of the world with low irrigation, low fertilizer input and on marginal lands (Hojati *et al*., 2011). In past, safflower was cultivated on limited area, as minor crop (Canavar *et al*., 2014). Now, the scenario has changed. Efforts have been made to raise the cultivated area and productivity of the crop all over the world. Naturally, safflower is a temperate zone crop, but has capability of bearing temperature ranges from -7 to 40 °C with zero frost injury during vegetative and flowering growth periods. Crop is widely grown in more than 60 countries of the world, being resistance to many abiotic stresses. India, China, USA, Ethiopia, Kenya, Mexico, Argentina, Australia, Canada, Italy, Spain, Turkey, Iraq, Syria, Kazakhstan, Iran, Uzbekistan, Morocco, Israel, Russia and Pakistan are the commercial growers of the Safflower in the world (Emongor and Oagile, 2017).

Cropping system of Pakistan is deficit in space for cultivation of both conventional and non-conventional oil seed crops and these are considered as minor crops. However, to meet the requirement of vegetable oil for humans, animals and industry, rearing of conventional oil seed crops over limited area is not fruitful. So, it is a dire need of the time to motivate the growers for sowing of non-conventional oil seed crops in Pakistan. Northern areas of Sindh and Baluchistan are suitable for cultivation of safflower as an oil seed crop. While, in Punjab and KPK provinces, arid and semi-arid regions have favorable environmental conditions for safflower production (Amjad, 2014). Pakistan expends a huge amount around US$ 1.5 billion to buy in the edible oil during 2018-19. The loss of foreign exchange reserves is much less than FY 2017-18, in which about US$ 3.0 billion were spent on import of edible oil. It is need of the time to enhance the cultivated area of the non-conventional oilseed crops like safflower and sunflower in Pakistan to meet the demand of annual vegetable oil of the country (Anonymous, 2018-19).

Present study was designed to investigate the importance of yield and its contributing parameters of a plant and to determine the high potential yielding germplasm based on different agronomic parameters by collecting and screening the national and international diverse genetic material. The selected genotypes may be included in further breeding programs enabling to help the safflower plant breeders to maintain and improve the genetic constitutions of the germplasm.

Materials and Methods

The genetic material was comprised of two hundred accessions (Table 1). Germplasm was collected from Institute of Agricultural Biotechnology and Genetic Resources (IABGR), NARC, Islamabad. Genetic material was evaluated for various yield contributing parameters during 2016-17 at experimental area of PARC Research and Training Station, Faculty of Agriculture, Bahauddin Zakariya University, Multan. Randomized Complete Block Design was implemented along with three replications by maintaining 15-20 cm interplant distance and row to row distance was 40-45cm. Balode *et al*. (2012) and Shinwari *et al*. (2014) screened 155 and 122 accessions of safflower for various screening purposes. All cultural practices were done as per requirement. Ten randomly chosen plants from each genotype were used to record data of the following parameters; days to flowering (DF), plant height (PH), pods per plant (PPP), no. of primary branches per plant (PBP), no. of secondary branches per plant (SBP), thousand grain weight (TGW), yield per plant (YPP) and days to maturity (DM).

Recorded data was put to estimate the analysis of variance (Steel *et al*., 1997) to check the existence of significant genetic variability. Heritability (h^2) in the broad sense and genetic advance for all parameters were estimated according to the formulae as described by Allard (1960) and Falconer (1981), respectively. Principal component analysis was performed by using XLSTAT 2014.

Results and Discussion

Analysis of variance with genetic advance and heritability for 200 lines revealed valuable differences for all the traits under study (Table 2). Magnitude of genetic advance among studied parameters ranged between 11.99-27.21% for PBP and YPP, respectively. Whereas, coefficient of variance (CV) ranged from 2.67 to 19.71% for DM and PBP, respectively. Estimation of heritability ranged between 77.4% to 99.0% for DF and PPP in observed traits (Table 2).

