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# Determining relationships among seed yield, yield components and morpho-phenological traits using multivariate analyses in safflower (*Carthamus tinctorious* L.)

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## ABSTRACT

*The objective of this study was to determine the relationships among yield, yield components and morpho-phenological traits using 64 genotypes of safflower. Days to budding, days to flowering, days to maturity, plant height, primary branches per plant, head diameter, heads per plant, seeds per head, 1000-seed weight and seed yield per plant were evaluated. Results showed that seed yield per plant correlated positively and significantly with heads per plant ( $r = 0.65^{**}$ ), seeds per head ( $r = 0.76^{**}$ ) and primary branches per plant ( $r = 0.38^*$ ). According to path analysis, days to maturity, primary branches per plant and seeds per head possessed the highest positive direct effect on seed yield, respectively. Stepwise multiple linear regression analysis showed that 86% of the total variation in seed yield could be explained by variation in seeds per head, heads per plant and 1000-seed weight. Therefore, it could be concluded that seeds per head and head per plant are the most suitable selection indices for improving seed yield in safflower.*

**Key words:** Safflower, seed yield, correlation, effect, path analysis.

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## INTRODUCTION

Safflower (*Carthamus tinctorius* L.) is an annual oilseed crop grown and has been grown for centuries in parts of Asia [1]. It is a multipurpose crop for oil, medicinal and industrial uses [2]. This crop is adapted to dryland or irrigated cropping systems [3]. It is considered to be an important crop to enlarge the high-quality edible oil sources [1, 4]. Iran is one of the rich germplasm source and origin centers of safflower [5]. With the growing demand of food and diminishing arable land due to urbanization, soil erosion, salinisation and other forms of land degradation increasing yield within existing land through developing high yielding cultivars and better crop

management practices is feasible [3]. Seed yield is a very complex trait, and can be dissected into various agronomic component traits.

The ultimate goal of the most plant breeding programs is to improve the productivity of grains as measured in terms of the yield per plant [6]. From a physiological point of view, all crop plants offer a great scope for yield improvement. The possibilities of achieving this goal through genetic manipulation by genetic designs have been elucidated by evolving high yielding hybrids of safflower by production of different F<sub>1</sub> hybrids via diallel crosses. Literature review showed that little efforts have been taken for development of F<sub>1</sub> hybrids of safflower through the exploitation of genetic variability present in the exotic parents. F<sub>1</sub> generation obtained from the crossing of parental genotypes provides all possible variations. To increase the genetic yield potential, the maximum utilization of the desirable characters for synthesizing of any ideal genotypes is essential.

Path analysis determines the relative importance of direct and indirect effects of agronomic component traits on seed yield. This method has been used by plant breeders to assist for identifying high-heritable traits associated with seed yield [7]. Stepwise regression analysis is used to determine the percentage contribution of more important traits that had significant association with seed yield. With considering that selection is one of the important tools in safflower improvement, it is important to realize the relative importance of traits in influencing the seed yield in a desired direction [8]. The relationships among different agro-morphological traits have been studied with calculation of simple correlations and path analysis method in safflower [3, 9-12]. Prasad *et al.* [7] studied path analysis in some hybrids of safflower. Path analysis has been conducted among parental genotypes and their F<sub>1</sub> hybrids in sesame [13], pearl millet [14], maize [15] and F<sub>2</sub> genotypes in tomato [16] to elucidate the contribution of agronomic traits on seed yield.

For improving yield and oil content of safflower genotypes, superior cultivars must be developed by selection strategies that efficiently utilize the existing genetic variation. Therefore, an understanding of the responses and relationships between yield-determining traits is required by the breeder who has to select for under conditions where the cultivars are to be deployed. In spite of correlation coefficients which provide simple linear relationships between traits, path coefficients present the relative contribution of various yield-determining traits, enabling breeders to choose between direct and indirect selection.

The objective of this study was to determine the relationships between some phenological, morphological, and yield components with seed yield in some safflower genotypes and their F<sub>1</sub> hybrids to estimate the best selection criteria for yield improvement in safflower breeding program using correlation coefficients, stepwise regression and path coefficients.

