NOTE

Evaluation of seed yield-related characters in spring safflower (*Carthamus tinctorius* L.) using factor analysis

J. Ashkani and H. Pakniyat[1]

[1]Department of Crop Production and Plant Breeding, College of Agriculture, Shiraz University, Shiraz, I.R. Iran.

ABSTRACT

Factor analysis is a general method for analyzing data and is used to investigate relationships among variables without distinguishing some as independent and others as dependent ones. Phenotypic and genetic factor analyses of 13 traits were carried out for eight genotypes of spring safflower (*Carthamus tinctorius* L.) under stress and non-stress irrigation regimes. Each experiment was conducted as a randomized complete block design with three replications. Genetic correlation matrix was used to obtain a genetic factor matrix to recognize seed yield-related characters and their associations with seed yield to determine the best criterion for identification of high-yielding genotypes under stress and non-stress irrigation regimes. Results indicated that selection based on biological yield, 1000-seed weight and plant capitula weight, may be desirable for high-yielding genotypes under stress conditions, whereas, selection based on biological yield, number of capitula/plant, plant capitula weight, capitula harvest index and harvest index, may be more efficient for identifying high-yield genotypes under non-stress conditions. Furthermore, biological yield and plant capitula weight may be suitable for screening of high-yield genotypes under both irrigation regimes.

Key words: Spring safflower, *Carthamus tinctorius* L., Factor analysis, Irrigation regimes.

ارزیابی صفات وابسته بـــه عملکـرد دانـــه در گلرنــگ بهـاره (*Carthamus tinctorius* L.) با استفاده از روش تجزیه به عامل ها

جهانشاه اشکانی و حسن پاک نیت

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1. Former Graduate Student and Assistant Professor, respectively (Correspondence: pakniyat@shirazu.ac.ir).

به ترتیب، دانشجوی پیشین کارشناسی ارشد و استادیار بخش زراعت و اصلاح نباتات دانشکده کشاورزی دانشگاه شیراز، شیراز، جمهوری اسلامی ایران.

چکیده

روش تجزیه به عاملها، روشی عمومی برای تجزیه داده ها است که برای بررسی روابط بین متغیرهـا بـه کار می رود، بدون در نظر گرفتن این موضوع کـه برخـی از آنهـا متغیرهـای غیروابسـته و برخـی دیگـر متغیرهـای وابسته هستند. تجزیه به عاملها برای ۱۳ صفت هشت ژنوتیپ گلرنگ بهـاره در شـرایط رژیمهـای تـنش رطوبتـی و بدون تنش رطوبتی انجام شد. هر آزمایش در قالب طرح بلوکهای کامل تصادفی و در سه تکرار اجـرا شـد. مـاتریکس همبستگی ژنتیکی، برای به دست آوردن ماتریکس ژنتیکی و تشخیص صفات وابسته به عملکرد دانه و ارتباط آنها بـا عملکرد دانه با هدف تعیین بهترین خصوصیت در تشخیص ژنوتیپ هـای پرمحصـول در شـرایط رژیمهـای آبیـاری تنش دار و بدون تنش به کار برده شد. نتایج نشان داد که گزینش بر پایه عملکرد بیولوژیکی وزن هـزار دانـه و وزن طبق برای تشخیص ژنوتیپهای با عملکرد بالا در شرایط تنش رطوبتی و گزینش بـر پایه عملکـرد بیولـوژیکی تعـداد طبق در گیاه، وزن طبق، شاخص برداشت طبقها و شاخص برداشت ممکن است در تشخیص ژنوتیپهـای پرمحصـول در شرایط بدون تنش رطوبتی مؤثر باشد. فـزون بـر ایـن، عملکـرد بیولـوژیکی و وزن طبـق در گیـاه در تشـخیص ژنوتیپهای پرمحصول در هر دو رژیم آبیاری است مؤثر باشند.