Table 1: *List of safflower germplasm.*

Sr. No.	Accessions	Genus	Species	Origin	Sr. No.	Accessions	Genus	Species	Origin
1	016173	*Carthamus*	*tinctorius*	India	101	016327	*Carthamus*	*tinctorius*	Afghanistan
2	016186	*Carthamus*	*tinctorius*	India	102	016329	*Carthamus*	*tinctorius*	Afghanistan
3	016188	*Carthamus*	*tinctorius*	India	103	016331	*Carthamus*	*tinctorius*	Afghanistan
4	016189	*Carthamus*	*tinctorius*	India	104	016333	*Carthamus*	*tinctorius*	Afghanistan
5	016190	*Carthamus*	*tinctorius*	India	105	016334	*Carthamus*	*tinctorius*	Afghanistan
6	016191	*Carthamus*	*tinctorius*	India	106	016335	*Carthamus*	*tinctorius*	Afghanistan
7	016192	*Carthamus*	*tinctorius*	India	107	016337	*Carthamus*	*tinctorius*	Afghanistan
8	016193	*Carthamus*	*tinctorius*	India	108	016338	*Carthamus*	*tinctorius*	Afghanistan
9	016194	*Carthamus*	*tinctorius*	India	109	016341	*Carthamus*	*tinctorius*	Iran
10	016195	*Carthamus*	*tinctorius*	Turkey	110	016342	*Carthamus*	*tinctorius*	Iran
11	016199	*Carthamus*	*tinctorius*	Kenya	111	016343	*Carthamus*	*tinctorius*	Iran
12	016200	*Carthamus*	*tinctorius*	Turkey	112	016345	*Carthamus*	*tinctorius*	Iran
13	016201	*Carthamus*	*tinctorius*	India	113	016346	*Carthamus*	*tinctorius*	Iran
14	016202	*Carthamus*	*tinctorius*	Afghanistan	114	016347	*Carthamus*	*tinctorius*	Ethiopia
15	016203	*Carthamus*	*tinctorius*	Afghanistan	115	016349	*Carthamus*	*tinctorius*	Portugal
16	016204	*Carthamus*	*tinctorius*	Iran	116	016351	*Carthamus*	*tinctorius*	Portugal
17	016205	*Carthamus*	*tinctorius*	Ethiopia	117	016353	*Carthamus*	*tinctorius*	Portugal
18	016206	*Carthamus*	*tinctorius*	Iran	118	016354	*Carthamus*	*tinctorius*	Portugal
19	016207	*Carthamus*	*tinctorius*	Australia	119	016356	*Carthamus*	*tinctorius*	Pakistan
20	016209	*Carthamus*	*tinctorius*	Morocco	120	016357	*Carthamus*	*tinctorius*	Pakistan
21	016210	*Carthamus*	*tinctorius*	Morocco	121	016358	*Carthamus*	*tinctorius*	Pakistan
22	016211	*Carthamus*	*tinctorius*	Spain	122	016359	*Carthamus*	*tinctorius*	Pakistan
23	016216	*Carthamus*	*tinctorius*	India	123	016360	*Carthamus*	*tinctorius*	India
24	016217	*Carthamus*	*tinctorius*	India	124	016361	*Carthamus*	*tinctorius*	India
25	016218	*Carthamus*	*tinctorius*	India	125	016362	*Carthamus*	*tinctorius*	India
26	016220	*Carthamus*	*tinctorius*	Pakistan	126	016364	*Carthamus*	*tinctorius*	India
27	016225	*Carthamus*	*tinctorius*	India	127	016365	*Carthamus*	*tinctorius*	India
28	016229	*Carthamus*	*tinctorius*	India	128	016366	*Carthamus*	*tinctorius*	India
29	016230	*Carthamus*	*tinctorius*	India	129	016367	*Carthamus*	*tinctorius*	India
30	016231	*Carthamus*	*tinctorius*	India	130	016368	*Carthamus*	*tinctorius*	India
31	016233	*Carthamus*	*tinctorius*	India	131	016369	*Carthamus*	*tinctorius*	India
32	016234	*Carthamus*	*tinctorius*	India	132	016373	*Carthamus*	*tinctorius*	India
33	016235	*Carthamus*	*tinctorius*	India	133	016374	*Carthamus*	*tinctorius*	Australia
34	016236	*Carthamus*	*tinctorius*	India	134	016375	*Carthamus*	*tinctorius*	Australia
35	016237	*Carthamus*	*tinctorius*	India	135	016377	*Carthamus*	*tinctorius*	Australia
36	016238	*Carthamus*	*tinctorius*	India	136	016379	*Carthamus*	*tinctorius*	Australia
37	016239	*Carthamus*	*tinctorius*	India	137	016381	*Carthamus*	*tinctorius*	Afghanistan
38	016240	*Carthamus*	*tinctorius*	India	138	016383	*Carthamus*	*tinctorius*	Ethiopia
39	016241	*Carthamus*	*tinctorius*	India	139	016386	*Carthamus*	*tinctorius*	Egypt
40	016242	*Carthamus*	*tinctorius*	India	140	016387	*Carthamus*	*tinctorius*	India
41	016243	*Carthamus*	*tinctorius*	India	141	016390	*Carthamus*	*tinctorius*	India
42	016245	*Carthamus*	*tinctorius*	India	142	016391	*Carthamus*	*tinctorius*	India
43	016246	*Carthamus*	*tinctorius*	India	143	016392	*Carthamus*	*tinctorius*	India
44	016247	*Carthamus*	*tinctorius*	India	144	016393	*Carthamus*	*tinctorius*	India
45	016249	*Carthamus*	*tinctorius*	India	145	016396	*Carthamus*	*tinctorius*	India
46	016250	*Carthamus*	*tinctorius*	India	146	016397	*Carthamus*	*tinctorius*	India
47	016252	*Carthamus*	*tinctorius*	India	147	016398	*Carthamus*	*tinctorius*	India
48	016253	*Carthamus*	*tinctorius*	India	148	016402	*Carthamus*	*tinctorius*	Israel
49	016254	*Carthamus*	*tinctorius*	India	149	016407	*Carthamus*	*tinctorius*	Iran
50	016259	*Carthamus*	*tinctorius*	Iran	150	016408	*Carthamus*	*tinctorius*	Iran