## MATERIALS AND METHODS

### Field Experiments

The plant material consisted of 64 genotypes (including 8 parental genotypes and their 56 F<sub>1</sub> hybrids) of safflower that were produced from a full-diallel mating design. Parental genotypes were originated from different geographical regions of Iran (C<sub>111</sub>, C<sub>4110</sub>, ISF<sub>14</sub>, A<sub>2</sub>, IL.111, K<sub>21</sub>) along with two exotic genotypes from Germany (GE<sub>62918</sub>) and Mexico (22-191). Iranian genotypes were produced by selection within different Iranian landraces. This study was conducted at Research Farm of College of Agriculture, Isfahan University of Technology located in Lavark, Najaf-Abad, Iran (51° 32' E and 32° 32' N, 1630 m asl) in spring 2008. This

experiment was conducted using a randomized complete block design with three replications. Each plot consisted of one central and two border rows with 1.5 m in length and 40 cm apart. The experiment was conducted on a Typic Haplargids of the arid tropic with pH=7.5. Days to emergence (DE), days to budding (DB) and days to flowering (DF) were recorded on plot basis, whereas plant height (PH), primary branches per plant (PB), number of heads per plant (HP), number of seeds per head (SH), 1000 seed weight (SW) (g), head diameter (HD) (cm) and seed yield per plant (g) were recorded using ten randomly selected plants from each plot.

### Statistical analysis

Analysis of variance (ANOVA) for evaluated traits, simple phenotypic correlation and stepwise regression analysis was performed using SAS program [17]. Path coefficient analysis and factor analysis were carried out by SPSS Ver.9 using seed yield as dependent variable and the remaining traits as independent variables.

## RESULTS AND DISCUSSION

Results of analysis of variance, maximum, minimum and means of the studied trait with their coefficient variation (CV) are summarized in Table 1. There was a highly significant difference among genotypes for all of the traits. The results showed that there was a high genetic variation among the studied genotypes. In this experiment CV ranged from 1.42 for days to maturity to 13.9 obtained from the seed yield per plant.

**Table 1 Results of analysis of variance and descriptive statistics of evaluated traits in 64 genotypes of safflower**

Source of variation	df	Mean squares										
		DE	DB	DF	DM	PH	PB	HD	HP	SH	SW	SY
Replication	2	64.3*	31.7**	259.9**	326.4**	792.3**	4.7**	0.02	208.1**	80.4**	16.0	500.8**
Genotype	63	10.4**	16.5**	10.9**	5.7**	271.4**	2.4**	0.08**	13.5**	134.6**	44.7**	124.6**
Residual	126	0.4	5.6	4.0	2.3	49.3	0.7	0.02	6.8	2.0	8.0	21.8
CV (%)		4.8	4.2	2.5	1.4	7.6	10.1	5.8	8.6	3.4	8.9	13.9
Max		15.7	62.1	81.6	111.3	112.3	10.3	3.1	34.9	52.8	39.1	55.2
Min		9.1	52.9	75.3	103	72.3	7.0	2.3	19.1	25.0	26.5	22.2
Mean		12.6	55.5	78.3	107.3	91.7	8.5	2.7	23.2	42.2	31.8	33.6

### Correlation coefficients

The results of this study showed that seed yield was highly and positively ( $P < 0.01$ ) associated with SH and HP (Table 2). This result suggests that indirect selection through increasing these three traits would be effective for yield improvement. The relationships among some agro-morphological and phenological traits have been reported in safflower [18, 19, 20].

SH highly and positively correlated with seed yield. Therefore, this trait could be considered as the most important for yield improvement in safflower. This result is in agreement with that of Roopa and Ravikumar [20], Pascual-Villalobos and Albuquerque [21] and Mozaffari and Asadi [3] who reported that seeds per plant possessed the highest positive correlation with seed yield. On the other hand Chaudhary [10] reported a highly positive correlation between head diameter and seed yield. In the present study, no significant correlation was found between seed yield and other agro-morphological and phenological traits (Table 2).

PB positively correlated with HP and SW. Mokhtassi et al. [11] reported a non-significant correlation between seed weight and primary branches per plant. In the present study, there was a positive significant correlation between primary branches per plant and days to flowering. This

result is in agreement with that of Roopa and Ravikumar [20] who also reported the positive relationship between these traits in safflower. Among the seed yield components, only 1000 seed weight did not significantly correlated with seed yield (Table 2). There was a negative correlation between plant height with 1000-seed weight and head diameter. These relationships were also supported by Camas et al. [22]. The finding of no significant correlation between plant height and seed yield in the present study is consistent with that of Camas et al. [22] and Roopa and Ravikumar [20].