INTRODUCTION

Developing crop varieties with high yield potentials through identification of drought tolerance mechanisms is important for increasing yields in dry areas (9, 18). Breeding for improving crop production either within given microenvironments (rainfed vs. irrigated) or in a wide range of growing conditions (5) is the goal of many breeding programs. The estimate of correlation coefficients indicates the inter-relationship of the characters (17). The correlations between characters consist of three main causes, namely pleiotropy, linkage and environmental effects. A gene with pleiotropic effects causes simultaneous variation in two or more characters when the gene is segregating and the genetic correlation arising from pleiotropy expresses the extent to which the two characters are influenced by the same gene (8).

Numerous researchers have used genetic correlation for evaluation of the relationship between yield and yield-related characters in several crops (1, 7, 16, 23). Compensation of yield components occurs as a result of competition for limited resources thus, simple correlations with seed yield may not provide a complete picture of the seed yield (10).

Factor analysis can be understood as a data-reduction technique by removing the duplicated information from among a set of correlated variables (13, 19). Factor analysis provides more information than a simple correlation matrix because it discriminates between groups of variables (factors) and indicates percentage contribution of variables to each factor (21), but factor analysis is impeded by genotype through environmental interaction. The advantage of a genetic correlation matrix would be that, the sets of derived factors are free of environmental effects and, therefore, the genetic composition of a factor can be shown more clearly. Also, inferences are made on a genetic basis, which is useful in a breeding program (22).

To determine the potential of genetically different cultivars and lines, breeders must observe many different characteristics in their breeding and selection programs. The sign of the loading indicates the direction of the relationship between the factor and the variable. Thus, two variables with high magnitude of loadings in the same factor would be expected to exhibit a high correlation (21).

Previous study by Sieber *et al.* (22), revealed that, using of a genetic correlation matrix to obtain a genetic factor matrix vs. a phenotypic analysis suggests reduction in number of derived factors. In addition, more total variation among the input variables could be explained by a genetic than a phenotypic analysis. Factor analysis has been used by many researchers (2, 3, 6, 21, 24) for determination of dependent relationship among characters associated with seed yield in several crops.

The objective of this research was to evaluate seed yield-related characters and their relationships to seed yield for determination of the best criteria for high-yield genotype screening under stress and non-stress irrigation regimes, using factor analysis technique.

MATERIALS AND METHODS

Eight spring safflower genotypes (Arak, Isfahan and Poshtkooh from Iran; Gila, Nebraska10 and UC10 from USA; RH8018 and RH410118 from F.A.O.) were grown in two separate experiments under stress and non-stress irrigation regimes at the Experimental Station of Agricultural College, Shiraz University in Badjgah, Iran (29°50' N, 52°46' E) in 2001. These genotypes were selected from different geographical origins to provide enough variation for evaluation of the variables. The soil texture was clay loam (fine, mixed, mesic, calcixerollic xerochrepts). The stress and non-stress experiments received water when 80±5 and 160±5 mm evaporation occurred from A class pan, respectively. Applied water was measured in each experiment. Soil moisture status was measured by weighing method. Each experiment was conducted as a randomized complete block design with three replications. Each plot consisted of six 4-m long rows spaced 60 cm apart. The four middle rows were used for sampling, and the two outside rows were considered as boarder rows. The sowing date was April 15, 2001 and each genotype was harvested at full maturity (starting from mid-August).

Recorded traits were: seed yield (g/m^2), number of capitula per plant, plant capitula weight (g), number of seeds per capitulum, 1000-seed weight (g), biological yield (g/m^2), harvest index, days to 50% flowering, days to 75% of maturity, plant height (cm), oil and protein content (%) and capitula harvest index (proportion of plant seed yield to plant capitula weight).

Statistical Analysis

Phenotypic and genetic correlation coefficients of the data were computed according to Miller *et al.* (15) formula. Principal factor analysis (PFA) was performed according to the procedures outlined by Cattell (4) and Guertin and Bailey (11), using phenotypic and genetic correlation matrices. The varimax rotation method (an orthogonal rotation) suggested by Kaiser (14) was used. Data of each experiment was analyzed, separately. All computations were conducted using SAS statistical program package (20).