Links Researchers

Sr. No.	Accessions	Genus	Species	Origin	Sr. No.	Accessions	Genus	Species	Origin
51	016260	*Carthamus*	*tinctorius*	Egypt	151	016409	*Carthamus*	*tinctorius*	Iran
52	016261	*Carthamus*	*tinctorius*	Egypt	152	016410	*Carthamus*	*tinctorius*	Iran
53	016262	*Carthamus*	*tinctorius*	Egypt	153	016411	*Carthamus*	*tinctorius*	Iran
54	016264	*Carthamus*	*tinctorius*	Egypt	154	016412	*Carthamus*	*tinctorius*	Iran
55	016265	*Carthamus*	*tinctorius*	Pakistan	155	016413	*Carthamus*	*tinctorius*	Iran
56	016266	*Carthamus*	*tinctorius*	Pakistan	156	016414	*Carthamus*	*tinctorius*	Iran
57	016267	*Carthamus*	*tinctorius*	Pakistan	157	016415	*Carthamus*	*tinctorius*	Iran
58	016268	*Carthamus*	*tinctorius*	Pakistan	158	016416	*Carthamus*	*tinctorius*	Iran
59	016269	*Carthamus*	*tinctorius*	Pakistan	159	016419	*Carthamus*	*tinctorius*	Iran
60	016270	*Carthamus*	*tinctorius*	Pakistan	160	016420	*Carthamus*	*tinctorius*	Iran
61	016271	*Carthamus*	*tinctorius*	Egypt	161	016421	*Carthamus*	*tinctorius*	Iran
62	016272	*Carthamus*	*tinctorius*	Egypt	162	016423	*Carthamus*	*tinctorius*	Iran
63	016273	*Carthamus*	*tinctorius*	Egypt	163	016425	*Carthamus*	*tinctorius*	Iran
64	016274	*Carthamus*	*tinctorius*	Egypt	164	016426	*Carthamus*	*tinctorius*	Turkey
65	016276	*Carthamus*	*tinctorius*	Egypt	165	016428	*Carthamus*	*tinctorius*	Afghanistan
66	016278	*Carthamus*	*tinctorius*	India	166	016430	*Carthamus*	*tinctorius*	Afghanistan
67	016279	*Carthamus*	*tinctorius*	Egypt	167	016431	*Carthamus*	*tinctorius*	Afghanistan
68	016280	*Carthamus*	*tinctorius*	Egypt	168	016432	*Carthamus*	*tinctorius*	India
69	016281	*Carthamus*	*tinctorius*	Iran	169	016434	*Carthamus*	*tinctorius*	India
70	016283	*Carthamus*	*tinctorius*	Iran	170	016435	*Carthamus*	*tinctorius*	India
71	016284	*Carthamus*	*tinctorius*	Iran	171	016436	*Carthamus*	*tinctorius*	India
72	016285	*Carthamus*	*tinctorius*	Iran	172	016438	*Carthamus*	*tinctorius*	India
73	016287	*Carthamus*	*tinctorius*	Iran	173	016439	*Carthamus*	*tinctorius*	India
74	016288	*Carthamus*	*tinctorius*	Iran	174	016441	*Carthamus*	*tinctorius*	Sudan