SH correlated positively and significantly with DF and DB and is in agreement with the report of Roopa and Ravikumar [20]. A positive relationship between SW and HD observed in this study is consistent with that of Camas et al. [22]. One-thousand seed weight correlated negatively and significantly with DB and DF. This result is in agreement with the finding of Mokhtassi et al. [11]. There was a significant correlation between DE and DF (Table 2). DF had a positive correlation with DE and PH. DF had a negative significant correlation with SW and PB (Table 2). This result was supported by earlier reports of Roopa and Ravikumar [20]. PH had a positive significant correlation with DE (Table 2). Mozaffari and Asadi [3] found a positive significant correlation between PH and DM and a negative correlation between PH with HP. A negative correlation between PH with SW and HD was also reported by Camas et al. [22]. Hence, seed yield in safflower could be improved indirectly by selecting genotypes producing a greater number of seeds per head and heads per plant.

**Table 2 Correlation coefficient between studied traits in 64 genotypes of safflower**

Trait	DE	DB	DF	DM	PH	PB	HD	HP	SH	SW	SY
DE	1										
DB	0.17	1									
DF	0.02	0.74**	1								
DM	0.24	0.68**	0.67**	1							
PH	0.27	0.69**	0.59**	0.60**	1						
PB	0.14	-0.28	-0.36*	-0.40*	-0.48**	1					
HD	-0.1	-0.42*	-0.2	-0.24	-0.47**	0.14	1				
HP	-0.17	-0.06	0.018	-0.07	-0.25	0.45**	-0.007	1			
SH	-0.02	0.55**	0.48**	0.26	0.30	0.06	-0.11	0.31	1		
SW	0.09	-0.63**	-0.65**	-0.62**	-0.8**	0.37*	0.55**	0.04	-0.22	1	
SY	-0.09	0.097	0.11	0.04	-0.14	0.38*	0.16	0.65**	0.76**	0.09	1

\* and \*\* significant at  $P < 0.05$  and  $P < 0.01$  respectively.

DE: Days to emergence; DB: days to budding; DF: days to flowering; DM: Days to maturity; PH: plant height; PB: primary branches per plant; HD: head diameter; HP: heads per plant; SH: seeds per head; SW: 1000-seed weight; SY: seed yield per plant

### Path analysis

Genotypic correlation coefficients were partitioned into direct and indirect effects through various yield contributing characters using path analysis in parental genotypes and F<sub>1</sub> hybrids. Path analysis in parental genotypes showed that DF had the greatest positive effect on seed yield (Table 3). Among agronomical traits, HD had the highest direct effect on seed yield. DB, DM and SH possessed negative direct effect on seed yield (Table 3). The results imply that HD can be used as a selection index to improve seed yield in safflower.

The results of path analysis on F<sub>1</sub> hybrids (56 genotypes) showed that DF, DM, PB, HP and SH possessed the positive direct effects on the seed yield while other traits had negative or negligible

direct effects on seed yield (Table 4). Among yield components SH had the highest positive direct effect on seed yield (Table 4).

**Table 3 Direct (diagonal and bolded) and indirect effects (upper and low of the diagonal line) of morpho-phenological traits and yield components on seed yield in parental genotypes of safflower using path coefficient analysis**