RESULTS AND DISCUSSION

Correlation Between Characters

In most instances, there was a close agreement between phenotypic and genetic correlations, while in some cases, the differences were high, suggesting the importance of environmental effects in estimating these parameters.

The phenotypic and genetic correlations among various characters under stress and non-stress conditions are presented in Tables 1 and 2, respectively. In general, the phenotypic and genetic correlations were of the same sign, but the genetic correlations in most cases were higher than the corresponding phenotypic correlations. In these cases, where the magnitude of the genetic and phenotypic correlations was nearly the same, the environmental variances and covariances were very small, i.e. the influences of environment on these relationships was minimal (8). Throughout the remainder of this section, reference will be made only to genetic correlation between various characters.

Under non-stress conditions, highly significant positive correlations were found between seed yield and biological yield (r=0.89, P<0.01), 1000-seed weight (r=0.95, P<0.01) and also plant capitula weight (r=0.95, P<0.01) whereas, negative correlation was present between seed yield and oil content (r=-0.89, P<0.01). Genetic correlation coefficients revealed that seed yield was not associated with number of capitula/plant, number of seeds/capitulum, days to 50% flowering, days to 75% maturity, plant height, protein content, capitula harvest index and harvest index (Table 2). However, in the study conducted by Pandya *et al.* (17) seed yield was also positively correlated with days to 75% maturity.

Under stress condition, a highly significant positive correlation was observed between seed yield and biological yield (r=0.92, P<0.01), number of seeds/capitulum (r=0.64, P<0.05), plant capitula weight (r=0.96, P<0.01), capitula harvest index (r=0.72 , P<0.01) and harvest index (r=0.61, P<0.05) Genetic correlation coefficients revealed that, seed yield was not related to number of capitula/plant, 1000-seed weight, days to 50% flowering, days to 75% maturity, plant height, oil content, protein content and harvest index (Table 2).

Factor Analysis

Factor analysis was used for grouping characteristics associated with seed yield under stress and non-stress conditions. Factor consisted of seed yield defined as *productivity* factor, with sign of characters indicating the direction of the relationship between seed yield and yield-related characters. Characters with high association to seed yield were selected under the two experiments. Since no test of significance was performed for factor loadings, the decision was rather arbitrary as to how many factors should be

Table 1. Phenotypic and genetic (in parenthesis) correlation coefficients amongst 13 traits under non-stress conditions.

Trait	No.	1	2	3	4	5	6	7	8	9	10	11	12	13	Mean	SD
Seed yield (g/m²)	1	1.00 (1.00)	0.92 (0.89)	0.44 (0.13)	0.07 (0.37)	0.56 (0.95)	0.97 (0.95)	0.25 (0.32)	0.31 (-0.31)	0.33 (0.28)	-0.33 (-0.89)	-0.47 (-0.41)	0.16 (-0.17)	0.18 (-0.24)	144.47	42.69
Biological yield (g/m²)	2		1.00 (1.00)	0.49 (0.37)	0.22 (0.33)	0.44 (0.62)	0.97 (0.99)	0.32 (0.41)	0.35 (0.03)	0.16 (-0.04)	-0.39 (-0.76)	-0.41 (-0.40)	-0.15 (-0.60)	-0.20 (-0.66)	558.40	162.46
No. capitula/plant	3			1.00 (1.00)	-0.10 (0.04)	0.13 (0.23)	0.50 (0.29)	0.24 (0.33)	0.09 (-0.10)	-0.21 (-0.51)	-0.39 (-0.56)	-0.04 (0.37)	-0.23 (-0.54)	-0.08 (-0.56)	16.66	3.27
No. seeds/capitulum	4				1.00 (1.00)	-0.27 (-0.04)	0.10 (0.43)	0.24 (0.00)	0.29 (0.52)	-0.09 (-0.05)	0.00 (0.13)	-0.11 (-0.34)	-0.07 (-0.21)	-0.36 (0.00)	51.68	6.33
1000-seed weight (g)	5					1.00 (1.00)	0.51 (0.73)	-0.18 (0.35)	-0.18 (-0.49)	0.23 (0.32)	-0.38 (-0.59)	-0.38 (-0.43)	0.18 (0.36)	0.26 (0.29)	33.06	3.69
Plant capitula weight (g)	6						1.00 (1.00)	0.27 (-0.29)	0.29 (-0.14)	0.21 (0.02)	-0.36 (-0.87)	-0.44 (-0.43)	-0.07 (-0.47)	0.02 (-0.56)	31.44	9.49
Days to 50% flowering	7							1.00 (1.00)	0.64 (0.57)	0.47 (0.46)	-0.22 (-0.28)	0.30 (0.64)	0.18 (-0.18)	-0.12 (-0.30)	91.37	4.10
Days to 75% maturity	8								1.00 (1.00)	0.29 (0.29)	0.19 (0.61)	-0.17 (0.21)	-0.07 (-0.34)	-0.09 (-0.56)	115.58	2.41
Plant height (cm)	9									1.00 (1.00)	-0.10 (-0.10)	0.09 (0.29)	-0.03 (0.71)	0.44 (0.59)	78.56	4.80
Oil content (%)	10										1.00 (1.00)	-0.09 (-0.08)	0.08 (0.27)	0.15 (0.15)	34.66	2.95
Protein content (%)	11											1.00 (1.00)	0.50 (0.28)	-0.10 (0.20)	19.82	1.03
Capitula harvest index	12												1.00 (1.00)	0.73 (0.99)	0.75	0.06
Harvest index	13													1.00 (1.00)	20.64	2.64