75	016289	*Carthamus*	*tinctorius*	Iran	175	016442	*Carthamus*	*tinctorius*	Sudan
76	016290	*Carthamus*	*tinctorius*	Iran	176	016443	*Carthamus*	*tinctorius*	Sudan
77	016291	*Carthamus*	*tinctorius*	Iran	177	016446	*Carthamus*	*tinctorius*	Russia
78	016292	*Carthamus*	*tinctorius*	Iran	178	016447	*Carthamus*	*tinctorius*	Egypt
79	016293	*Carthamus*	*tinctorius*	Iran	179	016451	*Carthamus*	*tinctorius*	Egypt
80	016295	*Carthamus*	*tinctorius*	Iran	180	016453	*Carthamus*	*tinctorius*	Egypt
81	016296	*Carthamus*	*tinctorius*	Iran	181	016458	*Carthamus*	*tinctorius*	India
82	016297	*Carthamus*	*tinctorius*	Iran	182	016459	*Carthamus*	*tinctorius*	India
83	016298	*Carthamus*	*tinctorius*	Iran	183	016460	*Carthamus*	*tinctorius*	India
84	016299	*Carthamus*	*tinctorius*	Iran	184	016464	*Carthamus*	*tinctorius*	India
85	016301	*Carthamus*	*tinctorius*	Iran	185	016465	*Carthamus*	*tinctorius*	India
86	016303	*Carthamus*	*tinctorius*	Iran	186	016466	*Carthamus*	*tinctorius*	India
87	016304	*Carthamus*	*tinctorius*	Iran	187	016467	*Carthamus*	*tinctorius*	India
88	016306	*Carthamus*	*tinctorius*	Iran	188	016469	*Carthamus*	*tinctorius*	India
89	016308	*Carthamus*	*tinctorius*	Iran	189	016470	*Carthamus*	*tinctorius*	Turkey
90	016310	*Carthamus*	*tinctorius*	Iran	190	016471	*Carthamus*	*tinctorius*	Iran
91	016312	*Carthamus*	*tinctorius*	Turkey	191	016474	*Carthamus*	*tinctorius*	Iran
92	016313	*Carthamus*	*tinctorius*	Turkey	192	016478	*Carthamus*	*tinctorius*	Iran
93	016314	*Carthamus*	*tinctorius*	Turkey	193	016479	*Carthamus*	*tinctorius*	Iran
94	016316	*Carthamus*	*tinctorius*	Turkey	194	016482	*Carthamus*	*tinctorius*	Iran
95	016317	*Carthamus*	*tinctorius*	Turkey	195	016483	*Carthamus*	*tinctorius*	USA
96	016318	*Carthamus*	*tinctorius*	Spain	196	016484	*Carthamus*	*tinctorius*	USA
97	016320	*Carthamus*	*tinctorius*	Germany	197	016489	*Carthamus*	*tinctorius*	China
98	016324	*Carthamus*	*tinctorius*	Iraq	198	016492	*Carthamus*	*tinctorius*	China
99	016325	*Carthamus*	*tinctorius*	Iraq	199	016495	*Carthamus*	*tinctorius*	China
100	016326	*Carthamus*	*tinctorius*	Iraq	200	016501	*Carthamus*	*tinctorius*	USA