Trait	DE *	DB	DF	DM	PH	PB	HD	HP	SH	SW
DE	<b>13.8</b>	5.52	-24.6	6.72	0.51	3.6	0.11	0.48	-0.38	-5.4
DB	-4.9	<b>-15.35</b>	29.24	-7.7	1.9	-1.70	-0.9	0.14	-0.95	0.30
DF	-9.52	-12.5	<b>35.66</b>	-11.46	1.14	-3.96	-0.38	-0.02	-0.24	1.53
DM	-7.04	-9.06	31.02	<b>-13.17</b>	0.92	-5.06	-0.47	0.36	1.24	1.15
PH	1.93	-8.29	11.05	-3.29	<b>3.68</b>	-1.22	-1.61	-0.05	-0.57	-1.68
PB	8.14	4.3	-23.1	10.93	-0.73	<b>6.10</b>	0.710	-0.05	-2.6	-3.6
HP	0.69	6.14	-6.06	2.76	-2.61	1.89	<b>2.26</b>	-0.99	-1.72	-2.22
SH	-4.69	1.53	0.71	3.42	0.14	0.24	1.58	<b>-1.41</b>	-1.57	0.53
SW	-1.10	3.71	-1.78	-3.42	-0.44	-3.41	-0.81	0.46	<b>4.78</b>	3.07
HD	-9.80	-0.61	-0.61	7.13	-1.97	-0.81	-2.86	-0.65	-0.10	<b>7.67</b>

DE: Days to emergence; DB: days to budding; DF: days to flowering; DM: Days to maturity; PH: plant height; PB: primary branches per plant, HD: head diameter; HP: heads per plant; SH: seeds per head; SW: 1000-seed weight; SY: seed yield per plant.

Overall, positive indirect effect via DF, DM, PB, SW and HD, with negative indirect effect via DB, PH and HP resulted in a positive genetic correlation between SH and seed yield (Table 4). This finding is in agreement with the reports of Abel and Driscoll [23] and Mozaffari and Asadi [3]. These findings suggest that the increasing of the yield component traits with high positive direct effects as the immensely efficient criteria is an efficient way to improve yield of safflower [7]. DB, PH, HD and SW had negative direct effects on seed yield. The highest negative direct effect was related to DB. But indirect effect through DM and PH and HP increased correlation coefficient of DB with seed yield (Table 4). DM had the highest positive direct effect on seed yield, but it had negative indirect effects via PH, PB, HP, DE and DB (Table 4). On the other hand, positive direct effect of days to maturity had been compensated via negative indirect effects of other traits. This phenomenon resulted in a negative correlation between seed yield and days to maturity.

**Table 4 Direct (diagonal and bolded) and indirect effects (upper and low of the diagonal line) of morpho-phenological traits and yield components on seed yield in F<sub>1</sub> hybrids of safflower genotypes using path coefficient analysis**

Trait	DE	DB	DF	DM	PH	PB	HD	HP	SH	SW	†Corr.(Y <sub>p</sub> )	Corr.(Y <sub>p</sub> ) ¥
DE	<b>-0.83</b>	-0.22	-0.06	0.73	-0.14	0.23	0.17	-0.01	0.09	0.01	-0.09	-0.09
DB	-0.17	<b>-1.08</b>	0.013	1.60	0.60	-0.49	-0.24	0.46	0.26	0.11	0.13-	0.097
DF	0.11	-0.03	<b>0.46</b>	0.078	-0.33	-0.060	0.12	0.40	-0.02	0.04	0.17	0.11
DM	-0.31	-0.90	0.01	<b>1.93</b>	-0.48	-0.72	-0.16	0.21	0.24	0.07	0.14-	0.04
PH	-0.16	-0.89	0.20	1.27	<b>-0.73</b>	-0.66	0.13	0.23	0.27	0.09	-0.24	-0.014
PB	-0.13	0.36	-0.19	-0.97	0.33	<b>1.44</b>	-0.09	0.05	-0.14	-0.02	0.65	0.38
HD	0.34	-0.62	-0.24	0.05	0.24	0.33	<b>0.42</b>	0.28	-0.12	0.016	0.59	0.65
HP	0.016	-0.7	0.25	0.58	-0.23	0.11	-0.16	<b>0.71</b>	0.07	0.02	0.68	0.76
SH	0.25	0.90	0.03	-1.53	0.62	0.66	-0.16	-0.17	<b>-0.31</b>	-0.11	0.19	0.09
SW	0.09	0.69	-0.10	-0.77	0.37	0.20	0.03	-0.09	-0.19	<b>-0.18</b>	0.05	0.16

†=Genotypic correlation of evaluated traits with seed yield

¥= †=Phenotypic correlation of evaluated traits with seed yield

DE: Days to emergence; DB: days to budding; DF: days to flowering; DM: Days to maturity; PH: plant height; PB: primary branches per plant, HD: head diameter; HP: heads per plant; SH: seeds per head; SW: 1000-seed weight; SY: seed yield per plant.