Significant values are underlined (P<0.05).

Table 2. Phenotypic and genetic (in parenthesis) correlation coefficients amongst 13 traits under stress conditions.

Trait	No.	1	2	3	4	5	6	7	8	9	10	11	12	13	Mean	SD
Seed yield (g/m²)	1	1.00 (1.00)	0.93 (0.92)	0.56 (0.28)	0.55 (0.64)	0.23 (0.11)	0.96 (0.96)	0.03 (0.07)	0.27 (0.41)	0.43 (0.46)	-0.12 (-0.31)	0.06 (-0.20)	0.42 (0.72)	0.47 (0.61)	58.5	14.45
Biological yield (g/m²)	2		1.00 (1.00)	0.64 (0.45)	0.56 (0.66)	0.14 (0.09)	0.95 (0.91)	0.11 (0.36)	0.36 (0.57)	0.47 (0.53)	-0.17 (-0.40)	0.08 (-0.17)	0.18 (0.62)	0.11 (0.25)	220.55	47.980
No. capitula/plant	3			1.00 (1.00)	-0.80 (-0.34)	0.26 (0.53)	0.63 (0.46)	-0.12 (-0.15)	0.02 (-0.03)	0.18 (0.15)	0.09 (0.17)	0.09 (-0.18)	-0.07 (-0.32)	0.01 (-0.30)	7.93	1.40
No. seeds/capitulum	4				1.00 (1.00)	-0.09 (-0.29)	0.45 (0.52)	0.35 (0.60)	0.52 (0.74)	0.43 (0.46)	-0.57 (-0.66)	0.09 (0.17)	0.48 (0.72)	0.13 (0.26)	41.49	9.94
1000-seed weight (g)	5					1.00 (1.00)	0.16 (0.04)	0.09 (0.02)	0.07 (0.06)	0.46 (0.59)	-0.20 (-0.32)	-0.04 (0.21)	0.23 (0.18)	0.21 (-0.01)	30.50	2.70
Plant capitula weight (g)	6						1.00 (1.00)	-0.08 (-0.09)	0.18 (0.28)	0.31 (0.30)	0.01 (-0.13)	0.07 (-0.18)	0.15 (0.51)	0.31 (0.55)	11.96	2.73
Days to 50% flowering	7							1.00 (1.00)	0.61 (0.83)	0.49 (0.71)	-0.53 (-0.72)	0.03 (0.06)	0.40 (0.47)	-0.12 (-0.59)	87.71	4.10
Days to 75% maturity	8								1.00 (1.00)	0.62 (0.71)	-0.42 (-0.59)	-0.08 (-0.18)	0.36 (0.58)	-0.10 (-0.14)	110.54	2.84
Plant height (cm)	9									1.00 (1.00)	-0.45 (-0.56)	0.99 (0.14)	0.50 (0.72)	-0.02 (0.01)	68.76	3.96
Oil content (%)	10										1.00 (1.00)	-0.24 (-0.36)	-0.45 (-0.59)	0.08 (0.09)	33.96	3.12
Protein content (%)	11											1.00 (1.00)	0.02 (-0.19)	-0.03 (-0.26)	21.56	2.32
Capitula harvest index	12												1.00 (1.00)	0.67 (0.51)	0.48	0.03
Harvest index	13													1.00 (1.00)	20.52	1.55