Table 2: *Means and analysis of variance (ANOVA) for eight traits among 200 safflower genotypes.*

Parameters	MS (R)	MS (V)	MS(E)	Means ± SE	h^2 (%)	GA (%)	CV (%)
DF	9.512	50.028	11.294	121.97	77.4	22.22	2.755
PH	8.202	567.962	13.287	104.77	97.7	19.6	3.479
DM	9.052	87.593	16.453	151.70	81.2	17.33	2.673
PPP	1.872	224.181	2.223	38.31	99.0	16.51	3.892
PBP	0.140	4.902	0.246	2.57	95.0	11.99	19.31
SBP	1.415	74.672	1.1369	8.54	98.5	23.51	12.48
TGW	5.612	157.537	4.012	37.78	97.5	14.73	5.301
YPP	15.247	1248.901	20.240	83.82	98.4	27.21	5.367

DF: days to flowering; PH: plant height; DM: days to maturity; PPP: pods per plant; PBP: number of primary branches per plant; SBP: number of secondary branches per plant; TGW: thousand grain weight; YPP: yield per plant; MS(R): mean square of replications; MS(V): mean square of varieties; MS(E): mean square of errors; h^2: heritability; GA: genetic advance; CV: coefficient of variability.

Table 3: *Genotypic (r_g) and phenotypic (r_p) correlation between various morpho-physiological traits of safflower.*

Traits	DF	PH	DM	PPP	PBP	SBP	TGW	YPP
DF								
G	1.000	-0.0279*	0.9275*	0.0325*	-0.0992*	-0.0371*	0.0679*	-0.0168*
P	1.000	-0.0246	0.7489**	0.0271	-0.0770	-0.0300	0.0561	-0.0619
PH								
G		1.0000	-0.1590*	0.6102*	-0.783*	-0.0690*	0.1032*	0.6551*
P		1.0000	-0.1399	0.5999*	-0.0784*	-0.0677*	0.0993	0.6423**
DM								
G			1.0000	-0.0989*	-0.0055	-0.0085	-0.0670*	-0.1165*
P			1.0000	-0.0847	-0.0019	-0.0047	-0.0582	-0.1051
PPP								
G				1.0000	-0.0005	-0.0694*	0.1099*	0.7520*
P				1.0000	0.0014	-0.0670	0.1082	0.7437**
PBP								
G					1.0000	0.7807*	-0.1782*	-0.0826*
P					1.0000	0.7541**	-0.1666	-0.0791
SBP								
G						1.0000	-0.1445*	-0.1388
P						1.0000	-0.1432	-0.1367
TGW								
G							1.0000	0.1231*
P							1.0000	0.1222
YPP								
G								1.0000
P								1.0000

For abbreviations, See Table 2; **Significant; ** Highly significant.*

Genotypic and phenotypic correlations were observed among eight (8) morpho-physiological parameters in safflower. Days to flowering (DF) showed negatively significant interrelationship with PH, PBP, SBP and YPP, while positive significant interrelationship was observed among DF, DM, PPP and TGW. Plant height (PH) showed negatively significant genotypic and phenotypic interrelations with DM, PBP and SBP. However, there was positive and significant genotypic interrelation among PH, PPP, TGW and YPP. Negatively significant genotypic and phenotypic interrelations were present among days to maturity and other yield related parameters. Pods per plant (PPP) had negatively significant interrelation with

PBP and SBP, while positively significant correlation was observed among PPP, TGW and YPP. Results revealed the existence of positive correlation among PBP and SBP, while both traits showed negative interrelation with TGW and YPP. However, TGW showed positive interrelation with YPP.