In view point of path analysis, PB and SW via DM resulted in the decreasing effect on the correlation coefficient between these traits with seed yield. Also, the negative indirect effects of HP through DB and DF decreased the correlation between seed yield and HP. Primary branches per plant had the highest positive direct effect after days to maturity (Table 4). SW had a negative direct effect on seed yield (Table 4), but positive indirect effects via PB, PH and DB resulted in the positive genetic correlation of seed weight with seed yield (Table 4). On the other hand, increasing in SH caused the reduction of seed weight because of the compensatory effects in yield components and limitation in photosynthesis sinks in plant. Inconsistence with this finding, Mokhtassi et al. [11] reported the negligible direct effects of HP and seeds per head on seed yield. The results of the present study indicated that even though the relationships among some yield components were statistically significant, their direct effect in path coefficient values was ranked after a trait that had a lower correlation coefficient. Plant height had the highest negative correlation with seed yield among the evaluated traits (Table 4). This correlation was resulted from negative direct and indirect effects via other traits. Altogether, the main effects of all yield components responsible for seed yield were mostly affected via days to maturity and plant branches per plant.

### Multiple stepwise regression

Overall 77% of the seed yield variation could be explained by two seed yield component of seeds per head (58%) and heads per plant (19%), while 1000-seed weight when entered to the regression model could only justify 11% of its variation (Table 5). The unexplained variation, 13.83% of the total may be due to variation in other components. Positive regression coefficient of the three variables implies that defining a logical index selection with these variables, with considering their narrow-sense heritability and correlation coefficient with seed yield, might be a good strategy for increasing seed yield in safflower.

**Table 5 Summary of stepwise multiple regression analysis of seed yield and 10 pheno-morphological traits in safflower**

Regression equations	Coefficient of partial determination	Cumulative coefficient determination
$SY^* = 2.87 + 0.68SH$	0.58	0.58
$SY = -20.08 + 0.55SH + 1.20HP$	0.19	0.77
$SY = -36.47 + 0.62SH + 1.11HP + 0.49SW$	0.08	0.86

\*SY= seed yield, SH = seeds per head, HP = Heads per plant and SW = 1000 seed weight

### Factor analysis

Variable data were subjected to factor analysis which divided the 11 variables into three factors with overall justifying 99% of the total genetic variation (Table 6). Factor 1 was strongly associated with phenological traits including DB, DF and DM as well as PH (Table 6). The positive signs of these traits (0.86, 0.82, 0.81 and 0.87) indicate the positive direction of the relationship between the factor and the variables [24]. This in turn shows that the traits may be influenced by the same genes and hence may be beneficial for screening desirable safflower genotypes. Considering the high magnitude of phenological traits loading signs in the first factor, this factor could be titled as phenological factor. Second factor explained 31% of the total genetic variation (Table 6). In this factor HD, HP, SH and yield per plant loaded with positive signs (0.60, 0.77, 0.76, 0.94, respectively). With considering that HP and SH are the main components of seed yield, thus this factor could be named as the yield factor. The third factor explained 14.7% of the total genetic variation and has less important in safflower improvement program. According to factor analysis, our results indicated that selection based on PH, DB, DF,

HP and SH can be considered as the desirable criteria for selecting superior safflower genotypes under field conditions.

**Table 6 Loading of the three important principal factors (PF) from a factor analysis of 11 traits in safflower**

Variables	Factor ( matrix of factor coefficients)		
	1	2	3
DE	0.26	-0.13	0.86
DB	0.86	0.17	-0.01
DF	0.82	0.19	-0.23
DM	0.81	0.01	0.08
PH	0.87	-0.16	0.06
PB	0.51-	0.51	0.52
HD	-0.50	0.60	-0.23
HP	-0.14	0.77	0.06
SH	0.44	0.76	-0.12
SW	-0.78	0.09	-0.09
YP	-0.004	0.94	-0.02
Variance (%)	53	85	99
Cumulative variance (%)	53	31	14.7

DE: Days to emergence; DB: days to budding; DF: days to flowering, DM: Days to maturity; PH: plant height; PB: primary branches per plant; HD: head diameter; HP: heads per plant; SH: seeds per head; SW: 1000-seed weight; SY: seed yield per plant