Significant values are underlined (P<0.05).

extracted from the data set and what magnitude of loading coefficient a variable should possess to be considered meaningful. Factors whose eigen values were greater than 1.0 were retained. Traits with loading in a factor greater than 0.6 in were deemed major (2).

Under non-stress conditions, the first four factors explained 97% of the total variation. Factor I was strongly associated with seed yield, biological yield, 1000-seed weight and plant capitula weight, whereas, days to 75% maturity, and oil content had negative signs (Table 3). It accounted for 40% of the total variation and was defined as *productivity* factor. This factor was regarded as the components of seed yield, and indicated that seed yield was related to biological yield, 1000-seed weight and plant capitula weight. Thus, these characters may be influenced by the same gene or genes. Factors II, III, and IV accounted for 26, 17 and 14% of the total variation, respectively. The loading variables in these factors were not associated with seed yield, thus, they are not important in safflower seed yield improvement programs.

Under stress conditions the first five factors, explained 96% of the total variation. Variable compositions of the five factors with loadings are given in Table 4. Factor I accounted for about 43% of variability. This factor was not associated with seed yield and can be described as *phenological characters* factor. This factor may screen suitable genotypes under stress conditions but cannot screen high-yielding genotypes. Factor II was defined as *productivity* factor, and accounted for 21% of the total variability. In this factor biological yield, plant capitula weight, number of seeds/capitulum, number of capitula/plant, capitula harvest index and harvest index had positive factor loadings, whereas, oil content had negative load. This factor indicated that seed yield was associated with biological yield, number of capitula/plant, capitula weight, number of seeds/capitulum, capitula harvest index and harvest index. These criteria are suitable for high-yield safflower genotype screening under stress conditions. Other factors (III, IV and V) explained 15, 10 and 7% of the total variation, respectively, and indicated no association with seed yield/plant. Thus, they are not important in safflower seed yield improvement programs.

CONCLUSIONS

The variation exhibited by the safflower genotypes for 13 quantitative characters indicates that selection for many of these characters may be effective. The association of plant characters with seed yield assumes a special importance as a basis for selecting high-yielding strains (7). Under two irrigation regimes, variables with significant coefficients in genetic correlation matrix had factor loadings larger than 0.6 in productivity factor, indicating that these variables have high percentage of contribution in productivity factor and selection based on these variables may be efficient under both conditions. Finally, selection based on biological yield, number of seeds/capitulum, plant capitula weight, capitula harvest index and harvest index may be desirable for high-yield genotype screening under stress conditions, whereas selection based on biological yield, 1000-seed weight and plant capitula weight may be more efficient for high-yielding genotype screening under non-stress conditions. Furthermore, biological yield and plant capitula weight may be suitable for screening of high-yielding genotypes under both irrigation regimes.

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Table 3. Factor loadings based on phenotypic and genetic (in parenthesis) correlation matrices under non-stress conditions.