Principal component analysis

Results of PCA showed that on basis of eigen value, data is considered up to three principal components. It was noted that 74 % variability of the total variation lies in three PC's. First PC has 30.6 % variability, while PC2 and PC3 has 22.9 % and 20.5 % variability of the total existing variation of the data. These PC's are orthogonal with each other. In first PC, four parameters i.e. PH, PPP, TGW and YPP were correlated with each other in negative direction, while remaining traits showed positive correlation with each other. In PC2, five yield related parameters viz; PH, PPP, PBP, SBP and YPP were negatively correlated with each other, while remaining traits were positively interrelated with each other. Under PC3, only one parameter (TGW) showed negative correlation with other parameters, which is a valuable yield index. The component with eigenvalues > 1 contributed 74% (Table 4) of the total variability among accessions of safflower for various morph-physiological traits. Two hundred accessions of safflower have been divided into eight cluster groups on the basis of their performance for studied parameters. Cluster 7 contain maximal (41) number of accessions, while cluster number 5 and 6 consist of lowest (15) number of accessions each. Cluster number 1 and 3 consist of 34 and 28 accessions respectively. While cluster number 4, 2 and 8 comprised of 26, 21 and 20 accessions respectively (Table 5).

Results of ANOVA revealed the presence of high genetic variability among all accessions of safflower for studied parameters and proved that data was fit for further statistical analysis. Existence of variation is useful for various genetic analysis and ultimately helpful in selection and improvement of crop (Kose *et al*., 2018). The basic purpose of correlation studies was to observe a common relationship between different characters and their level of the involvement to the yield (Panhwar *et al*., 2003). Plant parameters viz., DF, DM, PBP and SBP showed negative impact on yield and grain yield reduces with increase in number of DF, DM, PBP and SBP. However, plant attributes like PH, PPP and TGW had positive effect on yield of the crop as yield increases with increase in magnitude of these traits. It was observed that grain yield had significant interaction with PPP, PH and TGW (Ahmadzadeh, 2013; Kose *et al*., 2018). To intensify the crop yield, magnitude of plant attributes like PPP and TGW must be increased because these parameters had direct influence on YPP (Elfadl *et al*., 2010; Eslam *et al*., 2010; Safavi, 2011). Based upon the results of correlation, it is suggested that genotypes having higher magnitude of PH, branches per plant and grain weight will be selected for future breeding program to enhance yield (Kose *et al*., 2018). If value of 'r' (correlation) is near to 1, interrelation among two variables is positive and traits are highly dependent on each other. If 'r' is nearly zero among different variables no interdependency is observed, while 'r' with negative sign among variables proved negative relation among variables (Katar, 2013).

Table 4: *Principal Component Analysis (PCA) of germplasm.*

	PC 1	**PC 2**	**PC 3**
Eigen values	2.448	1.832	1.640
Proportion of variance	30.600	22.903	20.497
Cumulative variance	30.600	53.503	74.000
Eigen vectors			
Variables	**PC 1**	**PC 2**	**PC 3**
DF	0.108012	0.674046	0.644409
PH	-0.808049	-0.111115	0.199538
DM	0.255235	0.634851	0.640596
PPP	-0.831564	-0.104359	0.308155
PBP	0.287557	-0.685164	0.554232
SBP	0.331518	-0.656911	0.549469
TGW	-0.263355	0.214418	-0.143479
YPP	-0.874539	-0.068448	0.222903

Estimation of heritability is a promising indication about the transmittance of various parameters from parents to progeny. Appraisal of heritability is very helpful in selection of suitable genotypes/ accessions among various environmental and field conditions from a heterogeneous breeding population (Tahernezhad *et al*., 2018). Based upon percent (%) magnitude, heritability could be classified into low (0-30%), medium (30-60%) and high (>60%) (Reddy *et al*., 2013). Results revealed that magnitude of heritability was greater than 70% for all studied parameters (Table 2), indicating high transmittance percentage. It is also predicted that these parameters