## CONCLUSION

Results of the correlation coefficients showed that SH ( $r = 0.76$ ) and HP ( $r = 0.65$ ) are two major grain yield attributes that significantly affected grain yield in safflower. This finding was consistent with that of the multiple regression analysis that showed 77% of the seed yield variation could be explained by SH and HP. Likewise, according to path analysis SH had the highest positive direct effect on seed yield (Table 3). Overall, positive indirect effect via DF, DM, PB, SW and HD, with negative indirect effect via DB, PH and HP resulted in a positive genetic correlation between SH and seed yield. Among the seed yield components, only 1000 seed weight did not significantly correlated with seed yield. Vast range of genetic variation for all these traits indicated that there exists a good opportunity to select for a combinations of such traits.

## REFERENCES

- [1] E.A. Weiss. Oil seed Crops. 2nd edn. Blackwell Science Ltd, Oxford, UK, **2000**, P.364.
- [2] R.J. Singh. Genetic Resources, Chromosome Engineering and Crop Improvement. CRC Press Inc. Boca Raton, Florida, USA. **2007**, P.320.
- [3] K. Mozaffari; A.A. *Asian J. Plant Sci.* **2006**, 5, 977-983.
- [4] A.A. Jaradat, M. Shahid, *Genet Resour Crop Evol.* **2006**, 2, 129-140
- [5] P.F. Knowles. *Econ. Bot.* **1969**, 23, 324-329.
- [6] K.P. Ghosh; A.K.M.A. Islam; M.A.K. Mian; M.M. Hossain. *J. Appl. Sci. Environ. Manage.* **2010**, 14, 91-95.
- [7] S. Prasad; B.R. Chaudhary; R.K. Agrawal. *Sesame and Safflower Newsletter* **1993**, 8, 74-78.
- [8] V Singh; M.B. Deshpande; S.V. Choudhari; N. Nimbkar. *Sesame and Safflower Newsletter* **2004**, 19, 77-81.
- [9] O Gecer; S.N. Sinan; F. Gulyasar. *J. Agric. Fac.* **1987**, 2, 37-43.
- [10] S.K. Chaudhary. *Int. J. Tropical Agric.* **1990**, 8, 129-132.
- [11] A. Mokhtassi; G.A. Akbari; M. J. Mirhadi. *Euphytica* **2006**, 148,261-268.

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- [12] V. Rudra- Naik; M.G. Bentur; K.G. Parameshwarappa. *Karnataka J. Agric. Sci.* **2009**, 22, 44-46.
- [13] K. Bharathi; P. Vivekanandan. *Elec. J. Plant Breed.* **2009**, 1, 70-73.
- [14] A.U. Izge; A.M. Kadams; D.T. Gungula. *Afr. J. Agric. Res.* **2006**, 1,194-198.
- [15] O.B. Bello; S.Y. Abdulmalik; M.S. Afolabi; S.A. Ige. *Afr. J. Biotech.* **2010**, 9, 2633-2639.
- [16] K.P. Ghosh; A.K.M.A. Islam; M.A.K. Mian; M.M. Hossain. *J. Appl. Sci. Environ. Manage.* **2010**, 14, 91-95.
- [17] SAS Institute. SAS/ STAT software. **1997**. Changes and enhancements, through release 6.12. SAS Institute Inc., Cary, NC.
- [18] A. Ashri. *Euphytica* **1975**, 24, 651-659.
- [19] V. Ranga Rao, M. Ramachandram. *Theor. Appl. Genet.* **1977**, 50, 185-191.
- [20] V.K. Roopa; R.L. Ravikumar. *Karantaka J. Agric. Sci.* **2008**, 21, 436-437.
- [21] M.J. Pascual-Villalobos; N. Albuquerque. *Euphytica* **1996**, 92, 327-332.
- [22] N. Camas; C. Cirak; E. Esendal. *J. Fac. Agric.*, OMU. **2007**, 22, 98-104.
- [23] G.H. Abel; M.F. Driscoll. *Crop Sci.* **1976**, 16, 231-216.
- [24] C. Toker; M.I. Cagirgan. *Hereditas* **2004**, 140, 226-228.