Traits	Factors			
	1 (40%)*	2 (26%)	3 (17%)	4 (14%)
Seed yield (g/m^2)	0.92 (0.99)	0.24 (0.03)	0.18 (0.11)	-0.13 (-0.04)
Biological yield (g/m^2)	0.93 (0.88)	-0.09 (-0.40)	0.29 (0.25)	-0.07 (0.01)
No. capitula/plant	0.61 (0.27)	-0.28 (-0.67)	-0.07 (-0.31)	0.26 (0.43)
No. seeds/capitulum	0.00 (0.23)	-0.28 (-0.03)	0.65 (0.78)	-0.18 (-0.12)
1000-seed weight (g)	0.65 (0.88)	0.30 (0.32)	-0.44 (-0.22)	-0.18 (-0.15)
Plant capitula weight (g)	0.95 (0.96)	0.04 (-0.28)	0.19 (0.20)	-0.10 (-0.04)
Days to 50% flowering	0.23 (0.28)	0.12 (-0.03)	0.66 (0.47)	0.64 (0.85)
Days to 75% maturity	0.17 (-0.35)	0.15 (-0.22)	0.85 (0.87)	0.02 (0.29)
Plant height (cm)	0.17 (0.23)	0.77 (0.84)	0.24 (0.18)	0.33 (0.38)
Oil content (%)	-0.56 (-0.87)	0.16 (0.18)	0.27 (0.40)	-0.49 (-0.27)
Protein content (%)	-0.42 (-0.34)	-0.06 (0.08)	-0.07 (-0.20)	0.80 (0.94)
Capitula harvest index	-0.09 (-0.14)	0.86 (0.96)	0.10 (-0.22)	-0.16 (0.00)
Harvest index	-0.01 (-0.17)	0.85 (0.93)	-0.26 (-0.31)	-0.10 (-0.07)

Coefficients larger than 0.6 have been underlined.

* Proportion of total genetic variance.

Table 4. Factor pattern coefficients for four phenotypic and genetic (in parenthesis) factors under stress conditions.

Traits	Factors									
	1 (43%)*		2 (21%)		3 (15%)		4 (10%)		5 (7%)	
Seed yield (g/m^2)	0.91	(0.19)	0.15	(0.94)	0.37	(0.26)	0.04	(0.11)	0.02	(-0.07)
Biological yield (g/m^2)	0.96	(0.40)	0.25	(0.91)	0.01	(-0.07)	-0.01	(0.06)	0.03	(-0.06)
No. capitula/plant	0.75	(-0.19)	-0.16	(0.46)	-0.22	(-0.74)	0.38	(0.47)	0.04	(-0.17)
No. seed/capitula	0.40	(0.67)	0.64	(0.52)	0.29	(0.33)	-0.43	(-0.35)	0.14	(0.26)
1000-seed weight (g)	0.11	(0.05)	0.13	(0.03)	0.18	(-0.06)	0.89	(0.99)	0.00	(0.12)
Plant capitula weight (g)	0.97	(0.00)	0.01	(0.99)	0.16	(0.07)	-0.01	(0.03)	0.01	(-0.05)
Days to 50% flowering	-0.11	(0.99)	0.83	(-0.08)	-0.01	(-0.17)	0.06	(-0.02)	-0.06	(0.04)
Days to 75% maturity	0.20	(0.90)	0.83	(0.25)	-0.04	(-0.00)	-0.03	(-0.01)	-0.19	(-0.17)
Plant height (cm)	0.30	(0.71)	0.72	(0.25)	0.07	(0.12)	0.41	(0.57)	0.07	(0.04)
Oil content (%)	0.05	(-0.73)	-0.74	(-0.14)	-0.12	(-0.17)	-0.03	(-0.19)	-0.42	(-0.44)
Protein content (%)	0.06	(0.01)	-0.01	(-0.13)	-0.04	(-0.05)	0.00	(0.09)	0.95	(0.97)
Capitula harvest index	0.06	(0.58)	0.48	(0.43)	0.81	(0.64)	0.11	(0.18)	0.04	(-0.11)
Harvest index	0.17	(-0.35)	-0.19	(0.48)	0.94	(0.81)	0.09	(0.04)	-0.05	(-0.13)

Coefficients larger than 0.6 have been underlined.
* Proportion of total genetic variance.

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