Table 5: *Cluster-wise accession membership.*

Cluster No.	Accessions
I	A5, A9, A23, A24, A29, A35, A50, A52, A53, A54, A55, A78, A79, A86, A90, A96, A99, A100, A102, A105, A108, A109, A114, A118, A121, A122, A131, A137, A141, A150, A162, A163, A185, A189
II	A33, A41, A48, A58, A59, A73, A85, A97, A101, A106, A110, A119, A142, A143, A144, A164, A172, A175, A177, A182, A190
III	A14, A15, A16, A17, A28, A32, A37, A43, A47, A56, A57, A69, A70, A74, A84, A91, A92, A94, A98, A104, A111, A112, A115, A117, A126, A128, A132, A138
IV	A2, A3, A10, A13, A27, A36, A38, A40, A60, A63, A64, A65, A83, A87, A93, A95, A103, A107, A113, A124, A129, A133, A134, A135, A136, A139
V	A7, A8, A11, A18, A20, A21, A26, A34, A42, A49, A62, A68, A71, A72, A82
VI	A1, A6, A12, A19, A22, A25, A30, A31, A39, A61, A66, A67, A123, A127, A140
VII	A4, A44, A45, A46, A51, A75, A76, A77, A80, A81, A88, A89, A116, A120, A125, A130, A145, A148, A149, A152, A153, A154, A155, A156, A158, A159, A160, A161, A165, A166, A169, A173, A174, A178, A179, A186, A191, A193, A196, A199, A200
VIII	A146, A147, A151, A157, A167, A168, A170, A171, A176, A180, A181, A183, A184, A187, A188, A192, A194, A195, A197, A198

are less influenced by environment and highly suitable for early selection due to presence of additive nature of genetic inheritance. These results are in accordance with the findings of Arslan (2007), Sirisha (2009) and Elfadl *et al*. (2010).

PCA is a multivariate analysis technique, which is usually used to develop coordinated axis of an orthogonal and to estimate the relative importance of classified variables. This technique is characterized by conversion of complex plant data analysis into simple form (Slavkovic *et al*., 2004). Maximum variation was observed among first three PC's and it contained 74% of the total variability. Ahmadzadeh (2013) reported that 72.92 percent of the total variation was found in first three PC's, while Kose *et al*. (2018) found 65.4 percent of total variation in first two PC's. If the eigen values are greater than one, then diversity is not found in the traits and values are less than one, then diversity is found in all the characters. Negative eigen values were ignored because these values have no importance while positive values considered diversity is found in the characters. Cluster analysis classified the germplasm into eight groups on basis of similarity in their mean performance for observed parameters. Cluster analysis is a helpful technique to categorize the germplasm into well-defined subgroups and groups depending upon resemblance and deviation among mean performance of observed parameters (Biljana and Onjia, 2007).

Conclusions and Recommendations

Significant genetic variability was observed among germplasm regarding yield and its related attributes. The highest estimates of genetic advance and heritability for all traits showed their significance in selection of particular parents to be used in future breeding program. Higher heritability magnitude showed the predominance of additive genetic effects for studies traits, due to which direct and early selection is useful. From the results of correlation, it was concluded that three parameters viz., plant height, pods per plant and thousand grain weight had positively significant genotypic interrelationship with yield per plant. So, genotypes having higher value of PH, PPP and TGW can be selected to develop high yielding safflower varieties for Pakistan.

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Novelty Statement

Safflower is a good source of high-quality oil and mostly used for food, industry, ornamental purpose and as a biofuel. Pakistan expands a huge amount of foreign exchange on import of oil. By evaluation of available germplasm in the country, we will be able to develop high yielding safflower varieties with less input resources. This will not only helpful to meet the oil requirement of the country but also to improve health of the people and save the foreign exchange.

Author's Contributions

Rao Wali Muhammad and Abdul Qayyum planed the proposal and conducted the whole study. Methodology and analysis were carried out by Muhammad Qadir Ahmad and Waqas Malik. Hafiz Muhammad Wasif Ali completed the manuscript write up. Overall assessment of write up was done by Amir Hamza. Statistical analysis was accomplished by Etrat Noor.

Conflict of interest

The authors have declared no conflict of interest.

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